

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 14, 2003, 01:09:48 ; Search time 647 Seconds
(without alignments)
9667.477 Million cell updates/sec

Title: US-09-765-271-55

Perfect score: 2389
Sequence: 1 TTCTTACGAGTTGGAGCTGT.....TAAGTAGGAAAAATAAAC 2389

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 200 summaries

Database : N.Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2389	100.0	AAV27351	Streptococcus pneu
2	2389	100.0	ABO84819	S. pneumoniae SP03
3	2389	100.0	AAA47604	Recombinant varian
4	2338	97.9	ABX06886	S. pneumoniae type
5	2338	97.9	AAV52227	Streptococcus pneu
6	2338	97.9	ABX56454	Streptococcus pneu
7	148	6.2	AAA65731	Streptococcus pneu
8	148	6.2	AAA65736	Streptococcus pneu

9	148	6.2	2647	24	ABK15103	DNA encoding Strep
10	53	2.2	504	21	AAA08556	S. pneumoniae 20 k
11	53	2.2	2163	20	AAV25394	Streptococcus pneu
12	53	2.2	2290	19	AAV27356	Streptococcus pneu
13	53	2.2	2290	19	ABQ84824	S. pneumoniae SP04
14	53	2.2	2359	24	AAV52376	Streptococcus pneu
15	53	2.2	2457	25	ABX06885	S. pneumoniae type
16	53	2.2	2478	21	AAA08585	S. pneumoniae 92 k
17	53	2.2	2481	21	AAA05417	Streptococcus pneu
18	53	2.2	2517	25	ABX06705	S. pneumoniae type
19	53	2.2	2531	21	AAA47602	Recombinant varian
20	53	2.2	2531	21	AAA47605	Recombinant varian
21	53	2.2	2639	21	AAA65737	Streptococcus pneu
22	53	2.2	2639	24	ABK15104	DNA encoding Strep
23	53	2.2	2162598	25	ABX56454	Streptococcus pneu
24	50	2.1	492	20	AAV25393	Streptococcus pneu
25	44	1.8	973	19	AAV52488	Streptococcus pneu
26	38	1.6	3171	21	AAA65739	Streptococcus pneu
27	30	1.3	40	19	AAV27492	Streptococcus pneu
28	30	1.3	40	21	AAA47601	Primer for amplify
29	30	1.3	40	24	ABQ84960	Streptococcus pneu
30	27	1.1	36	21	AAA47599	Primer for amplify
31	27	1.1	37	19	AAV27491	Streptococcus pneu
32	27	1.1	37	24	ABQ84959	Streptococcus pneu
33	26	1.1	35	21	AAA47600	Primer for amplify
34	25	1.0	33	21	AAA65762	Streptococcus pneu
35	25	1.0	33	24	ABK33684	S. pneumoniae BVH-
36	25	1.0	34	21	AAA65764	Streptococcus pneu
37	25	1.0	34	24	ABK33686	S. pneumoniae BVH-
38	25	1.0	35	24	ABK33719	S. pneumoniae BVH-
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40	24	1.0	1442	24	ABQ84882	Streptococcus pneu
41	24	1.0	1398	24	ABN65839	Streptococcus poly
42	24	1.0	1455	21	AAA65733	Streptococcus pneu
43	24	1.0	1455	21	AAA47603	Recombinant varian
44	24	1.0	1455	21	AAA05473	Streptococcus pneu
45	24	1.0	1455	21	AAZ91804	Streptococcus pneu
46	24	1.0	2528	21	AAA65738	Streptococcus pneu
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50	24	1.0	5048	21	AAA65735	Streptococcus pneu
51	24	1.0	5048	24	ABK15101	DNA encoding Strep
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56	21	0.9	29	24	ABK33683	S. pneumoniae BVH-
57	21	0.9	462586	25	ABQ84281	Chromosome 2 Asthm
58	20	0.8	501	24	AAI69344	C. albicans hyphal
59	20	0.8	1146	21	AAA05814	Group B Streptococ
60	20	0.8	2466	24	ABN65935	Streptococcus poly
61	20	0.8	2466	24	ABN70334	Streptococcus poly
62	20	0.8	2469	21	AAA65740	Streptococcus pneu
63	20	0.8	2469	21	AAA05811	Group B Streptococ
64	20	0.8	2469	22	AAV54820	Streptococcus agal
65	20	0.8	2472	21	AAA65741	Streptococcus pneu
66	20	0.8	2478	24	ABN65838	Streptococcus poly
67	20	0.8	2478	22	AAV50036	Streptococcus pyog
68	20	0.8	5158	24	AAI69348	C. albicans contig
69	20	0.8	5215	20	AAV91105	Group B Streptococ
70	19	0.8	164	25	ABX54820	Streptococcus agal
71	19	0.8	426	23	ABV02215	Human prostate exp
72	19	0.8	427	22	AAV30789	Human prostate exp
73	19	0.8	468	23	ABV11384	Human prostate exp
74	19	0.8	481	23	AAV13259	Human prostate exp
75	19	0.8	481	23	ABV41454	Human prostate exp
76	19	0.8	693	24	ABO89355	Human prostate exp
77	19	0.8	1203	23	ABV21401	Human prostate exp
78	19	0.8	1205	23	AAV27219	Human prostate exp
79	19	0.8	1455	21	AAA05838	Human prostate exp
80	19	0.8	1650	21	AAA70231	Plasmodium falciipa
81	19	0.8	7492	22	AAV90510	Mouse factor VIII

82	19	0.8	7493	19	AAV25812	Murine factor VIII
83	19	0.8	7493	19	AAV12115	Mus musculus facto
84	19	0.8	7493	20	AAK91164	Mouse factor VIII
85	19	0.8	143306	24	ABK49586	Human transporter
86	18	0.8	51	21	AAK77296	Human clone cg4399
87	18	0.8	324	25	ABK55599	Bovine EST associa
88	18	0.8	327	21	AAK05686	Human secreted pro
89	18	0.8	372	21	AAK05686	Lung cancer associ
90	18	0.8	372	24	ABV94637	Human pancreatic c
91	18	0.8	379	22	AAK64590	Human polynucleoti
92	18	0.8	423	21	AAK00113	Human secreted pro
93	18	0.8	448	21	AAK77174	Human ORFX ORF2729
94	18	0.8	495	24	ABN65206	Human cancer relat
95	18	0.8	499	21	AAK57418	Arachidonic acid m
96	18	0.8	499	21	AAK57938	A thaliana AMP dea
97	18	0.8	914	24	AAK45031	Salmonella typhi D
98	18	0.8	924	23	AAK56173	Drosophila melanog
99	18	0.8	1038	23	ABK12667	Arabidopsis thalia
100	18	0.8	1077	21	AAK44226	Arabidopsis thalia
101	18	0.8	1258	21	AAK88831	Arabidopsis thalia
102	18	0.8	1279	23	ABK43425	DNA encoding novel
103	18	0.8	1309	21	AAK55026	Arabidopsis thalia
104	18	0.8	1311	21	AAK32909	Arabidopsis thalia
105	18	0.8	1436	20	AAK79857	SAE1 coding sequen
106	18	0.8	1587	20	AAK13215	Enterococcus faeca
107	18	0.8	1587	24	ABK99010	HTRM clone 2284580
108	18	0.8	1635	21	AAK52469	Human polynucleoti
109	18	0.8	1737	22	AAK88285	Human cancer assoc
110	18	0.8	1750	21	AAK78009	Romaine lettuce ep
111	18	0.8	1780	21	AAK46328	Lettuce cDNA encod
112	18	0.8	1803	24	ABK91236	Arabidopsis thalia
113	18	0.8	1803	24	ABK13910	Fructan exohydrola
114	18	0.8	2074	22	AAK45511	A thaliana AMP dea
115	18	0.8	2520	24	AAK45016	SEN virus genome f
116	18	0.8	2646	21	AAK61122	Human polynucleoti
117	18	0.8	2840	22	AAK160818	A. thaliana AMP-de
118	18	0.8	2880	20	AAK22395	Human DNA for a no
119	18	0.8	2956	22	AAK31541	Human polynucleoti
120	18	0.8	2956	24	ABK66865	Human immune/haema
121	18	0.8	3058	22	AAK83876	Drosophila melanog
122	18	0.8	3063	23	ABK13444	Human cDNA #38 dif
123	18	0.8	3154	25	ABK63038	SEN virus genome f
124	18	0.8	3347	21	AAK61121	Drosophila melanog
125	18	0.8	3457	23	ABK06786	Drosophila melanog
126	18	0.8	4679	23	ABK12665	Human nervous syst
127	18	0.8	5962	22	ABK19263	Human cDNA encodin
128	18	0.8	6524	25	ABK70653	Human ATP binding
129	18	0.8	7323	21	AAK294746	Human cytoskeleton
130	18	0.8	7557	25	AAK49607	ATP binding cassat
131	18	0.8	7784	19	AAV33392	Drosophila melanog
132	18	0.8	7800	23	ABK24460	Drosophila melanog
133	18	0.8	10036	23	ABK10488	Genomic sequence #
134	18	0.8	12051	22	AAK41999	Human immune/haema
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136	18	0.8	18416	22	AAK41998	Human immune/haema
137	18	0.8	18416	22	AAK70235	Human immune/haema
138	18	0.8	21354	22	AAK46815	Tumour suppressor
139	18	0.8	22870	22	AAK41989	Genomic sequence #
140	18	0.8	22870	22	AAK42010	Genomic sequence #
141	18	0.8	22870	22	AAK80760	Human immune/haema
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143	18	0.8	61890	23	ABK16586	Drosophila melanog
144	18	0.8	66685	22	AAK07380	Human genomic DNA
145	18	0.8	66686	24	ABK73149	Human CLASP-5 geno
146	18	0.8	910715	20	AAK20248	Borrelia burgdorferi
147	18	0.8	1664976	19	AAV21209	Methanococcus jann
148	18	0.8	2944528	24	AAK03041	Listeria monocytoc
149	18	0.7	20	15	AAK68205	Human D2 dopamine
150	17	0.7	20	18	AAK68561	Human 3D6 VL-B o11
151	17	0.7	131	24	ABK59431	Human 3D6 VL-C o11
152	17	0.7	146	24	ABK59432	Human secreted exp
153	17	0.7	163	21	AAK42081	Polymorphic region
154	17	0.7	254	21	AAK45758	
155	17	0.7	261	22	AAK22115	Human breast cance
156	17	0.7	271	25	ABK24487	Human GBP-mannose
157	17	0.7	279	24	ABK76700	Human ORF1647 cDNA
158	17	0.7	316	22	AAK35075	Human colon cancer
159	17	0.7	321	14	AAK06738	Sequence 1 which e
160	17	0.7	322	19	AAK27398	Streptococcus pneu
161	17	0.7	322	24	ABK96743	Human pancreatic c
162	17	0.7	322	24	ABK96743	S. pneumoniae SP08
163	17	0.7	332	21	AAK28943	Human secreted pro
164	17	0.7	335	21	AAK00856	Human secreted pro
165	17	0.7	358	21	AAK69612	Human cervical can
166	17	0.7	359	21	AAK75614	Human ORFX ORF1169
167	17	0.7	369	22	ABK11743	Human nervous syst
168	17	0.7	371	25	ABK21536	Human GDP-mannose
169	17	0.7	375	24	ABK97848	Human ARP-2 cDNA f
170	17	0.7	377	21	AAK0890	Breast cancer DDPC
171	17	0.7	377	22	ABK12942	Human nervous syst
172	17	0.7	394	23	ABK13601	Human prostate exp
173	17	0.7	400	22	AAK73060	Human cervical can
174	17	0.7	400	22	AAK66057	Novel human polynu
175	17	0.7	402	24	ABK59446	Humanised 3D6 vers
176	17	0.7	402	24	ABK59447	Humanised 3D6 vers
177	17	0.7	411	25	ABK07845	S. pneumoniae type
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180	17	0.7	428	23	AAK70352	Human cervical can
181	17	0.7	431	25	ABK50263	Bovine EST associa
182	17	0.7	432	23	ABK4715	Human prostate exp
183	17	0.7	432	23	ABK43570	Human prostate exp
184	17	0.7	436	22	AAK62913	Human immune/haema
185	17	0.7	440	23	ABK04432	Human prostate exp
186	17	0.7	454	24	ABK89870	Human polynucleoti
187	17	0.7	457	23	ABK33304	Human prostate exp
188	17	0.7	457	23	ABK42237	Human prostate exp
189	17	0.7	458	22	AAK199524	Human polynucleoti
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191	17	0.7	467	24	ABK21637	Human ovarian canc
192	17	0.7	470	20	AAK219370	Human ORFX polynuc
193	17	0.7	470	20	AAK219158	M. tuberculosis an
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196	17	0.7	497	24	ABK72614	Human MDT encodin
197	17	0.7	504	22	AAK70055	Human cervical can
198	17	0.7	517	21	AAK52234	Arabidopsis thalia
199	17	0.7	522	21	AAK52500	Arabidopsis thalia
200	17	0.7	523	19	AAK14494	H. pylori GHPO 117

ALIGNMENTS

RESULT 1
ID AAV27351 standard; DNA; 2389 BP.

AAV27351:

02-OCT-1998 (first entry)

Streptococcus pneumoniae SP0036 nucleotide.

Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;

detection; pneumonia; Otitis media; meningitis; ss.

Streptococcus pneumoniae.

Key Location/Qualifiers

CDS 2..2389

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FT /product= "SP0036"

FT /transl_except= (pos:1367..1369,aa:Xaa)

FT /note= "no stop codon given; Xaa is unspecified"

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PD	07-MAY-1998.		
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Pf	30-OCT-1997;	97WO-US19422.	
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PR	31-OCT-1996;	96US-0029960.	
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PA	(HUMA-) HUMAN GENOME SCI INC.		
PI	Choi GH, Hromockyj A, Johnson LS, Kunsch CA;		
XX			
DR	WPI; 1998-272224/24.		
DR	P-PDB; AAU55090.		
PT	Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis		
PS	Claim 1; Page 59; 118pp; English.		
CC	The present sequence encodes a protein from Streptococcus pneumoniae.		
CC	The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridization or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.		
SQ	Sequence 2389 BP; 830 A; 461 C; 486 G; 611 T; 1 other:		
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	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 2389; Conservative	0; Mismatches	0; Indels
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Dd	121 GCGTAAAGAAATCATVGCATGACCAATCGTCATCAAGATPACAGACCAGGCTATGTCC		180
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Dd	181 TTCACATGGCGAACATCATATTATTAACAATGTAAGGTTCCCTTATGACGCTATCATCG		240
OY	241 TGANAATTTACTCAGAAAAGATCCCAAATTAAGCTAAAGATGAGATATGTTAATCA		300
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Db	1501	ACTTGGCAACCAAAATTCCTCAAAATTTGAGTATACGGAAGACGAAGTGTGATATTCCTCAAT	1560

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QY 1561 AGCTGATTAAGTATCAACGTCAGATGTTACATTTTGTGTAACATGATATATACAGTGA 1620
DB 1561 AGCTGATTAAGTATCAACGTCAGATGTTACATTTTGTGTAACATGATATATACAGTGA 1620
QY 1621 TGAAGGAGATGATATGTAAGCGCTCATATGGCCATATGTCATCTGATTTGAAAAAGATAG 1680
DB 1621 TGAAGGAGATGATATGTAAGCGCTCATATGGCCATATGTCATCTGATTTGAAAAAGATAG 1680
QY 1681 CCTTTCGATTAAGGAAAAAGTTGACGCTCAAGCCATATCTTAAAGAAAAAGGATCTCTAC 1740
DB 1681 CCTTTCGATTAAGGAAAAAGTTGACGCTCAAGCCATATCTTAAAGAAAAAGGATCTCTAC 1740
QY 1741 TCCATCTTCAGACGACAGATGTTAAAGCAATCCAATGAGATGTGACAGACGATATTTA 1800
DB 1741 TCCATCTTCAGACGACAGATGTTAAAGCAATCCAATGAGATGTGACAGACGATATTTA 1800
QY 1801 CAATCGTGTGAAGGGGAAAAAGCAATTCACCTGTTGACTTCCATATATGTTGAGCA 1860
DB 1801 CAATCGTGTGAAGGGGAAAAAGCAATTCACCTGTTGACTTCCATATATGTTGAGCA 1860
QY 1861 TACAGTTGAGGTTAAAAAGGTAATTTGATATTCCTCATAGGATGATTCATCAATATAT 1920
DB 1861 TACAGTTGAGGTTAAAAAGGTAATTTGATATTCCTCATAGGATGATTCATCAATATAT 1920
QY 1921 TAAATTTGCTTGTGTTGATGATCAACATACAAAGCTCAATGCTTACCTTGAGAGA 1980
DB 1921 TAAATTTGCTTGTGTTGATGATCAACATACAAAGCTCAATGCTTACCTTGAGAGA 1980
QY 1981 TTTGTTTGCAGCATTAAGTACTATGTAAGAACACCTTGACGAGACGTCATTTCTATGA 2040
DB 1981 TTTGTTTGCAGCATTAAGTACTATGTAAGAACACCTTGACGAGACGTCATTTCTATGA 2040
QY 2041 TGGATGGGGCAATGCGCAGTGAAGCATGTGTTAGGCAAGAACCAAGTGAAGATCCAAA 2100
DB 2041 TGGATGGGGCAATGCGCAGTGAAGCATGTGTTAGGCAAGAACCAAGTGAAGATCCAAA 2100
QY 2101 TAAAGACTTCAAGCGGATGAAGAGCCAGTAGAGAGAAACACCTGTGAGCCAGAAAGTCC 2160
DB 2101 TAAAGACTTCAAGCGGATGAAGAGCCAGTAGAGAGAAACACCTGTGAGCCAGAAAGTCC 2160
QY 2161 TCAAGTAGAGACTGAAAAAGTGAAGGCCCACTCAAGAGACAGAAAGTTTGTTCGCA 2220
DB 2161 TCAAGTAGAGACTGAAAAAGTGAAGGCCCACTCAAGAGACAGAAAGTTTGTTCGCA 2220
QY 2221 AGTAACGGATCTGATCTGAAGGCAATGCAACAGAACTCTAGCTGTTTACGAAATTA 2280
DB 2221 AGTAACGGATCTGATCTGAAGGCAATGCAACAGAACTCTAGCTGTTTACGAAATTA 2280
QY 2281 TTTGACTCTTCAAAATTATGATTAACAATAGTATCATGACAGAGAGAAAAATTACTTGC 2340
DB 2281 TTTGACTCTTCAAAATTATGATTAACAATAGTATCATGACAGAGAGAAAAATTACTTGC 2340
QY 2341 GTTGTAAAGGAAGTAATCTCTCATCTGTAAGTGAAGAAAAATAAAC 2389
DB 2341 GTTGTAAAGGAAGTAATCTCTCATCTGTAAGTGAAGAAAAATAAAC 2389

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RESULT 2

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AB084819 ID AB084819 standard; DNA; 2389 BP.
XX AC AB084819;
XX DT 04-SEP-2002 (first entry)
XX DE S. pneumoniae SP036 nucleotide sequence SEQ ID NO:55.
XX KM Streptococcus pneumoniae; epitope; vaccine; antigenic protein;
XX KW antibacterial; Streptococcal infection; detection; gene; ds.
OS Streptococcus pneumoniae.
XX PN US2002061545-A1.

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XX 23-MAY-2002.
PD 22-JAN-2001; 2001US-0765272.
XX 30-OCT-1997; 97US-0961083.
XX (CHOI/) CHOI G H.
PA (KUNS/) KUNSCH C A.
PA (BARA/) BARASH S C.
PA (DILL/) DILLON P J.
PA (DOUG/) DOUGHERTY B.
PA (FANN/) FANNON M R.
XX (ROSE/) ROSEN C A.
PI Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR;
PI Rosen CA;
DR WPI; 2002-479261/51.
DR P-PSDB; ABP54584.
XX New Streptococcus pneumoniae antigens, useful for detecting
FT Streptococcus and for preventing or attenuating disease caused by
PT Streptococcus infection -
PS Claim 1; Page 27; 70pp; English.
XX AB084792 to AB084904 represents nucleic acids which encode the
CC Streptococcus pneumoniae antigens given in ABP54557 to ABP54669.
CC The S. pneumoniae antigens have antibacterial activity and can be
CC used in vaccines. The S. pneumoniae antigens can also be used to
CC prevent or attenuate a Streptococcal infection in an animal. The
CC polynucleotides encoding the S. pneumoniae antigens can be used to
CC detect Streptococcus nucleic acids. AB084905 to AB085130 represent
CC primers used in the cloning of S. pneumoniae ORFs (open reading frames)
CC which are used in an example from the present invention.
XX SQ Sequence 2389 BP; 830 A; 461 C; 486 G; 611 T; 1 other;
Query Match 100.0%; Score 2389; DB 24; Length 2389;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTACGATGGGAGCTGTATCAAGCTAGAAACGTTAAGAAAAATATCGTGTCTTA 60
DB 1 TTTTACGATGGGAGCTGTATCAAGCTAGAAACGTTAAGAAAAATATCGTGTCTTA 60
QY 61 TATAGATGAAAAACAACGACGCGAAAAACGAGAAATTTGACTCTGATGAGTTAGCAA 120
DB 61 TATAGATGAAAAACAACGACGCGAAAAACGAGAAATTTGACTCTGATGAGTTAGCAA 120
QY 121 GCGTGAAGGAATCAATCTGAGCAAAATCGTCATCAATACATACAGACCAAGGCTTGTAC 180
DB 121 GCGTGAAGGAATCAATCTGAGCAAAATCGTCATCAATACATACAGACCAAGGCTTGTAC 180
QY 181 TTTGATGAGGACACCATATCATTTTCAATGATGTAAGGTTCTTATACGCTATCATCAG 240
DB 181 TTTGATGAGGACACCATATCATTTTCAATGATGTAAGGTTCTTATACGCTATCATCAG 240
QY 241 TGAAGAAATTACTCATGAAAGATCCAACTTAAGCTTAAAGATGAGATATTTGTAATGA 300
DB 241 TGAAGAAATTACTCATGAAAGATCCAACTTAAGCTTAAAGATGAGATATTTGTAATGA 300
QY 301 GGTCAAGGCTGATATGTTTCAAGGATGATGAAAAATCTATGTTTACCTTAAGATGC 360
DB 301 GGTCAAGGCTGATATGTTTCAAGGATGATGAAAAATCTATGTTTACCTTAAGATGC 360
QY 361 TGCCACGCGGATTAAGCTCGTACAAAGAGAAATCAATCGACAAACCAAGACATAG 420
DB 361 TGCCACGCGGATTAAGCTCGTACAAAGAGAAATCAATCGACAAACCAAGACATAG 420
QY 421 TCAACATCGTGAAGGTGAATCCCAAGAAAGATGTGCTGTGCTTGGCAGCTTGCGCA 480

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Db 421 TCACATCGTGAAGGTGAACCTCAAGAAACGATGCTGTGCTTGGACGCTTGGCA 480
 QY 481 AGAGCGCTACTACAGATGATGTTATCTTTATGCTTGATGATGATGAGGATAC 540
 Db 481 AGAGCGCTACTACAGATGATGTTATCTTTATGCTTGATGATGATGAGGATAC 540
 QY 541 TGGTATGCTTATATGCTTCTCATGAGATCATTAACCTTACCTTAAAGATGAT 600
 Db 541 TGGTATGCTTATATGCTTCTCATGAGATCATTAACCTTACCTTAAAGATGAT 600
 QY 601 ATCAGCTACGAGTGGCTGCTGCGAGAACCTTCTATGCTGCGAGAAATCTGCAAA 660
 Db 601 ATCAGCTACGAGTGGCTGCTGCGAGAACCTTCTATGCTGCGAGAAATCTGCAAA 660
 QY 661 TTCAGAACCTATCGCGCAAAATAGCATTAACCTTCAAGAACAACTGGGTACCTTC 720
 Db 661 TTCAGAACCTATCGCGCAAAATAGCATTAACCTTCAAGAACAACTGGGTACCTTC 720
 QY 721 TGTAAAGCAATCCAGAACTCAAAATCTAACAACAGCAACAGCACTAACAGTCA 780
 Db 721 TGTAAAGCAATCCAGAACTCAAAATCTAACAACAGCAACAGCACTAACAGTCA 780
 QY 781 AGCAAGTCAAAAGTATGATGATGATGCTTGTGAACAGCTCTCAAACTGCTTTGAG 840
 Db 781 AGCAAGTCAAAAGTATGATGATGATGCTTGTGAACAGCTCTCAAACTGCTTTGAG 840
 QY 841 TCAAGCACTGTAGATCTGATGCTTGTGCTTGTGATCCAGCAAAATCAAGTGCAG 900
 Db 841 TCAAGCACTGTAGATCTGATGCTTGTGCTTGTGATCCAGCAAAATCAAGTGCAG 900
 QY 901 AGCTAGAGTGTGTCAGTGCACACAGAGATCATTCACCTTACCTTACCTCAAT 960
 Db 901 AGCTAGAGTGTGTCAGTGCACACAGAGATCATTCACCTTACCTTACCTCAAT 960
 QY 961 GTCTGAATTTGAAGAAAGATGCTGCTGATTAATTCCTTGTGATGCTTCAACCAT 1020
 Db 961 GTCTGAATTTGAAGAAAGATGCTGCTGATTAATTCCTTGTGATGCTTCAACCAT 1020
 QY 1021 GGTACCAAGTTCAAGGCGCAAGCAACAGTCCACACAGCTCCGGAACCTAGTCCAG 1080
 Db 1021 GGTACCAAGTTCAAGGCGCAAGCAACAGTCCACACAGCTCCGGAACCTAGTCCAG 1080
 QY 1081 CCCGCAACCTGACCAAACTTTAAATGATCAATCTTCTTGTGATGCTGCTGCT 1140
 Db 1081 CCCGCAACCTGACCAAACTTTAAATGATCAATCTTCTTGTGATGCTGCTGCT 1140
 QY 1141 ACGAAAGTTGGGGAAGATGATGATTCGAAGAAAGGCGATCTCTGTTATGCTTTGC 1200
 Db 1141 ACGAAAGTTGGGGAAGATGATGATTCGAAGAAAGGCGATCTCTGTTATGCTTTGC 1200
 QY 1201 GAAAGATTTACATCTGAAACCTGTTAAATCTTGAAGACAGTATCAAAACAGAG 1260
 Db 1201 GAAAGATTTACATCTGAAACCTGTTAAATCTTGAAGACAGTATCAAAACAGAG 1260
 QY 1261 TGTTCACACACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 Db 1261 TGTTCACACACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 QY 1321 TGATAAGCATTAATCTGTTAACTGAGGCTCATAAAGCTTGTGTTAAATTAAGGCTG 1380
 Db 1321 TGATAAGCATTAATCTGTTAACTGAGGCTCATAAAGCTTGTGTTAAATTAAGGCTG 1380
 QY 1381 TAAATCTGATTTCCAAAGCTTGAACAAATTAATTAAGAACTGAAATGCACTAA 1440
 Db 1381 TAAATCTGATTTCCAAAGCTTGAACAAATTAATTAAGAACTGAAATGCACTAA 1440
 QY 1441 TAAAGAAATTTGATGATGATTTATGCTTCTGATGACCAATTAACCATCCAGAG 1500
 Db 1441 TAAAGAAATTTGATGATGATTTATGCTTCTGATGACCAATTAACCATCCAGAG 1500
 QY 1501 ACTTGGCAACCAATTTCTCAATGATGATGATGATGATGATGATGATGATGATGAT 1560
 Db 1501 ACTTGGCAACCAATTTCTCAATGATGATGATGATGATGATGATGATGATGATGAT 1560

QY 1561 AGCTGATAGATATACAAAGCTGATGATGATGATGATGATGATGATGATGATGAT 1620
 Db 1561 AGCTGATAGATATACAAAGCTGATGATGATGATGATGATGATGATGATGATGAT 1620
 QY 1621 TGAAGAGATGATATGTAACGCTCATATGAGGCTATGATGATGATGATGATGATGAT 1680
 Db 1621 TGAAGAGATGATATGTAACGCTCATATGAGGCTATGATGATGATGATGATGATGAT 1680
 QY 1681 CCTTTCTGATAGAGAAAGTTGCGAGCTCAAGCTTATCTAAGAAAGATGATCTTAC 1740
 Db 1681 CCTTTCTGATAGAGAAAGTTGCGAGCTCAAGCTTATCTAAGAAAGATGATCTTAC 1740
 QY 1741 TCCATCTCAGACGAGATGTTAAAGCAATCCAACTGAGATGATGATGATGATGAT 1800
 Db 1741 TCCATCTCAGACGAGATGTTAAAGCAATCCAACTGAGATGATGATGATGATGAT 1800
 QY 1801 CAATGCTGTAAGAGGAGAAAGCAATTCATCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
 Db 1801 CAATGCTGTAAGAGGAGAAAGCAATTCATCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
 QY 1861 TACAGTTGAGTTAAAGCGTAAATTTGATTAATCTCATAGATGATGATGATGAT 1920
 Db 1861 TACAGTTGAGTTAAAGCGTAAATTTGATTAATCTCATAGATGATGATGATGAT 1920
 QY 1921 TAAATTTGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
 Db 1921 TAAATTTGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
 QY 1981 TTTGTTTGCAGATTAAGTACTAGTGAACCACTTCAAGCAAGCTTCAATTAATGA 2040
 Db 1981 TTTGTTTGCAGATTAAGTACTAGTGAACCACTTCAAGCAAGCTTCAATTAATGA 2040
 QY 2041 TGGATGGGGCAATGCGAGTGAATGATGATGATGATGATGATGATGATGATGAT 2100
 Db 2041 TGGATGGGGCAATGCGAGTGAATGATGATGATGATGATGATGATGATGATGAT 2100
 QY 2101 TAAAGATTTCAAGGAGTGAAGAGCAGTGAAGAAACACTGCTGAGCCGAAAGTCCC 2160
 Db 2101 TAAAGATTTCAAGGAGTGAAGAGCAGTGAAGAAACACTGCTGAGCCGAAAGTCCC 2160
 QY 2161 TCAAGTGAAGTGAAGAAAGTGAAGAGCCCACTCAAGAGAGAGAGAGAGAGAGAG 2220
 Db 2161 TCAAGTGAAGTGAAGAAAGTGAAGAGCCCACTCAAGAGAGAGAGAGAGAGAGAG 2220
 QY 2221 AGTAACGATTTCTAGTCTGAAGAGCAATGCAACAGAACTCTAGCTGCTGCTGCT 2280
 Db 2221 AGTAACGATTTCTAGTCTGAAGAGCAATGCAACAGAACTCTAGCTGCTGCTGCT 2280
 QY 2281 TTTGACTCTTCAAAATTATGATGATGATGATGATGATGATGATGATGATGAT 2340
 Db 2281 TTTGACTCTTCAAAATTATGATGATGATGATGATGATGATGATGATGATGAT 2340
 QY 2341 GTTGTAAAGAGATTAATCTTCACTGTAAGTGAAGAGAGAGAGAGAGAGAGAG 2399
 Db 2341 GTTGTAAAGAGATTAATCTTCACTGTAAGTGAAGAGAGAGAGAGAGAGAGAG 2399

RESULT 3
 AAA47604
 ID AAA47604 standard; DNA; 2451 bp.
 XX
 AC AAA47604;
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE Recombinant variant of Sp36 gene (Sp36A) of *S. pneumoniae*.
 XX
 KW Streptococcus pneumoniae; infection; vaccine; coiled coil region;
 KW histidine triad residue; Sp36; antibody; otitis media;
 KW nasopharyngeal infection; bronchial infection; bronchitis; sepsis;
 KW meningitis; lobar pneumonia; ds.
 XX

OS	Streptococcus pneumoniae.
XX	
XX	
FH	Key Location/Qualifiers
FT	CDS 1..2451
FT	/tag= a
FT	/product= Sp36a polypeptide
XX	
XX	
PM	MO200037105-A2.
PD	29-JUN-2000.
XX	
PF	21-DEC-1999; 99WO-US30390.
XX	
PR	21-DEC-1998; 98US-0113048.
XX	
PA	(MEDI-) MEDIMUNE INC.
XX	
PI	Johnson LS, Koenig S, Adamou JE;
XX	
DR	WPI: 2000-452129/39.
XX	P-PBDB; AAB01468.
PT	Vaccine useful for prophylaxis and treatment of pneumococcal infections such as otitis media, nasopharyngeal and bronchial infections,
PT	comprises Streptococcus pneumoniae proteins
XX	
PS	Disclosure; Page 64-65; 70pp; English.
XX	
CC	Although a number of proteins have been suggested as being involved in the pathogenicity of Streptococcus pneumoniae, there still remains a need to identify polypeptides having epitopes in common from various strains of S. pneumoniae in order to utilize such polypeptides in vaccines to protect against a wide variety of S. pneumoniae. New vaccine compositions are described which comprise a Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino acids in length that comprise at least one histidine triad residue (HxxHxM) or a coiled-coil region, or an antibody directed against these features. The vaccine is useful in protecting against infection by Streptococcus pneumoniae. The vaccine composition comprising antibodies to it is useful for passive immunization for treating pneumococcal infections which includes otitis media, nasopharyngeal and bronchial infections.
CC	
CC	
CC	
SQ	Sequence 2451 BP; 849 A; 467 C; 499 G; 635 T; 1 other:
	Query Match . 100.0%; Score 2389; DB 21; Length 2451;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 TTCTTACAGATTGGGACTGTATCAAGCTAGAACGGTTAAGAAATAATCGTGTTCCCTA 60
Db	60 TTCCTTAGCAGTTGGGACTGTATCAAGCTAGAACGGTTAAGAAATAATCGTGTTCCCTA 119
OY	61 TATAGATGAAAAACAAGCGAACGCAAAAAACGGAATTTGACTCCTGATAGGTTAGCAA 120
Db	120 TATAGATGAAAAACAAGCGAACGCAAAAAACGGAATTTGACTCCTGATAGGTTAGCAA 179
OY	121 GCGTGAAGGAATCATGCTGAGCAAAATGCTCATCAAGATATACAGACCAAGGTAATGCAC 180
Db	180 GCGTGAAGGAATCAATGCTGAGCAAAATGCTCATCAAGATATACAGACCAAGGTAATGCAC 239
OY	181 TTCAATGGCGACCACTATCATATTATTAACATGTAAGGTTCTTATGACGCTATCATCAG 240
Db	240 TTCAATGGCGACCACTATCATATTATTAACATGTAAGGTTCTTATGACGCTATCATCAG 299
OY	241 TGAGAAATTACTCATGAAGAAGTCAAACTATAAGCTAAAAGATGAGATATTGTTAATGA 300
Db	300 TGAAGAAATTACTCATGAAGAAGTCAAACTATAAGCTAAAAGATGAGATATTGTTAATGA 359
OY	301 GGTCAGGGTGGATATGTTATCAAGGTGATGGAATAATCTATGTTACCTTAAGATGC 360
Db	360 GGTCAGGGTGGATATGTTATCAAGGTGATGGAATAATCTATGTTACCTTAAGATGC 419

QY	361	GGCCACGGGATACGTCGGCTACAAAAGGAAATCAATGACAAAAACAAGGCATAG	420
Db	420	TGCCACGGGGATACGTCGGTACAAAAGGAAATCAATGACAAAAACAAGGCATAG	479
QY	421	TCAACATCGTAAAGGTGGAACTCCAAAGAAACGATGAGTGTCTTGGCAGCGTTCGA	480
Db	480	TCAACATCGTAAAGGTGGAACTCCAAAGAAACGATGAGTGTCTTGGCAGCGTTCGA	539
QY	481	AGAACGCTATACACAGATGATGCTTATCTTTAATGCTTCGATATCATAGAGATAC	540
Db	540	AGAACGCTATCTACAGATGATGCTTATCTTTAATGCTTCGATATCATAGAGATAC	599
QY	541	TGGGATGCTTATATTCGTCCTCATGAGAGATCATTCACATTAACATCCTAAGATGAGTT	600
Db	600	TGGGATGCTTATATTCGTCCTCATGAGAGATCATTCACATTAACATCCTAAGATGAGTT	659
QY	601	ATCAGCTAGCAGATGGCTGCTGAGAAAGCCTTCCTATCTGGTGGAGAAATCTGTCAA	660
Db	660	ATCAGCTAGCAGATGGCTGCTGAGAAAGCCTTCCTATCTGGTGGAGAAATCTGTCAA	719
QY	661	TTCAAGAACTTATCGCCGACAAATPAGCATTAACATTCAGAAACAACTGGGTACCTTC	720
Db	720	TTCAAGAACTTATCGCCGACAAATPAGCATTAACATTCAGAAACAACTGGGTACCTTC	779
QY	721	TGTAAAGCAATCCAGAAACTACAAATCTAACACAGCAACAAACAGCAACATAACAGTCA	780
Db	780	TGTAAAGCAATCCAGAAACTACAAATCTAACACAGCAACAAACAGCAACATAACAGTCA	839
QY	781	AGCAAGTCAAAAGTATGATTCATTCATTCAGTCTTTAACAAGCTCTACAAACCTGCTTGAG	840
Db	840	AGCAAGTCAAAAGTATGATTCATTCATTCAGTCTTTAACAAGCTCTACAAACCTGCTTGAG	899
QY	841	TCAAAGCATGTAGAAATCTGATGSCCTTTGCTTTGATCCAGACAAATCACAAGTCGAAC	900
Db	900	TCAAAGCATGTAGAAATCTGATGSCCTTTGCTTTGATCCAGACAAATCACAAGTCGAAC	959
QY	901	AGCTAGAGAGTGTTCAGATGCGCCACACAGAGATCATTAACACTTCATCCCTTACTCTCAAT	960
Db	960	AGCTAGAGAGTGTTCAGATGCGCCACACAGAGATCATTAACACTTCATCCCTTACTCTCAAT	1019
QY	961	GTCGAAATTTGAAGAACGAATCGCTCGATATATCCCTTGCTTATCGTTCAAAACATTG	1020
Db	1020	GTCGAAATTTGAAGAACGAATCGCTCGATATATCCCTTGCTTATCGTTCAAAACATTG	1079
QY	1021	GGTACACAGATTCAAAGCCAGAACAAACCAAGTCCAAACCGAATCCGGAACCTAGTCCAGG	1080
Db	1080	GGTACACAGATTCAAAGCCAGAACAAACCAAGTCCAAACCGAATCCGGAACCTAGTCCAGG	1139
QY	1081	CCCGCAACCTTGACCCAAATCTTAAATATGACTCAATCTTCTTTGGTATGCTCAGCTGCT	1140
Db	1140	CCCGCAACCTTGACCCAAATCTTAAATATGACTCAATCTTCTTTGGTATGCTCAGCTGCT	1199
QY	1141	ACGAAAGTGGGGGAAGGATATGATTCGAAAGAAAGGAGCATCTCTGTTATGCTTTGCTTC	1200
Db	1200	ACGAAAGTGGGGGAAGGATATGATTCGAAAGAAAGGAGCATCTCTGTTATGCTTTGCTTC	1259
QY	1201	GAAAGATTTACATCTGAACCTGTTAAAAATCTTGAAGCAAGTATCAAAAACAAGAGAG	1260
Db	1260	GAAAGATTTACATCTGAACCTGTTAAAAATCTTGAAGCAAGTATCAAAAACAAGAGAG	1319
QY	1261	TGTTTACACACTTAACTGCTTAAAAAAGAAATGTTGCTCTCTGTGACCAAGATTTTA	1320
Db	1320	TGTTTACACACTTAACTGCTTAAAAAAGAAATGTTGCTCTCTGTGACCAAGATTTTA	1379
QY	1321	TGATTAAGCATATATCTGTTAACTGAGGCTCATTAAGCCTTGTTTGAATTAAGGGTCG	1380
Db	1380	TGATTAAGCATATATCTGTTAACTGAGGCTCATTAAGCCTTGTTTGAATTAAGGGTCG	1439
QY	1381	TAAATTCGATTTCCAAAGCCTTAGACAAATTTATGAAGCCTTGATATGATATGACACTTA	1440
Db	1440	TAAATTCGATTTCCAAAGCCTTAGACAAATTTATGAAGCCTTGATATGATATGACACTTA	1499
QY	1441	TAAAGAAAATTTGGTAGATGATTTATTGGCATTCCTGACACCAATTAACCATCCAGAGCG	15000

Db 1500 TAAAGAAAAATGGATGATGATTTATTTGGCATTCTAGAGCAACCAATTCACAGAGG 1559
 QY 1501 ACTTGCAAAACCAATTTCTCAATGAGATATCTGAAGCAAGTTGGTATGCTCAAT 1560
 Db 1560 ACTTGCAAAACCAATTTCTCAATGAGATATCTGAAGCAAGTTGGTATGCTCAAT 1619
 QY 1561 AGCTGATAGATATACACCTGAGATGTTTACATTTTGTGAATGATATATATGATGA 1620
 Db 1620 AGCTGATAGATATACACCTGAGATGTTTACATTTTGTGAATGATATATATGATGA 1679
 QY 1621 TGAAGAGATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 Db 1680 TGAAGAGATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1739
 QY 1681 CTTTCTGATAGAAAAAGTTGAGCTCAACCTATATTAAGAAAAAGATGCTTACC 1740
 Db 1740 CTTTCTGATAGAAAAAGTTGAGCTCAACCTATATTAAGAAAAAGATGCTTACC 1799
 QY 1741 TCCATCTCCAGACGAGATGTTAAAGCAAACTGAGAGATGATGAGAGCTATTTA 1800
 Db 1800 TCCATCTCCAGACGAGATGTTAAAGCAAACTGAGAGATGATGAGAGCTATTTA 1859
 QY 1801 CAATGCTGAAAGGGGAAAAAGCAATTCCTCTGCTGATTCATATATGTTGAGCA 1860
 Db 1860 CAATGCTGAAAGGGGAAAAAGCAATTCCTCTGCTGATTCATATATGTTGAGCA 1919
 QY 1861 TACAGTGAAGTTAAACCGTAAATTTGATTTCTCTATAGATCATATACATATAT 1920
 Db 1920 TACAGTGAAGTTAAACCGTAAATTTGATTTCTCTATAGATCATATACATATAT 1979
 QY 1921 TAAATTTGCTGTTGATGATCACAACATCAAAAGTCCCAATGGTATATCTGAGAGA 1980
 Db 1980 TAAATTTGCTGTTGATGATCACAACATCAAAAGTCCCAATGGTATATCTGAGAGA 2039
 QY 1981 TTTGTTGCGAGATTAAGTACTAGTAGACACCTGCGAAGCTGCAATTTCTATATGA 2040
 Db 2040 TTTGTTGCGAGATTAAGTACTAGTAGACACCTGCGAAGCTGCAATTTCTATATGA 2099
 QY 2041 TGGATGGGCGCATGCGACGATGATGTTAGGCAAGAAAGCCACAGTGAAGATCCAA 2100
 Db 2100 TGGATGGGCGCATGCGACGATGATGTTAGGCAAGAAAGCCACAGTGAAGATCCAA 2159
 QY 2101 TAAAGACTTCAAGCGGATGAAGAGCAGTAGAGGAAACCTGCTGAGCCAGAGTCCC 2160
 Db 2160 TAAAGACTTCAAGCGGATGAAGAGCAGTAGAGGAAACCTGCTGAGCCAGAGTCCC 2219
 QY 2161 TCAAGTAGAGCTGAAAAAGTGAAGCCCACTCAAGAGAGAGAGTTTCTTGCAGAA 2220
 Db 2220 TCAAGTAGAGCTGAAAAAGTGAAGCCCACTCAAGAGAGAGAGTTTCTTGCAGAA 2279
 QY 2221 AGTAAAGGATTTAGTCTGAAAGCCATGCAACAGAACTCTAGCTGGTTTACGAATTA 2280
 Db 2280 AGTAAAGGATTTAGTCTGAAAGCCATGCAACAGAACTCTAGCTGGTTTACGAATTA 2339
 QY 2281 TTTGACTCTTCAATATATGATATACATATGATATGATATGATATGATATGATAT 2340
 Db 2340 TTTGACTCTTCAATATATGATATACATATGATATGATATGATATGATATGATAT 2399
 QY 2341 GTTGTAAAGAGATTAATCTTCACTGTATAGTAAAGAAAAATTAAC 2389
 Db 2400 GTTGTAAAGAGATTAATCTTCACTGTATAGTAAAGAAAAATTAAC 2448

RESULT 4
 ID ABX06886 standard; DNA; 2406 BP.
 AC ABX06886;
 XX
 DT 11-FEB-2003 (first entry)
 XX
 DE S. pneumoniae type 4 strain coding region #1174.

XX Gene; ds; bacterial meningitis; pneumonia; sepsis; otitis media;
 KM ear infection; anti-inflammatory; antibacterial; immunostimulant;
 KM auditory; respiratory; gene therapy; vaccine.
 OS Streptococcus pneumoniae type 4 strain.
 PN WO200277021-A2.
 XX 03-OCT-2002.
 PD 27-MAR-2002; 2002WO-IB02163.
 XX 27-MAR-2001; 2001GB-0007658.
 PR (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Masignani V, Tettelin H, Fraser C;
 DR WPI: 2003-040579/03.
 DR P-PSDB: AB01598.
 XX
 PT New proteins and nucleic acid molecules from Streptococcus pneumoniae,
 PT useful as medicaments for treating or preventing a disease or infection
 PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
 PT or ear infection
 XX
 PS Claim 6; SEQ ID NO 2347; 56bp; English.
 XX
 CC The invention relates to a protein comprising of having at least 50%
 CC identity to any of the 2469 amino acid sequences, identified in the
 CC specification (available on a computer readable format), or its fragment,
 CC expressed from 2469 or 2489 identified DNA coding regions from the
 CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
 CC AB556454. Also included are an antibody which binds one of the
 CC proteins, treating a patient by administering the protein, DNA or
 CC antibody (in a composition), a kit comprising first and second primers,
 CC which are the nucleic acid, cited above or fragments between nucleotides
 CC 8-100 of a sequence not defined in the specification, for amplifying a
 CC target sequence contained within a Streptococcus nucleic acid sequence,
 CC where the first primer is substantially complementary to the target
 CC sequence and the second primer is substantially complementary to the
 CC complement of the target sequence, and where the parts of the primers
 CC having substantial complementarity define the termini of the target
 CC sequence to be amplified, assay comprising contacting a test compound
 CC with the protein, and determining whether the test compound binds to the
 CC protein and a Streptococcus pneumoniae bacterium, where one or more
 CC genes encoding the proteins has been rendered inactive. The proteins,
 CC nucleic acid molecules, antibody and compositions are useful as
 CC medicaments for treating or preventing a disease or infection due to
 CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia,
 CC sepsis, otitis media or ear infection. They are also useful in developing
 CC vaccines, diagnostics and antibiotics. The methods are useful for
 CC identifying immunodominant proteins. The present sequence is one of
 CC the 2469 identified coding region from the genomic sequence.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 2406 BP; 834 A; 461 C; 490 G; 621 T; 0 other;

Query Match 97.9%; Score 2338; DB 25; Length 2406;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTCTTACAGATTTGGAGCTGTATCAAGCTTGAAGCGTTAAGAAAAATATCGTTTCTTA 60
 Db 18 TTCTTACAGATTTGGAGCTGTATCAAGCTTGAAGCGTTAAGAAAAATATCGTTTCTTA 77
 QY 61 TATAGATGAAAAACAAGGAGCGCAAAAAAGAGATTTGACTCTGATGAGGTTAGCAA 120

D 78 TATAGATGAAAAACAAGCGACGCAAAAAACGAGATTGACTCCTGATGAGTTAGCA 137
Q 121 GCGTGAAGGATTCATATGCTGAGCAAAATGTCATCAAGATTAACAGACCAAGGCTATGTCAC 180
D 138 GCGTGAAGGATTCATATGCTGAGCAAAATGTCATCAAGATTAACAGACCAAGGCTATGTCAC 197
Q 181 TTCAATGAGGACCACTATCATTTATTTACAAATGTAAGGTCCTTATGACGCTATCATCAG 240
D 198 TTCAATGAGGACCACTATCATTTATTTACAAATGTAAGGTCCTTATGACGCTATCATCAG 257
Q 241 TGAAGATTAATCTCATGAAAGATCCAACTATTAAGTAAAGATGAGATTTGTTAATGA 300
D 258 TGAAGATTAATCTCATGAAAGATCCAACTATTAAGTAAAGATGAGATTTGTTAATGA 317
Q 301 GGTCAAGGAGGATATGTTATCAAGGTAGTGAATAATCTATGTTTACCTTAAGGATGC 360
D 318 GGTCAAGGAGGATATGTTATCAAGGTAGTGAATAATCTATGTTTACCTTAAGGATGC 377
Q 361 TGCCCAAGCGGATTAACGTCGTCACAAAGAGGAAATCAATCGACAAACAAAGACATAG 420
D 378 TGCCCAAGCGGATTAACGTCGTCACAAAGAGGAAATCAATCGACAAACAAAGACATAG 437
Q 421 TCACATGTTGAAGTGAATCTCCAGAAAGATGTCGTCGTCCTTGCCTTGCACGTTGCA 480
D 438 TCACATGTTGAAGTGAATCTCCAGAAAGATGTCGTCGTCCTTGCCTTGCACGTTGCA 497
Q 481 AGGACGCTATCTACAGATGATGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540
D 498 AGGACGCTATCTACAGATGATGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 557
Q 541 TGTGATGCTTATATCGTTCTCTCATGAGATCATATTCATTATTAATCTTAAGAAATGAGTT 600
D 558 TGTGATGCTTATATCGTTCTCTCATGAGATCATATTCATTATTAATCTTAAGAAATGAGTT 617
Q 601 ATCAAGTACGAGATTTGCTGCTGACAAAGCCTTCTATCTGTCGAGGAAATCTGTCAA 660
D 618 ATCAAGTACGAGATTTGCTGCTGACAAAGCCTTCTATCTGTCGAGGAAATCTGTCAA 677
Q 661 TTCAAGAACTATGCGCGACAAATAGGATTAACCTTCAGAAACAACTGGGATACCTTC 720
D 678 TTCAAGAACTATGCGCGACAAATAGGATTAACCTTCAGAAACAACTGGGATACCTTC 737
Q 721 TGTAAAGCAATCCAGAACTAATAATCTAACAACAAGCAACAAAGCACTTAACAGTCA 780
D 738 TGTAAAGCAATCCAGAACTAATAATCTAACAACAAGCAACAAAGCACTTAACAGTCA 797
Q 781 AGCAAGTCAAAAGTATGATCATTTGATGTCCTTGAACAGCTCTTCAAACTGCTTTGAG 840
D 798 AGCAAGTCAAAAGTATGATCATTTGATGTCCTTGAACAGCTCTTCAAACTGCTTTGAG 857
Q 841 TCAACGATATGATGATGTCCTGTCCTTGAATCCAGCAAAATCAAGTCGAGAC 900
D 858 TCAACGATATGATGATGTCCTGTCCTTGAATCCAGCAAAATCAAGTCGAGAC 917
Q 901 AGCTAAGAGTGTGAGTGCACACAGAGATCATTAACACTTCACTTCTACTCAAT 960
D 918 AGCTAAGAGTGTGAGTGCACACAGAGATCATTAACACTTCACTTCTACTCAAT 977
Q 961 GTCTGAATTTGAAGAAAGATGCTGTTATATTCCTTCTGTTATGCTTCAAACTATG 1020
D 978 GTCTGAATTTGAAGAAAGATGCTGTTATATTCCTTCTGTTATGCTTCAAACTATG 1037
Q 1021 GGTACCGATTCAGAGCCAGAAACAAAGTCACCAACCGACTCCGAAACCTAGTCCAGG 1080
D 1038 GGTACCGATTCAGAGCCAGAAACAAAGTCACCAACCGACTCCGAAACCTAGTCCAGG 1097
Q 1081 CCCGCAACTGTCACCAAAATCTTTAAATAGACTCAAAATCTTCTTGTGTTAGTCACTGCT 1140
D 1098 CCCGCAACTGTCACCAAAATCTTTAAATAGACTCAAAATCTTCTTGTGTTAGTCACTGCT 1157
Q 1141 ACGAAAGTGTGGGAGAGATATGTTTGAAGAAAGGCACTTCTGTTATGCTTCTTGC 1200
D 1158 ACGAAAGTGTGGGAGAGATATGTTTGAAGAAAGGCACTTCTGTTATGCTTCTTGC 1217

Q 1201 GAAAGATTTACATCTGAAAATCTTTAAATAATCTTGAAGCAAGTTATCAAAACAAGAGAG 1260
D 1218 GAAAGATTTACATCTGAAAATCTTTAAATAATCTTGAAGCAAGTTATCAAAACAAGAGAG 1277
Q 1261 TGTTCACACACTTTAACTGCTAAAAAAGAAATGTTGCTCTCTGACCAAGAAATTTTA 1320
D 1278 TGTTCACACACTTTAACTGCTAAAAAAGAAATGTTGCTCTCTGACCAAGAAATTTTA 1337
Q 1321 TGAATTAAGCATATATCTGTTAACTGAGGCTCATTAAGCCTTGTGTTGAAATAAGGCTGC 1380
D 1338 TGAATTAAGCATATATCTGTTAACTGAGGCTCATTAAGCCTTGTGTTGAAATAAGGCTGC 1397
Q 1381 TAAATTCGATTTCCAAAGCCTTAGACAATTAATTAAGACGCTTAATGATGAATGACATTA 1440
D 1398 TAAATTCGATTTCCAAAGCCTTAGACAATTAATTAAGACGCTTAATGATGAATGACATTA 1457
Q 1441 TAAAGAAAAATGGTAGATGATTTATTTGGCATTTCTAGACCAATTAACCATCCAGAGCG 1500
D 1458 TAAAGAAAAATGGTAGATGATTTATTTGGCATTTCTAGACCAATTAACCATCCAGAGCG 1517
Q 1501 ACTTGGCAACCAAAATTTCTCAAAATGAGTATCTGAAGACGAAGTTGTTGTTGCTCAAT 1560
D 1518 ACTTGGCAACCAAAATTTCTCAAAATGAGTATCTGAAGACGAAGTTGTTGTTGCTCAAT 1577
Q 1561 AGCTGATAGATATCAACGTCAGATGTTACATTTTGTATGAACATGATATTAACAGTGA 1620
D 1578 AGCTGATAGATATCAACGTCAGATGTTACATTTTGTATGAACATGATATTAACAGTGA 1637
Q 1621 TGAAGAGATGATATATGTAACGCTCATATGAGGCAATGTCATGATTTGAAAAAGATAG 1680
D 1638 TGAAGAGATGATATATGTAACGCTCATATGAGGCAATGTCATGATTTGAAAAAGATAG 1697
Q 1681 CCTTTCTGATTAAGAAAAAGTTGAGCTCAAGCTTATCTTAAGAAAAAGATATCTTAAC 1740
D 1698 CCTTTCTGATTAAGAAAAAGTTGAGCTCAAGCTTATCTTAAGAAAAAGATATCTTAAC 1757
Q 1741 TCCATCTCCAGACGACAGATGTTAAAGCAATCCAACTGAGATGTCAGAGCTATTTTA 1800
D 1758 TCCATCTCCAGACGACAGATGTTAAAGCAATCCAACTGAGATGTCAGAGCTATTTTA 1817
Q 1801 CAATCGTGTGAAGGGGAAAAAGCAATTCACCTGTTGCACTTTCATATATGTTGAGCA 1860
D 1818 CAATCGTGTGAAGGGGAAAAAGCAATTCACCTGTTGCACTTTCATATATGTTGAGCA 1877
Q 1861 TACAGTTGAGGTTAAAAAGGTAATTTGATTTTCTTCATTAAGATATTAATTAATTAAT 1920
D 1878 TACAGTTGAGGTTAAAAAGGTAATTTGATTTTCTTCATTAAGATATTAATTAATTAAT 1937
Q 1921 TAAATTTGCTGTTGTTGATGATCAACATTAACAAAGCTCCAAATGCTATACCTTGAAGA 1980
D 1938 TAAATTTGCTGTTGTTGATGATCAACATTAACAAAGCTCCAAATGCTATACCTTGAAGA 1997
Q 1981 TTTGTTTGCAGCATTAAGTACTAGTAGAACACCTTGAAGAGCTGCACATTTCTAATGA 2040
D 1998 TTTGTTTGCAGCATTAAGTACTAGTAGAACACCTTGAAGAGCTGCACATTTCTAATGA 2057
Q 2041 TGTGTTGGGCAATGCCAGTGAATGTTGTTAGGCAAAAAAGACCAAGTGAAGTCCAAA 2100
D 2058 TGTGTTGGGCAATGCCAGTGAATGTTGTTAGGCAAAAAAGACCAAGTGAAGTCCAAA 2117
Q 2101 TAAAGACTTCAAAAGCGATGTAAGAGCAGTAGAGAAACCTGCTGAGCAGAAAGTCCC 2160
D 2118 TAAAGACTTCAAAAGCGATGTAAGAGCAGTAGAGAAACCTGCTGAGCAGAAAGTCCC 2177
Q 2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAAGACGAAGATTTTGTCTTGCAA 2220
D 2178 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAAGACGAAGATTTTGTCTTGCAA 2237
Q 2221 AGTAACGATTTCTAGTGTGAAGCAATGCAACGAAATCTTAGCTGTTTACGAATTA 2280
D 2238 AGTAACGATTTCTAGTGTGAAGCAATGCAACGAAATCTTAGCTGTTTACGAATTA 2297

QY 2281 TTGACTCTTCAATTTATGATACATATGATCATGCGAGACGAGAAAATTAATTCTTGC 2340
 Db 2298 TTTGACTCTTCAATTTATGATACATATGATCATGCGAGACGAGAAAATTAATTCTTGC 2357
 QY 2341 GTTGTAAAGAGAGATATCTTCTCATCTGTAGTAGGAAAAATTAAC 2389
 Db 2358 GTTGTAAAGAGAGATATCTTCTCATCTGTAGTAGGAAAAATTAAC 2406

RESULT 5

AAV52227
 ID AAV52227 standard; DNA; 8195 BP.

AAV52227;
 AC 23-OCT-1998 (first entry)

XX Streptococcus pneumoniae genome fragment SEQ ID NO:94.
 DE Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
 KM Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
 XX computer readable medium; vaccine; pharmaceutical composition; ds.

OS Streptococcus pneumoniae.
 XX WO9818931-A2.

PN 07-MAY-1998.
 XX 30-OCT-1997; 97MO-US19588.

PR 31-OCT-1996; 96US-0029960.
 XX (HUMA-) HUMAN GENOME SCI INC.

PA Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M;
 PI Kunsch CA, Rosen CA;
 XX WPI; 1998-272225/24.

PT Computer-readable medium with recorded Streptococcus pneumoniae
 PT polynucleotide sequences - useful in diagnostic kits and assays, and
 PT pharmaceutical compositions and vaccines for Streptococcus
 PT pneumoniae

PS Claim 1; Page 727-732; 1409pp; English.

XX The present invention describes a computer readable medium which has
 CC the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)
 CC recorded on it, or a representative fragment or a sequence at least 95%
 CC identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in
 CC SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
 CC Streptococcus pneumoniae. The present invention also describes an
 CC isolated nucleic acid molecule encoding a homologue of any of the
 CC fragments of the S. pneumoniae genome (SEQ ID NO:1 to 391) where the
 CC nucleic acid molecule is produced by a process comprising: (a) screening
 CC a genomic DNA library using as a probe a target sequence defined by any
 CC of the sequences in SEQ ID NO:1 to 391, identifying members of the
 CC library which contain sequences that hybridize to the target sequence and
 CC isolating the nucleic acid molecules from the members; or (b) isolating
 CC mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid
 CC molecules whose nucleotide sequence is homologous to amplification
 CC primers derived from the fragment of the S. pneumoniae genome to prime
 CC the amplification and isolating the amplified sequences. The computer
 CC readable medium can be used in a computer-based system for identifying
 CC fragments of the S. pneumoniae genome of commercial importance, or
 CC expression modulating fragments of the S. pneumoniae genome. Products
 CC from the present invention can be used in diagnosis kits and assays, and
 CC pharmaceutical compositions and vaccines for S. pneumoniae.

XX Sequence 8195 BP; 2688 A; 1622 C; 1777 G; 2105 T; 3 other;

Query Match 97.9%; Score 2338; DB 19; Length 8195;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 2388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	TTCTTACAGAGTGGGACTGTATCAAGCTAAGACGGTTAAGGAAATTAATCGTGTCCGA	60
Db	3053	TTCTTACAGAGTGGGACTGTATCAAGCTAAGACGGTTAAGGAAATTAATCGTGTCCGA	3112
QY	61	TATAGATGAAAACAAAGCGACGCAAAAACGAGAAATTTGAATCTCTGATAGGTTAGCA	120
Db	3113	TATAGATGAAAACAAAGCGACGCAAAAACGAGAAATTTGAATCTCTGATAGGTTAGCA	3172
QY	121	GGGTGAAGAAATCAATGCTGAGCAAAATGTCATCAAGATTAACAGCAAGGCTATGTCAC	180
Db	3173	GGGTGAAGAAATCAATGCTGAGCAAAATGTCATCAAGATTAACAGCAAGGCTATGTCAC	3232
QY	181	TTTCAATGGGACCACTATCAATTTATTAAGTGAAGTCTTATGACGCTATCATGAG	240
Db	3233	TTTCAATGGGACCACTATCAATTTATTAAGTGAAGTCTTATGACGCTATCATGAG	3292
QY	241	TGAAGAAATTAATCAATGAAAGATCCAAACTATTAAGCTAAAGATGAGATATTTAATGA	300
Db	3293	TGAAGAAATTAATCAATGAAAGATCCAAACTATTAAGCTAAAGATGAGATATTTAATGA	3352
QY	301	GGTCAAGGCTGATATGTTATCAAGTATGAGAAATATATGTTAATCTTAAGATGC	360
Db	3353	GGTCAAGGCTGATATGTTATCAAGTATGAGAAATATATGTTAATCTTAAGATGC	3412
QY	361	TGCCACGCGGATTAACGTCGTAACAAGAGAAATCAATGACAAAACAAAGACATAG	420
Db	3413	TGCCACGCGGATTAACGTCGTAACAAGAGAAATCAATGACAAAACAAAGACATAG	3472
QY	421	TCAACATGCTGAAGGTGAACTCCAAAGAAAGATGCTGTGCTTGCGACGTTCCGA	480
Db	3473	TCAACATGCTGAAGGTGAACTCCAAAGAAAGATGCTGTGCTTGCGACGTTCCGA	3532
QY	481	AGGACGCTATATCTACAGATGATGTTATATCTTTAATCTTGTATATCATAGAGATAC	540
Db	3533	AGGACGCTATATCTACAGATGATGTTATATCTTTAATCTTGTATATCATAGAGATAC	3592
QY	541	TGGTGAATGCTTATATCGTCTCTCATGAGATCATTAATCATTAAGATGATG	600
Db	3593	TGGTGAATGCTTATATCGTCTCTCATGAGATCATTAATCATTAAGATGATG	3652
QY	601	ATCAGCTGACGAGTGGCTGTCGAGAAAGCCTTCTTATCTGTGAGGAAATCTGTCAA	660
Db	3653	ATCAGCTGACGAGTGGCTGTCGAGAAAGCCTTCTTATCTGTGAGGAAATCTGTCAA	3712
QY	661	TTCAAGAACTATATGCGCCGACAAATAGGATTAACATTCAGAAACAACTGGTACCTTC	720
Db	3713	TTCAAGAACTATATGCGCCGACAAATAGGATTAACATTCAGAAACAACTGGTACCTTC	3772
QY	721	TGTAAAGCAATCAGGAATCTAATAATCTTAACAAGCAACAACGAACTACTACAGTCA	780
Db	3773	TGTAAAGCAATCAGGAATCTAATAATCTTAACAAGCAACAACGAACTACTACAGTCA	3832
QY	781	AGCAAGTCAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG	840
Db	3833	AGCAAGTCAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG	3892
QY	841	TCAAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	900
Db	3893	TCAAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	3952
QY	901	AGCTAGAGGTGTGAGAGTCCACACGAGATCATTAACATTCATCCTTACTTCAAT	960
Db	3953	AGCTAGAGGTGTGAGAGTCCACACGAGATCATTAACATTCATCCTTACTTCAAT	4012
QY	961	GCTCAATTTGAAGAAAGATGCGTCAATATTCCTGTTGCTTCAACCATTTG	1020
Db	4013	GCTCAATTTGAAGAAAGATGCGTCAATATTCCTGTTGCTTCAACCATTTG	4072
QY	1021	GGTACCAATTCAGAGCCAGAAACAAAGTCCAAACGAGCTCGGAACCTAGTCCAGG	1080
Db	4073	GGTACCAATTCAGAGCCAGAAACAAAGTCCAAACGAGCTCGGAACCTAGTCCAGG	4132

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Qy 1081 CCCGCAACCTGCACCAATCTTAAATAGACTCAATCTTCTTGTTAGTACGCTGCT 1140
Db 4133 CCCGCAACCTGCACCAATCTTAAATAGACTCAATCTTCTTGTTAGTACGCTGCT 4192
Qy 1141 ACGAAAGTGGGGAGGATATGTTTGAAGAAAAGGCGATCTCTGTTATGTTCTTGC 1200
Db 4193 ACGAAAGTGGGGAGGATATGTTTGAAGAAAAGGCGATCTCTGTTATGTTCTTGC 4252
Qy 1201 GAAAGATTACCATCTGAAACGTGTAAATCTTGAAGCAAGTATCAAAAACAAGAG 1260
Db 4253 GAAAGATTACCATCTGAAACGTGTAAATCTTGAAGCAAGTATCAAAAACAAGAG 4312
Qy 1261 TGTTCACACACTTAACTGTGCTAAAAAATGTTGCTCCTCGTGCACCAAGATTTTA 1320
Db 4313 TGTTCACACACTTAACTGTGCTAAAAAATGTTGCTCCTCGTGCACCAAGATTTTA 4372
Qy 1321 TGATTAAGCATATAATCTGTTACTGAGGCTCATTAAGCCTTGTGTAATAAGGCTG 1380
Db 4373 TGATTAAGCATATAATCTGTTACTGAGGCTCATTAAGCCTTGTGTAATAAGGCTG 4432
Qy 1381 TAAATTCGATTCCAGGCTTAGACAAATTAATTAAGCTTGAATGTAATGCACTAA 1440
Db 4433 TAAATTCGATTCCAGGCTTAGACAAATTAATTAAGCTTGAATGTAATGCACTAA 4492
Qy 1441 TAAAGAAAATTTGGTAGATGATTTATTTGGCAATCTCTAGACCAATTAACCAAGAG 1500
Db 4493 TAAAGAAAATTTGGTAGATGATTTATTTGGCAATCTCTAGACCAATTAACCAAGAG 4552
Qy 1501 ACTTGGCAACCAATTTCTCAATTTAGTATATCTGAAGCAAGAGTTCGATTGCTCAAT 1560
Db 4553 ACTTGGCAACCAATTTCTCAATTTAGTATATCTGAAGCAAGAGTTCGATTGCTCAAT 4612
Qy 1561 AGCTGATAGATATACAGTCAAGTGTATACATTTTATGAACATGATATATACAGTGA 1620
Db 4613 AGCTGATAGATATACAGTCAAGTGTATACATTTTATGAACATGATATATACAGTGA 4672
Qy 1621 TGAAGGAGATGATATGTAAGGCTCATATGAGGCTCATATGAGATTTGAAAAAGATAG 1680
Db 4673 TGAAGGAGATGATATGTAAGGCTCATATGAGGCTCATATGAGATTTGAAAAAGATAG 4732
Qy 1681 CCTTTCTGATAGGAAAAAGTTGAGCTCAAGCCTATATCTAAAGAAAAAGGATCTTACC 1740
Db 4733 CCTTTCTGATAGGAAAAAGTTGAGCTCAAGCCTATATCTAAAGAAAAAGGATCTTACC 4792
Qy 1741 TCCATCTTCACAGCAGATGTTAAAGCAATTCCACTGGAAGTATGAGACGCTATTTA 1800
Db 4793 TCCATCTTCACAGCAGATGTTAAAGCAATTCCACTGGAAGTATGAGACGCTATTTA 4852
Qy 1801 CAATCGTGTGAAGGGGAAAAAGCAATTCCTGCTGAGCTTCATATATGTTGAGCA 1860
Db 4853 CAATCGTGTGAAGGGGAAAAAGCAATTCCTGCTGAGCTTCATATATGTTGAGCA 4912
Qy 1861 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATTAAGATCACTAATATAT 1920
Db 4913 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATTAAGATCACTAATATAT 4972
Qy 1921 TAAATTTGCTTGTTGATGATCAGACATACAAAGCTCCAAATGCTTACTTGGGAAGA 1980
Db 4973 TAAATTTGCTTGTTGATGATCAGACATACAAAGCTCCAAATGCTTACTTGGGAAGA 5032
Qy 1981 TTTGTTTGGCGAGTTAGTACTAGTGAACACCTGACGAAAGCTCCAAATTCGAAGA 2040
Db 5033 TTTGTTTGGCGAGTTAGTACTAGTGAACACCTGACGAAAGCTCCAAATTCGAAGA 5092
Qy 2041 TGATGGGGCAATGCACATGAGCATGTGTTAGGCAAGAAAGCAACAGTGAAGATCCAAA 2100
Db 5093 TGATGGGGCAATGCACATGAGCATGTGTTAGGCAAGAAAGCAACAGTGAAGATCCAAA 5152
Qy 2101 TAAAGACTTCAAAAGCGATGAAGAGCCAGTGAAGAAACCTGTGAGCCAGAAAGTCCC 2160
Db 5153 TAAAGACTTCAAAAGCGATGAAGAGCCAGTGAAGAAACCTGTGAGCCAGAAAGTCCC 5212

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Qy 2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAAGACAGAGTTTGTGCGAA 2220
Db 5213 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAAGACAGAGTTTGTGCGAA 5272
Qy 2221 AGTAAAGGATTTTGTGTTGAAAGCCCAATGCAACAGAAATCTTACTGTTTGAAGATA 2280
Db 5273 AGTAAAGGATTTTGTGTTGAAAGCCCAATGCAACAGAAATCTTACTGTTTGAAGATA 5332
Qy 2281 TTTGACTCTTCAATTTATGATTAACATATGATATGATGATGATGATGATGATGATGAT 2340
Db 5333 TTTGACTCTTCAATTTATGATTAACATATGATATGATGATGATGATGATGATGATGAT 5392
Qy 2341 GTTGTAAAAAGAGTAATCTTCTATCTGTATAGTAAAGAAAAATAAAC 2389
Db 5393 GTTGTAAAAAGAGTAATCTTCTATCTGTATAGTAAAGAAAAATAAAC 5441

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RESULT 6
 ABS56454/C
 ID ABS56454 standard; DNA; 2162598 BP.
 XX
 AC ABS56454;
 XX
 DT 10-FEB-2003 (first entry)
 XX
 DE Streptococcus pneumoniae type 4 strain complete genome.
 XX
 KW ds; bacterial meningitis; pneumonia; sepsis; otitis media; genome;
 KW ear infection; antiinflammatory; antibacterial; immunostimulant;
 KW auditory; respiratory; gene therapy; vaccine.
 OS Streptococcus pneumoniae type 4 strain.
 XX
 FN W0200277021-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 27-MAR-2002; 2002WO-1B02163.
 XX
 PR 27-MAR-2001; 2001GB-0007658.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Maignani V, Tettelein H, Fraser C;
 DR WPI; 2003-040579/03.
 XX
 PT New proteins and nucleic acid molecules from Streptococcus pneumoniae,
 PT useful as medicaments for treating or preventing a disease or infection
 PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
 PT or ear infection -
 XX
 PS Claim 17; SEQ ID No 4979; 56bp; English.
 XX
 CC The invention relates to a protein comprising or having at least 50%
 CC identity to any of the 2469 amino acid sequences, identified in the
 CC specification (available on a computer readable format), or its fragment,
 CC expressed from 2469 of 2489 identified DNA coding regions from the
 CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
 CC ABS56454. Also included are an antibody which binds one of the
 CC proteins, treating a patient by administering the protein, DNA or
 CC antibody (in a composition), a kit comprising first and second primers,
 CC which are the nucleic acid cited above or fragments between nucleotides
 CC 8-100 of a sequence not defined in the specification, for amplifying a
 CC target sequence contained within a Streptococcus nucleic acid sequence,
 CC where the first primer is substantially complementary to the target
 CC sequence and the second primer is substantially complementary to the
 CC complement of the target sequence, and where the parts of the primers
 CC having substantial complementarity define the termini of the target
 CC sequence to be amplified, assay comprising contacting a test compound
 CC with the protein, and determining whether the test compound binds to the
 CC protein and a Streptococcus pneumoniae bacterium, where one or more

CC genes encoding the proteins has been rendered inactive. The proteins,
CC nucleic acid molecules, antibody and compositions are useful as
CC medicaments for treating or preventing a disease or infection due to
CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia,
CC sepsis, otitis media or ear infection. They are also useful in developing
CC vaccines, diagnostics and antibiotics. The methods are useful for
CC identifying immunodominant proteins. The present sequence is the
CC Streptococcus pneumoniae type 4 strain genome sequence.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIP0 at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2162598 BP; 654373 A; 427176 C; 431369 G; 649680 T; 0 other;

Query Match 97.9%; Score 2338; DB 25; Length 2162598;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTTACGAGTTGGAGCTGTATCAAGCTAGAAAGGTTAAGAAATAATCGTGTCTTA 60
DB 1006950 TTCTTACGAGTTGGAGCTGTATCAAGCTAGAAAGGTTAAGAAATAATCGTGTCTTA 1006891
QY 61 TATPAGTGAAGAAACAAGCGACCGCAAAAACGAGAAATTTGACTCTGTATGAGTTAGCAA 120
DB 1006890 TATPAGTGAAGAAACAAGCGACCGCAAAAACGAGAAATTTGACTCTGTATGAGTTAGCAA 1006831
QY 121 GGTGTAAGGAATCAATGCTGAGCAATCGTCATCAAGATACAGACCAAGGCTATGTCAC 180
DB 1006830 GGTGTAAGGAATCAATGCTGAGCAATCGTCATCAAGATACAGACCAAGGCTATGTCAC 1006771
QY 181 TTCACATGCGACCACTATCATTTATTAACATGGTAAAGTTCCCTTATGACGCTATCATGAC 240
DB 1006770 TTCACATGCGACCACTATCATTTATTAACATGGTAAAGTTCCCTTATGACGCTATCATGAC 1006711
QY 241 TGAAGATTTACTTCATGAAAAGATCCAAACTATAAGCTMAAAGATGAGATATTGTTATGA 300
DB 1006710 TGAAGATTTACTTCATGAAAAGATCCAAACTATAAGCTMAAAGATGAGATATTGTTATGA 1006651
QY 301 GGTCAAGGTTGATATGTTATCAAGGTAGTGAATAATCTATGTTTACCTTAAGATGTC 360
DB 1006650 GGTCAAGGTTGATATGTTATCAAGGTAGTGAATAATCTATGTTTACCTTAAGATGTC 1006591
QY 361 TSCCCACGCGGATTAAGCTCCGTACAAAGAGAAATCAATCGACAAACCAAGAGCATAG 420
DB 1006590 TSCCCACGCGGATTAAGCTCCGTACAAAGAGAAATCAATCGACAAACCAAGAGCATAG 1006531
QY 421 TCAACATCGTGAAGGTGAACCTCAAGAAACGATGGTGTGTTGCTTGGCAGCTTCCGA 480
DB 1006530 TCAACATCGTGAAGGTGAACCTCAAGAAACGATGGTGTGTTGCTTGGCAGCTTCCGA 1006471
QY 481 AGGAGGCTTACTACAGATGATGTTATATCTTTAATGCTTCTGTATATATAGAGATAC 540
DB 1006470 AGGAGGCTTACTACAGATGATGTTATATCTTTAATGCTTCTGTATATATAGAGATAC 1006411
QY 541 TGGTATGCTTATATGCTTCTCATGAGATATTAACATTCATTCCTTAAGATAGTT 600
DB 1006410 TGGTATGCTTATATGCTTCTCATGAGATATTAACATTCATTCCTTAAGATAGTT 1006351
QY 601 ATCAGCTAGCAGATTGGCTGTGTCAGAAAGCTTCTCATCTGTGTCAGAAATCTGTCAA 660
DB 1006350 ATCAGCTAGCAGATTGGCTGTGTCAGAAAGCTTCTCATCTGTGTCAGAAATCTGTCAA 1006291
QY 661 TTCAAGAACCTATCGCCGCAAAAATATGCGATTAACCTTCAAGAACCAACCTGGGTACTTC 720
DB 1006290 TTCAAGAACCTATCGCCGCAAAAATATGCGATTAACCTTCAAGAACCAACCTGGGTACTTC 1006231
QY 721 TSTAAGCAATCCAGGAATACAAATCTATAACAAGCAACCAAGCAACTTAACAGTCA 780
DB 1006230 TSTAAGCAATCCAGGAATACAAATCTATAACAAGCAACCAAGCAACTTAACAGTCA 1006171
QY 781 ACCAAGTCAAGTAATGACATTTGATGCTCTTGAACAGCTCTACAACTGCTTTGAG 840
DB 1006170 ACCAAGTCAAGTAATGACATTTGATGCTCTTGAACAGCTCTACAACTGCTTTGAG 1006110
QY 841 TCAAGGACATGTAAGATCGATGCGCTCTTATGATCCAGACAAATACAGTCGAC 900
DB 1006110 TCAAGGACATGTAAGATCGATGCGCTCTTATGATCCAGACAAATACAGTCGAC 1006051
QY 901 ACCTAGAGTGTGGAGTGCACACAGGATCATTAACCACTTATCCCTTACTTCAAT 960
DB 1006050 ACCTAGAGTGTGGAGTGCACACAGGATCATTAACCACTTATCCCTTACTTCAAT 1005991
QY 961 GTCTAATTGGAAGACGAATGCTGTATTAATTCCTTGTATTCGTTCAACCATG 1020
DB 1005990 GTCTAATTGGAAGACGAATGCTGTATTAATTCCTTGTATTCGTTCAACCATG 1005931
QY 1021 GGTACCAATTCAGGCGACGAACCAAGTCACACCGATCCGGAACCTAGTCCAG 1080
DB 1005930 GGTACCAATTCAGGCGACGAACCAAGTCACACCGATCCGGAACCTAGTCCAG 1005871
QY 1081 CCCGCAACCTGACCAAAATCTTAATAATGACTCAAAATCTTCTTGTAGTACGCTG 1140
DB 1005870 CCCGCAACCTGACCAAAATCTTAATAATGACTCAAAATCTTCTTGTAGTACGCTG 1005811
QY 1141 ACGAAAGTTGGGGAAGATATGATTCGAAGAAAAGGCACTCTGTTATGCTTTGC 1200
DB 1005810 ACGAAAGTTGGGGAAGATATGATTCGAAGAAAAGGCACTCTGTTATGCTTTGC 1005751
QY 1201 GAAAGATTTACATCTGTAACCTGTTAAATCTTGAAGCAAGTTATCAAAACAAGAG 1260
DB 1005750 GAAAGATTTACATCTGTAACCTGTTAAATCTTGAAGCAAGTTATCAAAACAAGAG 1005691
QY 1261 TGTTCACACACTTAACTGCTTAAGAAAAGAAATGTTGCTCTGTCGACCAAGATTTTA 1320
DB 1005690 TGTTCACACACTTAACTGCTTAAGAAAAGAAATGTTGCTCTGTCGACCAAGATTTTA 1005631
QY 1321 TGATTAAGCATTAATCTGTTAACTGAGGCTCATTAAGGCTTGTGTAATAAGGCTG 1380
DB 1005630 TGATTAAGCATTAATCTGTTAACTGAGGCTCATTAAGGCTTGTGTAATAAGGCTG 1005571
QY 1381 TAAATTCGATTTCCAGGCTTGAACAATTTATTAAGGCTTGAATGATATCACTTA 1440
DB 1005570 TAAATTCGATTTCCAGGCTTGAACAATTTATTAAGGCTTGAATGATATCACTTA 1005511
QY 1441 TAAAGAAAATTTGTAAGATTTATTTAGGCAATTCCTAGACCAATTAACCAACGAGG 1500
DB 1005510 TAAAGAAAATTTGTAAGATTTATTTAGGCAATTCCTAGACCAATTAACCAACGAGG 1005451
QY 1501 ACTTGCAAAACCAATTTCTCAAATTAAGTATTAAGTGAAGCAAGTTCGATTCAT 1560
DB 1005450 ACTTGCAAAACCAATTTCTCAAATTAAGTATTAAGTGAAGCAAGTTCGATTCAT 1005391
QY 1561 AGCTGATTAAGTATTAAGGCTGATGTTTACATTTTGTGTAACATGATATATCACTGA 1620
DB 1005390 AGCTGATTAAGTATTAAGGCTGATGTTTACATTTTGTGTAACATGATATATCACTGA 1005331
QY 1621 TGAAGGAGTGAATGTAAGGCTCATATGAGGCAATGCTCATGATTTGGAAGATAG 1680
DB 1005330 TGAAGGAGTGAATGTAAGGCTCATATGAGGCAATGCTCATGATTTGGAAGATAG 1005271
QY 1681 CTTTCTGATTAAGAAAAGTTGACGCTCAAGCTTATTAAGAAAAGGATCTTACC 1740
DB 1005270 CTTTCTGATTAAGAAAAGTTGACGCTCAAGCTTATTAAGAAAAGGATCTTACC 1005211
QY 1741 TCCATCTCAGACGAGATGTTTAAAGCAATTCGAACCTGAGATAGTGCAGGCTATTTA 1800
DB 1005210 TCCATCTCAGACGAGATGTTTAAAGCAATTCGAACCTGAGATAGTGCAGGCTATTTA 1005151
QY 1801 CAATCGTGAAGAAAGGGAAGAAAAGCAATTCGATTCGATTCATATATGTTGAGCA 1860
DB 1005150 CAATCGTGAAGAAAGGGAAGAAAAGCAATTCGATTCGATTCATATATGTTGAGCA 1005091
QY 1861 TACAGTTAGGTTTAAAGGATATTTGATTAATTCCTATTAAGATTCATTAACATTAAT 1920
DB 1005090 TACAGTTAGGTTTAAAGGATATTTGATTAATTCCTATTAAGATTCATTAACATTAAT 1005031

QY 1921 TAAATTCCTGTTGTTGATGATACATACAAAGCTCCAAATGCTATACCTTGAAGA 1980
 Db 1005030 TAAATTCCTGTTGTTGATGATACATACAAAGCTCCAAATGCTATACCTTGAAGA 1004971
 QY 1981 TTTGTTCCGACGATTAAGTACTAGTGAACACCTTGAAGACCTCCACATTTCAATGA 2040
 Db 1004970 TTTGTTCCGACGATTAAGTACTAGTGAACACCTTGAAGACCTCCACATTTCAATGA 1004911
 QY 2041 TGGATGGGCAATGCGACATGATGTTAGGCAAGAAAGCCACAGTGAAGATCCAAA 2100
 Db 1004910 TGGATGGGCAATGCGACATGATGTTAGGCAAGAAAGCCACAGTGAAGATCCAAA 1004851
 QY 2101 TAAAGACTTCAAAAGCGAGTGAAGAGCCAGTAGAGAAAACCTGCTGAGCCAGAACTCC 2160
 Db 1004850 TAAAGACTTCAAAAGCGAGTGAAGAGCCAGTAGAGAAAACCTGCTGAGCCAGAACTCC 1004791
 QY 2161 TCAAGTAGAGACTGAAAAAGTGAAGCCCACTCAAGAAAGCAGAAAGTTTGTGGCAA 2220
 Db 1004790 TCAAGTAGAGACTGAAAAAGTGAAGCCCACTCAAGAAAGCAGAAAGTTTGTGGCAA 1004731
 QY 2221 AGTAACGATCTGCTGTAAGAGCCCAATGCAACAGAACTCTAGCTGTTTACGAAATTA 2280
 Db 1004730 AGTAACGATCTGCTGTAAGAGCCCAATGCAACAGAACTCTAGCTGTTTACGAAATTA 1004671
 QY 2281 TTTGACTCTTCAAAATTTATGATTAACATAGTATCATGCGAGAGCAGAAAAATTACTTGC 2340
 Db 1004670 TTTGACTCTTCAAAATTTATGATTAACATAGTATCATGCGAGAGCAGAAAAATTACTTGC 1004611
 QY 2341 GTTGTAAAGAGAGTAATCTCTTCACTGTAAGTGAAGAAAAATTAAC 2389
 Db 1004610 GTTGTAAAGAGAGTAATCTCTTCACTGTAAGTGAAGAAAAATTAAC 1004562

RESULT 7

AAA65731 ID AAA65731 standard; DNA; 2523 BP.

AC AAA65731;

DT 21-NOV-2000 (first entry)

DE Streptococcus pneumoniae BVH-11 gene SEQ ID NO:3.

KM Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
 KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
 KM otitis media; pneumonia; immunisation; bactericidal; ds.

XX Streptococcus pneumoniae.

OS MO200039299-A2.

PN 06-JUL-2000.

XX 20-DEC-1999; 99WO-CA01218.

XX 23-DEC-1998; 98US-0113800.

XX (BIOC-) BIOCHEM PHARMA INC.

PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;

DR WPI: 2000-452397/39.

XX P-PSDB: AAB12716.

XX Streptococcal antigens useful for vaccinating against e.g. meningitis,
 PT otitis media, bacteraemia and/or pneumonia -

XX Example 2; Fig 3; 106pp; English.

CC The present invention describes nucleic acids (I) encoding protein
 CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein

CC antigens, may be used for the recombinant production of the proteins
 CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals
 CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence encodes the
 CC S. pneumoniae BVH-11 protein antigen.
 XX

SQ Sequence 2523 BP; 879 A; 523 C; 526 G; 595 T; 0 other;

Query Match 6.2%; Score 148; DB 21; Length 2523;

Best Local Similarity 100.0%; Pred. No. 2.3e-64;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 699 CAAGACAAACTGGGTAACCTTCTGTAAGCAATCCAGAACTCAAAATTAACACAAGCA 758

Db 758 CAAGACAAACTGGGTAACCTTCTGTAAGCAATCCAGAACTCAAAATTAACACAAGCA 817

QY 759 ACAACAGCAACACTAACAGTCAAGCAAGTCAAGTAATGACATTGATGCTCTTGAAC 818

Db 818 ACAACAGCAACACTAACAGTCAAGCAAGTCAAGTAATGACATTGATGCTCTTGAAC 877

QY 819 AGCTCTCAAACTGCTTGAAGTCAAG 846

Db 878 AGCTCTCAAACTGCTTGAAGTCAAG 905

RESULT 8

AAA65736 ID AAA65736 standard; DNA; 2647 BP.

AC AAA65736;

DT 21-NOV-2000 (first entry)

DE Streptococcus pneumoniae BVH-11 gene SEQ ID NO:12.

KM Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
 KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
 KM otitis media; pneumonia; immunisation; bactericidal; ds.

XX Streptococcus pneumoniae.

OS MO200039299-A2.

PN 06-JUL-2000.

XX 20-DEC-1999; 99WO-CA01218.

XX 23-DEC-1998; 98US-0113800.

XX (BIOC-) BIOCHEM PHARMA INC.

PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;

DR WPI: 2000-452397/39.

XX Streptococcal antigens useful for vaccinating against e.g. meningitis,
 PT otitis media, bacteraemia and/or pneumonia -

XX Example 6; Fig 15; 106pp; English.

CC The present invention describes nucleic acids (I) encoding protein
 CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein
 CC antigens, may be used for the recombinant production of the proteins
 CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals
 CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence encodes the
 CC S. pneumoniae BVH-11 protein antigen.
 XX

SQ Sequence 2647 BP; 934 A; 538 C; 556 G; 619 T; 0 other;

CC proteins can be used to inhibit *S. pneumoniae*-mediated C3 degradation.
CC C3-mediated inflammation and rejection in xenotransplantation can be
CC inhibited by expressing the nucleic acid sequences on the surface of an
CC organ of an animal. In particular, the polypeptides are useful for
CC stimulating the immune system and are effective to immunize or treat a
CC mammalian subject against *Streptococcus pneumoniae* infection or
CC colonization.
CC
SQ Sequence 504 BP; 153 A; 125 C; 98 G; 128 T; 0 other;

Query Match 2.2%; Score 53; DB 21; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 983 GCTCGTATTATTCCTTCGTATCGTTCAACCATGGGTACGATTCAAG 1035
DB 184 GCTCGTATTATTCCTTCGTATCGTTCAACCATGGGTACGATTCAAG 236
|||||
RESULT 11
ID AAY25394 standard; DNA; 2163 BP.
AC AAY25394;
XX 19-JUL-1999 (first entry)
DT
XX
DE Streptococcus pneumoniae complement C3-degrading protease DNA.
XX
KW Human complement C3-degrading protease; vaccine; infection;
KW meningitis; pneumonia; xerotransplantation; transplant rejection;
KW inflammation; ds.
XX
OS Streptococcus pneumoniae.
XX
PN WO9115675-A1.
XX
PD 01-APR-1999.
XX
PE 24-SEP-1998; 98WO-US20186.
XX
PR 24-SEP-1997; 97US-0059907.
XX
PA (AMCY) AMERICAN CYANAMID CO.
XX (MINU) UNIV MINNESOTA.
XX
PI Cheng Q, Finkel DJ, Green BA, Hostetter MK, Masi AW;
XX WPI, 1999-254719/21.
XX P-PSDB; AAY05753.
XX
PT New isolated human complement C3-degrading proteinase
PS
XX Claim 54; Page 52-54; 66pp; English.
XX
CC This DNA sequence encodes a 79 kDa protein (see AAY05753) of
CC Streptococcus pneumoniae serotype 4 that is capable of degrading
CC human complement protein C3 (HCP3). It was identified in the *S.*
CC pneumoniae serotype 4 genome by alignment to another novel open
CC reading frame (see AAY25393) that codes for a 20 kDa HCP3 protease
CC (AAY05752) of *S. pneumoniae* serotype 3. This suggested the open
CC reading frame that codes for the 20 kDa protein may be part of a
CC larger open reading frame. Amino acids 1-58 and 90-132 of the 20
CC kDa protein have substantial sequence identity with amino acids
CC 170-227 and 258-300 of the 79 kDa protein. Proteins and peptides or
CC polypeptides containing these regions, and DNA sequences encoding
CC them (nucleotides 507-661 and 827-999 of the present sequence) are
CC claimed. HCP3 proteases and polypeptides can be used as immune
CC system stimulating compositions (claimed). They can produce an
CC immune response against *S. pneumoniae* to immunize or treat a
CC mammalian subject against infection or colonization (claimed).
CC They can produce a B cell response, a T cell response, an
CC epithelial cell response, or an endothelial cell response

CC (claimed). The expression of the proteins on the surface of an
CC organ of an animal used in xenotransplantation can be used to
CC inhibit C3-mediated inflammation and rejection.
XX
SQ Sequence 2163 BP; 737 A; 450 C; 462 G; 514 T; 0 other;

Query Match 2.2%; Score 53; DB 20; Length 2163;
Best Local Similarity 100.0%; Pred. No. 3.9e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 983 GCTCGTATTATTCCTTCGTATCGTTCAACCATGGGTACGATTCAAG 1035
DB 688 GCTCGTATTATTCCTTCGTATCGTTCAACCATGGGTACGATTCAAG 740
|||||
RESULT 12
ID AAY27356 standard; DNA; 2290 BP.
AC AAY27356;
XX 02-OCT-1998 (first entry)
DT
XX
DE Streptococcus pneumoniae SP0042 nucleotide.
XX
KW Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
KW detection; pneumonia; otitis media; meningitis; ss.
XX
OS Streptococcus pneumoniae.
XX
FH Key Location/Qualifiers
FT CDS 2..2290
FT
FT /*Cag= a
FT /product= "Sp0042"
FT /transl_except= (pos:152..154,aa:Xaa)
FT /transl_except= (pos:1406..1408,aa:Xaa)
FT /transl_except= (pos:1430..1432,aa:Xaa)
FT /note= "no stop codon given; Xaa is unspecified"
XX
XX
PN WO9816930-A2.
XX
PD 07-MAY-1998.
XX
PE 30-OCT-1997; 97WO-US19422.
XX
PR 31-OCT-1996; 96US-0029960.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Choi GH, Hromockyj A, Johnson LS, Kunsch CA;
XX WPI, 1998-272224/24.
XX P-PSDB; AAM55095.
XX
PT Nucleic acid encoding antigenic peptide(s) from Streptococcus
PT pneumoniae - or their epitope-containing fragments, useful in
PT protective or therapeutic vaccines, and for diagnosis
PS
XX Claim 1; Page 61-62; 118pp; English.
XX
CC The present sequence encodes a protein from Streptococcus pneumoniae.
CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein
CC can be useful in vaccines for inducing protective antibodies against
CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.
CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid
CC are used to detect Streptococcus infection (by usual hybridisation or
CC amplification methods), also for isolating Streptococcus genes or their
CC allelic variants. The protein can be used similarly to detect specific
CC antibodies in standard immunoassays, especially for diagnosing or
CC monitoring infections. Antibodies which bind the protein are used to
CC detect corresponding antigens, to purify the protein and for passive
CC immunisation (optionally coupled to a toxin). Vaccines are administered,
CC e.g. by injection, orally or through the skin, typically at 0.01-1000

CC (especially 10-300) mu g/ml per dose.

XX Sequence 2290 BP; 766 A; 474 C; 498 G; 547 T; 5 other;

Query Match 2.2%; Score 53; DB 19; Length 2290;
Best Local Similarity 100.0%; Pred. No. 3.9e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 983 GCTCGATTATATCCCTTCGTTATCGTTCAACCATTTGGGTACGATTCAAG 1035
DB 944 GCTCGATTATATCCCTTCGTTATCGTTCAACCATTTGGGTACGATTCAAG 996

RESULT 13

AB084824
ID AB084824 standard; DNA; 2290 BP.

AC AB084824;

DT 04-SEP-2002 (first entry)

DE S. pneumoniae SP042 nucleotide sequence SEQ ID NO:65.

XX Streptococcus pneumoniae; epitope; vaccine; antigenic protein;
KW antibacterial; Streptococcal infection; detection; gene; ds.

XX Streptococcus pneumoniae.

OS US2002061545-A1.

PN 23-MAY-2002.

PD 22-JAN-2001; 2001US-0765272.

PF 30-OCT-1997; 97US-0961083.

PR (CHOI/) CHOI G H.

PA (KUNS/) KUNSCH C A.

PA (BARA/) BARASH S C.

PA (DILL/) DILLON P J.

PA (DOUG/) DOUGHERTY B.

PA (FANN/) FANNON M R.

PA (ROSE/) ROSEN C A.

XX Chai GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR;

PI Rosen CA;

PI WPI; 2002-479261/51.

DR P-PSDB; ABP54589.

PT New Streptococcus pneumoniae antigens, useful for detecting

PT Streptococcus and for preventing or attenuating disease caused by

PT Streptococcus infection -

XX Claim 1; Page 28-29; 70pp; English.

XX AB084792 to AB084804 represents nucleic acids which encode the

XX Streptococcus pneumoniae antigens given in ABP5457 to ABP5469.

XX The S. pneumoniae antigens have antibacterial activity and can be

XX used in vaccines. The S. pneumoniae antigens can also be used to

XX prevent or attenuate a Streptococcal infection in an animal. The

XX CC polynucleotides encoding the S. pneumoniae antigens can be used to

XX detect Streptococcus nucleic acids. AB084805 to AB08510 represent

XX primers used in the cloning of S. pneumoniae ORFs (open reading frames)

XX which are used in an example from the present invention.

XX Sequence 2290 BP; 766 A; 474 C; 498 G; 547 T; 5 other;

XX Query Match 2.2%; Score 53; DB 24; Length 2290;

XX Best Local Similarity 100.0%; Pred. No. 3.9e-16;

XX Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 944 GCTCGATTATATCCCTTCGTTATCGTTCAACCATTTGGGTACGATTCAAG 996

RESULT 14
AAV52376
ID AAV52376 standard; DNA; 2359 BP.

AC AAV52376;

DT 23-OCT-1998 (first entry)

DE Streptococcus pneumoniae genome fragment SEQ ID NO:243.

XX Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;

XX computer readable medium; vaccine; pharmaceutical composition; ds.

OS Streptococcus pneumoniae.

PN -WO9818931-A2.

PD 07-MAY-1998.

PF 30-OCT-1997; 97WO-US19588.

PR 31-OCT-1996; 96US-0029960.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Barash SC, Chai GH, Dillon PJ, Dougherty BA, Fannon M;

PI Kunsch CA, Rosen CA;

PI WPI; 1998-272225/24.

PT Computer-readable medium with recorded Streptococcus pneumoniae

PT polynucleotide sequences - useful in diagnostic kits and assays, and

PT pharmaceutical compositions and vaccines for Streptococcus

PT pneumoniae

PS Claim 1; Page 1265-1266; 1409pp; English.

XX The present invention describes a computer readable medium which has

XX the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)

XX recorded on it, or a representative fragment or a sequence at least 95%

XX identical to SEQ ID NO:1 to 391. The nucleotide sequences depicted in

XX SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from

XX Streptococcus pneumoniae. The present invention also describes an

XX isolated nucleic acid molecule encoding a homologue of any of the

XX fragments of the S. pneumoniae genome (SEQ ID NO:1 to 391) where the

XX nucleic acid molecule is produced by a process comprising: (a) screening

XX a genomic DNA library using as a probe a target sequence defined by any

XX of the sequences in SEQ ID NO:1 to 391, identifying members of the

XX library which contain sequences that hybridize to the target sequence and

XX isolating the nucleic acid molecules from the members; or (b) isolating

XX cDNA or RNA produced from an organism, amplifying nucleic acid

XX molecules whose nucleotide sequence is homologous to amplification

XX primers derived from the fragment of the S. pneumoniae genome to prime

XX the amplification and isolating the amplified sequences. The computer

XX readable medium can be used in a computer-based system for identifying

XX fragments of the S. pneumoniae genome of commercial importance, or

XX expression modulating fragments of the S. pneumoniae genome. Products

XX from the present invention can be used in diagnosis kits and assays, and

XX pharmaceutical compositions and vaccines for S. pneumoniae.

XX Sequence 2359 BP; 786 A; 451 C; 511 G; 611 T; 0 other;

XX Query Match 2.2%; Score 53; DB 19; Length 2359;

XX Best Local Similarity 100.0%; Pred. No. 3.9e-16;

XX Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 983 GCTCGATTATATCCCTTCGTTATCGTTCAACCATTTGGGTACGATTCAAG 1035
DB 1879 GCTCGATTATATCCCTTCGTTATCGTTCAACCATTTGGGTACGATTCAAG 1931

RESULT 15
ABX06885
ID ABX06885 standard; DNA; 2457 BP.
XX
AC ABX06885;
XX
DT 11-FEB-2003 (first entry)
XX
DE S. pneumoniae type 4 strain coding region #1173.
XX
KW Gene; ds; bacterial meningitis; pneumonia; sepsis; otitis media;
KM ear infection; antiinflammatory; antibacterial; immunostimulant;
XX auditory; respiratory; gene therapy; vaccine.
XX
OS Streptococcus pneumoniae type 4 strain.
XX
PN WO200277021-A2.
XX
PD 03-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-1B02163.
XX
PR 27-MAR-2001; 2001GB-0007658.
XX
PA (CHIR-) CHIRON SPA.
XX (GENO-) INST GENOMIC RES.
PI Maignani V, Tettelin H, Fraser C;
XX
XX WPI; 2003-040579/03.
DR P-PSDB; ABU01597.
XX
XX New proteins and nucleic acid molecules from Streptococcus pneumoniae,
PT useful as medicaments for treating or preventing a disease or infection
PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
PT or ear infection -
XX
PS Claim 6; SEQ ID No 2345; 56bp; English.
XX
XX The invention relates to a protein comprising or having at least 50%
CC identity to any of the 2469 amino acid sequences, identified in the
CC specification (available on a computer readable format), or its fragment,
CC expressed from 2469 of 2489 identified DNA coding regions from the
CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
CC ABS66454. Also included are an antibody which binds one of the
CC proteins, treating a patient by administering the protein, DNA or
CC antibody (in a composition), a kit comprising first and second primers,
CC which are the nucleic acid cited above or fragments between nucleotides
CC 8-100 of a sequence not defined in the specification, for amplifying a
CC target sequence contained within a Streptococcus nucleic acid sequence,
CC where the first primer is substantially complementary to the target
CC sequence and the second primer is substantially complementary to the
CC complement of the target sequence, and where the parts of the primers
CC having substantial complementarity define the termini of the target
CC sequence to be amplified, assay comprising contacting a test compound
CC with the protein, and determining whether the test compound binds to the
CC protein and a Streptococcus pneumoniae bacterium, where one or more
CC genes encoding the proteins has been rendered inactive. The proteins,
CC nucleic acid molecules, antibody and compositions are useful as
CC medicaments for treating or preventing a disease or infection due to
CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia,
CC sepsis, otitis media or ear infection. They are also useful in developing
CC vaccines, diagnostics and antibiotics. The methods are useful for
CC identifying immunodominant proteins. The present sequence is one of
CC the 2469 identified coding region from the genomic sequence.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 2457 BP; 836 A; 497 C; 531 G; 593 T; 0 other;

Query Match 2.2%; Score 53; DB 25; Length 2457;
Best Local Similarity 100.0%; Pred. No. 3,9e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 983 GCTCGTATTATTCCTCGTTATCGTTCAAAACCATGGGTACAGATTCAAG 1035
DB 1000 GCTCGTATTATTCCTCGTTATCGTTCAAAACCATGGGTACAGATTCAAG 1052
RESULT 16
AAA08557
ID AAA08557 standard; DNA; 2478 BP.
XX
AC AAA08557;
XX
DT 19-JUL-2000 (first entry)
XX
DE S. pneumoniae 92 kDa human C3-degrading protein coding sequence.
XX
KW Human C3-degrading protein; 92 kDa; immunostimulatory; vaccine;
KM inhibitor; inflammation; organ rejection; xenotransplantation; ss.
XX
OS Streptococcus pneumoniae.
XX
PN WO200017370-A1.
XX
PD 30-MAR-2000.
XX
PF 24-SEP-1999; 99WO-US22362.
XX
PR 24-SEP-1998; 98US-0101736.
XX 31-MAR-1999; 99US-0283094.
XX
XX (MINU) UNIV MINNESOTA.
XX (ANCY) AMERICAN CYANAMID CO.
PI Hostetter MK, Finkel DJ, Cheng Q, Green BA, Masi AM;
XX
XX WPI; 2000-283594/24.
DR P-PSDB; AAY91939.
XX
XX Isolated polypeptide is used to stimulate immune system and immunize or
PT treat a mammalian subject against Streptococcus pneumoniae infection or
PT colonization
XX
PS Claim 1; Page 55-57; 63bp; English.
XX
XX The present sequence, isolated from Streptococcus pneumoniae, encodes a
CC human C3-degrading protein (see AAY91939) of about 92 kDa. This
CC sequence may encompass a smaller 20 kDa polypeptide coding sequence
CC (AAA08556) also having human C3-degrading activity.
CC The DNA sequences can be used for producing an immune response to
CC Streptococcus pneumoniae in a mammal. Antibodies against the proteins
CC can be used to inhibit S. pneumoniae-mediated C3 degradation.
CC C3-mediated inflammation and rejection in xenotransplantation can be
CC inhibited by expressing the nucleic acid sequences on the surface of an
CC organ of an animal. In particular, the polypeptides are useful for
CC stimulating the immune system and are effective to immunize or treat a
CC mammalian subject against Streptococcus pneumoniae infection or
CC colonization.
XX
XX Sequence 2478 BP; 837 A; 510 C; 535 G; 596 T; 0 other;
Query Match 2.2%; Score 53; DB 21; Length 2478;
Best Local Similarity 100.0%; Pred. No. 3,9e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 983 GCTCGTATTATTCCTCGTTATCGTTCAAAACCATGGGTACAGATTCAAG 1035
DB 1003 GCTCGTATTATTCCTCGTTATCGTTCAAAACCATGGGTACAGATTCAAG 1055

RESULT 17
AAA05417
ID AAA05417 standard; DNA; 2481 BP.
XX
XX
AC AAA05417;
XX
XX
DT 24-MAY-2000 (first entry)
XX
XX
DE Streptococcus pneumoniae nucleotide sequence ID11.
XX
XX
KW Streptococcus pneumoniae; vaccine; screening; protein antigen;
KM antibacterial; antiinflammatory; meningitis; infection; diagnosis;
XX pneumococcal disease; ds.
XX
OS Streptococcus pneumoniae.
XX
PN WO200006737-A2.
XX
PD 10-FEB-2000.
XX
PF 27-JUL-1999; 99WO-GB02451.
XX
PR 27-JUL-1998; 98GB-0016337.
XX 19-MAR-1999; 99US-0125164.
XX
XX (MICR-) MICROBIAL TECHNICS LTD.
XX
XX
PI Gilbert CFG, Hansbro PM;
XX
XX WPI; 2000-1995300/17.
XX P-PSDB; AAY81662.
XX
XX New Streptococcal protein, useful as a vaccine, for diagnosis of
PT pneumococcal diseases and for screening agents capable of antagonizing
or inhibiting expression of the protein
XX
XX Claim 2; Page 99; 108pp; English.
XX
XX AAY81501 to AAY81679 represent specifically claimed protein sequences
CC isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent
CC specifically claimed nucleotide sequences isolated from S. pneumoniae.
CC The sequences have antibacterial and antiinflammatory properties.
CC The protein sequences, and fragments of them, are useful as immunogens
CC and/or antigens. The nucleotide sequences can be used in vaccines and in
CC diagnostic assays. The proteins and nucleotides can be useful for the
CC detection and diagnosis of S. pneumoniae. The protein sequences are also
CC useful for screening an agent capable of antagonizing, inhibiting or
CC interfering with the function or expression of the proteins in which the
CC agent is useful for treatment or prophylaxis of S. pneumoniae infection
CC and meningitis. AAA05591 to AAA05614 represent primers used in the
CC exemplification of the present invention.
XX
XX Sequence 2481 BP; 839 A; 514 C; 538 G; 590 T; 0 other;
SO
Query Match 2.2%; Score 53; DB 21; Length 2481;
Best Local Similarity 100.0%; Pred. No. 3.9e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 983 GCTGATATTATCCCTTCGTTATGTTCAACCATTTGGGTACGAGATTCAAG 1035
Db 1003 GCTGATATTATCCCTTCGTTATGTTCAACCATTTGGGTACGAGATTCAAG 1055
RESULT 18
ABX06705
ID ABX06705 standard; DNA; 2517 BP.
XX
XX
AC ABX06705;
XX
XX
DT 11-FEB-2003 (first entry)
XX
XX
DE S. pneumoniae type 4 strain coding region #993.
XX

KW Gene; ds; bacterial meningitis; pneumonia; sepsis; otitis media;
KM ear infection; antiinflammatory; antibacterial; immunostimulant;
XX auditory; respiratory; gene therapy; vaccine.
XX
XX
OS Streptococcus pneumoniae type 4 strain.
XX
XX
PN WO200277021-A2.
XX
XX
PD 03-OCT-2002.
XX
XX
PF 27-MAR-2002; 2002WO-IB02163.
XX
XX
PR 27-MAR-2001; 2001GB-0007658.
XX
XX
PA (CHIR-) CHIRON SPA.
XX (GENO-) INST GENOMIC RES.
XX
XX Maignani V, Tettelin H, Fraser C;
XX
XX WPI; 2003-040579/03.
XX P-PSDB; ABU01418.
XX
XX
XX New proteins and nucleic acid molecules from Streptococcus pneumoniae,
PT useful as medicaments for treating or preventing a disease or infection
PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
PT or ear infection
XX
XX
PS Claim 6; SEQ ID No 1985; 56pp; English.
XX
XX
XX The invention relates to a protein comprising or having at least 50%
CC identity to any of the 2469 amino acid sequences, identified in the
CC specification (available on a computer readable format), or its fragment,
CC expressed from 2469 of 2489 identified DNA coding regions from the
CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
CC ABS66454. Also included are an antibody which binds one of the
CC proteins, treating a patient by administering the protein, DNA or
CC antibody (in a composition), a kit comprising first and second primers,
CC which are the nucleic acid cited above or fragments between nucleotides
CC 8-100 of a sequence not defined in the specification, for amplifying a
CC target sequence contained within a Streptococcus nucleic acid sequence,
CC where the first primer is substantially complementary to the target
CC sequence and the second primer is substantially complementary to the
CC complement of the target sequence, and where the parts of the primers
CC having substantial complementarity define the termini of the target
CC sequence to be amplified, assay comprising contacting a test compound
CC with the protein, and determining whether the test compound binds to the
CC protein and a Streptococcus pneumoniae bacterium, where one or more
CC genes encoding the proteins has been rendered inactive. The proteins,
CC nucleic acid molecules, antibody and compositions are useful as
CC medicaments for treating or preventing a disease or infection due to
CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia,
CC sepsis, otitis media or ear infection. They are also useful in developing
CC vaccines, diagnostics and antibiotics. The methods are useful for
CC identifying immunodominant proteins. The present sequence is one of
CC the 2489 identified coding region from the genomic sequence.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SO Sequence 2517 BP; 830 A; 509 C; 545 G; 633 T; 0 other;
Query Match 2.2%; Score 53; DB 25; Length 2517;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 983 GCTGATATTATCCCTTCGTTATGTTCAACCATTTGGGTACGAGATTCAAG 1035
Db 1003 GCTGATATTATCCCTTCGTTATGTTCAACCATTTGGGTACGAGATTCAAG 1055
RESULT 19
AAA47602


```

ID  AAA47602 standard; DNA; 2531 BP.
XX
AC  AAA47602;
XX
DT  20-OCT-2000 (first entry)
XX
DE  Recombinant variant of Sp36 gene (Sp36D) of S. pneumoniae.
XX
KW  Streptococcus pneumoniae; infection; vaccine; coiled coil region;
KW  histidine triad residue; Sp36; antibody; otitis media;
KW  nasopharyngeal infection; bronchial infection; bronchitis; sepsis;
KW  meningitis; lobar pneumonia; ds.
XX
CS  Streptococcus pneumoniae.
XX
FH  Key Location/Qualifiers
FT  CDS 1..2517
FT  /tag= a
FT  /product= Sp36D polypeptide
XX
XX  WO200037105-A2.
XX
XX  29-JUN-2000.
XX
XX  21-DEC-1999; 99WO-US30390.
XX
XX  21-DEC-1998; 98US-0113048.
XX
XX  (MEDI-) MEDIMMUNE INC.
XX
XX  Johnson LS, Koenig S, Adamou JB;
XX
XX  WPI: 2000-452129/39.
XX  P-PSDB; AAB01466.
XX
XX  Vaccine useful for prophylaxis and treatment of pneumococcal infections
XX  such as otitis media, nasopharyngeal and bronchial infections,
XX  comprises Streptococcus pneumoniae proteins
XX
XX  Disclosure; Page 57-58; 70pp; English.
XX
XX  Although a number of proteins have been suggested as being involved
XX  in the pathogenicity of Streptococcus pneumoniae, there still remains
XX  a need to identify polypeptides having epitopes in common from
XX  various strains of S. pneumoniae in order to utilise such
XX  polypeptides in vaccines to protect against a wide variety of
XX  S. pneumoniae. New vaccine compositions are described which comprise a
XX  Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino
XX  acids in length that comprise at least one histidine triad residue
XX  (HxxHxH) or a coiled-coil region, or an antibody directed against
XX  these features. The vaccine is useful in protecting against infection
XX  by Streptococcus pneumoniae. The vaccine composition comprising
XX  antibodies to is useful for passive immunization for treating
XX  pneumococcal infections which includes otitis media, nasopharyngeal
XX  and bronchial infections.
XX
XX  Sequence 2531 BP; 836 A; 511 C; 547 G; 637 T; 0 other;
XX
XX  Query Match 2.2%; Score 53; DB 21; Length 2531;
XX  Best Local Similarity 100.0%; Pred. No. 4e-16;
XX  Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY  983 GCTGTAATATTCCTCGTATCGTTCAACCATGGGTACCGATTCAAG 1035
DB  1003 GCTGTAATATTCCTCGTATCGTTCAACCATGGGTACCGATTCAAG 1055
XX
XX  RESULT 20
XX  AAA47605
XX  ID AAA47605 standard; DNA; 2531 BP.
XX  AC AAA47605;
XX

```

```

DT  20-OCT-2000 (first entry)
XX
XX  Recombinant variant of Sp36 gene (Sp36B) of S. pneumoniae.
XX
XX  Streptococcus pneumoniae; infection; vaccine; coiled coil region;
XX  histidine triad residue; Sp36; antibody; otitis media;
XX  nasopharyngeal infection; bronchial infection; bronchitis; sepsis;
XX  meningitis; lobar pneumonia; ds.
XX
XX  Streptococcus pneumoniae.
XX
XX  Key Location/Qualifiers
XX  FT  CDS 1..2531
XX  /tag= a
XX  /product= Sp36B polypeptide
XX
XX  WO200037105-A2.
XX
XX  29-JUN-2000.
XX
XX  21-DEC-1999; 99WO-US30390.
XX
XX  21-DEC-1998; 98US-0113048.
XX
XX  (MEDI-) MEDIMMUNE INC.
XX
XX  Johnson LS, Koenig S, Adamou JB;
XX
XX  WPI: 2000-452129/39.
XX  P-PSDB; AAB01469.
XX
XX  Vaccine useful for prophylaxis and treatment of pneumococcal infections
XX  such as otitis media, nasopharyngeal and bronchial infections,
XX  comprises Streptococcus pneumoniae proteins
XX
XX  Disclosure; Page 69-70; 70pp; English.
XX
XX  Although a number of proteins have been suggested as being involved
XX  in the pathogenicity of Streptococcus pneumoniae, there still remains
XX  a need to identify polypeptides having epitopes in common from
XX  various strains of S. pneumoniae in order to utilise such
XX  polypeptides in vaccines to protect against a wide variety of
XX  S. pneumoniae. New vaccine compositions are described which comprise a
XX  Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino
XX  acids in length that comprise at least one histidine triad residue
XX  (HxxHxH) or a coiled-coil region, or an antibody directed against
XX  these features. The vaccine is useful in protecting against infection
XX  by Streptococcus pneumoniae. The vaccine composition comprising
XX  antibodies to is useful for passive immunization for treating
XX  pneumococcal infections which includes otitis media, nasopharyngeal
XX  and bronchial infections.
XX
XX  Sequence 2531 BP; 861 A; 508 C; 550 G; 609 T; 3 other;
XX
XX  Query Match 2.2%; Score 53; DB 21; Length 2531;
XX  Best Local Similarity 100.0%; Pred. No. 4e-16;
XX  Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY  983 GCTGTAATATTCCTCGTATCGTTCAACCATGGGTACCGATTCAAG 1035
DB  1000 GCTGTAATATTCCTCGTATCGTTCAACCATGGGTACCGATTCAAG 1052
XX
XX  RESULT 21
XX  AAA65737
XX  ID AAA65737 standard; DNA; 2639 BP.
XX  AC AAA65737;
XX
XX  21-NOV-2000 (first entry)
XX
XX  Streptococcus pneumoniae BVH-11-2 gene SEQ ID NO:13.
XX

```


KM Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
 KM prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
 KM otitis media; pneumonia; immunisation; bactericidal; ds.
 OS Streptococcus pneumoniae.
 XX
 PN WO20039299-A2.
 XX
 PD 06-JUL-2000.
 XX
 PF 20-DEC-1999; 99WO-CA01218.
 XX
 XX 23-DEC-1998; 98US-0113800.
 XX
 PA (BIOC-) BIOCHEM PHARMA INC.
 XX
 PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N,
 DR WPI; 2000-452397/39.
 DR P-PSDB; AAB12720.
 XX
 PT Streptococcal antigens useful for vaccinating against e.g. meningitis,
 PT otitis media, bacteraemia and/or pneumonia -
 XX
 PS Example 6; Fig 16; 106pp; English.
 XX
 CC The present invention describes nucleic acids (I) encoding protein
 CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein
 CC antigens, may be used for the recombinant production of the proteins
 CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals
 CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence encodes the
 CC S. pneumoniae BVH-11-2 protein antigen.
 XX
 SQ Sequence 2639 BP; 889 A; 518 C; 567 G; 665 T; 0 other;
 XX
 Query Match 2.2%; Score 53; DB 21; Length 2639;
 Best Local Similarity 100.0%; Pred. No. 4e-16;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 983 GCTCGATTATTCCCTTCGTTATGTTCAACCATTTGGTACGATTCAAG 1035
 DB 1113 GCTCGATTATTCCCTTCGTTATGTTCAACCATTTGGTACGATTCAAG 1165
 XX
 RESULT 22
 ABK15104
 ID ABK15104 standard; DNA; 2639 BP.
 XX
 AC ABK15104;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE DNA encoding Streptococcus pneumoniae BVH-11-2.
 XX
 KM BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
 KM pneumonia; streptococcal bacterial infection; gene; ds; BVH-11-2.
 XX
 OS Streptococcus pneumoniae.
 XX
 XX Key Location/Qualifiers
 FH CDS 114..2630
 FT /*tag= a
 FT /product= "BVH-11-2"
 FT /note= "The gene is flanked by sequences from the
 FT vector SP64, no information on which is
 FT given in the specification"
 XX
 PN WO200198334-A2.
 XX
 PD 27-DEC-2001.
 XX

XX
 PF 19-JUN-2001; 2001WO-CA00908.
 XX
 PR 20-JUN-2000; 2000US-212683P.
 XX
 PA (SHIR-) SHIRE BIOCHEM INC.
 XX
 PI Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
 DR WPI; 2002-122272/16.
 DR P-PSDB; AA075934.
 XX
 PT New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
 PT epitope-bearing polypeptides, useful as vaccine components for treating
 PT or preventing streptococcal infections such as otitis media,
 PT meningitis, and bacteraemia -
 XX
 PS Example 3; Fig 5; 113pp; English.
 XX
 CC The invention describes an isolated polypeptide (I) with 70-90%
 CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
 CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
 CC comprising (I) is useful for therapeutic or prophylactic treatment of
 CC meningitis, otitis media, bacteraemia or pneumonia infection in an
 CC individual susceptible to these disorders. (II) is also useful for
 CC therapeutic or prophylactic treatment of any streptococcal bacterial
 CC infection (e.g., caused by Streptococcus pneumoniae, group A
 CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
 CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardiae or
 CC Streptococcus aureus) in an individual susceptible to the infection.
 CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
 CC techniques. The Streptococcus polypeptides are useful in a diagnostic
 CC test for S. pneumoniae infection. (III) is useful for designing DNA
 CC probes for use in detecting the presence of Streptococcus in a biological
 CC sample suspected of containing the bacteria. The DNA probes may also be
 CC used for detecting circulating S. pneumonia nucleic acid in a sample for
 CC diagnosing streptococcal infections. This sequence encodes the
 CC Streptococcus pneumoniae protein BVH-11-2, used to create the antigenic
 CC peptides described in the method of the invention.
 XX
 SQ Sequence 2639 BP; 889 A; 518 C; 567 G; 665 T; 0 other;
 XX
 Query Match 2.2%; Score 53; DB 24; Length 2639;
 Best Local Similarity 100.0%; Pred. No. 4e-16;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 983 GCTCGATTATTCCCTTCGTTATGTTCAACCATTTGGTACGATTCAAG 1035
 DB 1113 GCTCGATTATTCCCTTCGTTATGTTCAACCATTTGGTACGATTCAAG 1165
 XX
 RESULT 23
 ABS56454
 ID ABS56454 standard; DNA; 2162598 BP.
 XX
 AC ABS56454;
 XX
 DT 10-FEB-2003 (first entry)
 XX
 DE Streptococcus pneumoniae type 4 strain complete genome.
 XX
 KM ds; bacterial meningitis; pneumonia; sepsis; otitis media; genome;
 KM ear infection; antiinflammatory; antibacterial; immunostimulant;
 KM auditory; respiratory; gene therapy; vaccine.
 XX
 OS Streptococcus pneumoniae type 4 strain.
 XX
 PN WO200277021-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 27-MAR-2002; 2002WO-IB02163.
 XX

PR 27-MAR-2001; 2001GB-0007658.
XX
XX (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
XX Maignani V, Tettein H, Fraser C;
XX WPI; 2003-040579/03.
DR
XX
PT New proteins and nucleic acid molecules from Streptococcus pneumoniae,
PT useful as medicaments for treating or preventing a disease or infection
PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
PT or ear infection
XX
XX
PS Claim 17; SEQ ID No 4979; 56pp; English.
XX
XX The invention relates to a protein comprising or having at least 50%
CC identity to any of the 2469 amino acid sequences, identified in the
CC specification (available on a computer readable format), or its fragment,
CC expressed from 2469 of 2489 identified DNA coding regions from the
CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
CC AB556454. Also included are an antibody which binds one of the
CC proteins, treating a patient by administering the protein, DNA or
CC antibody (in a composition), a kit comprising first and second primers,
CC which are the nucleic acid cited above or fragments between nucleotides
CC 8-100 of a sequence not defined in the specification, for amplifying a
CC target sequence contained within a Streptococcus nucleic acid sequence,
CC where the first primer is substantially complementary to the target
CC sequence and the second primer is substantially complementary to the
CC complement of the target sequence, and where the parts of the primers
CC having substantial complementarity define the termini of the target
CC sequence to be amplified, assay comprising contacting a test compound
CC with the protein, and determining whether the test compound binds to the
CC protein and a Streptococcus pneumoniae bacterium, where one or more
CC genes encoding the proteins has been rendered inactive. The proteins,
CC nucleic acid molecules, antibody and compositions are useful as
CC medicaments for treating or preventing a disease or infection due to
CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia,
CC sepsis, otitis media or ear infection. They are also useful in developing
CC vaccines, diagnostics and antibiotics. The methods are useful for
CC identifying immunodominant proteins. The present sequence is the
CC Streptococcus pneumoniae type 4 strain genome sequence.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pcf_sequences.
XX
SQ Sequence 2162598 BP; 654373 A; 427176 C; 431369 G; 649680 T; 0 other;
XX
Query Match 2.2%; Score 53; DB 25; Length 2162598;
Best Local Similarity 100.0%; Pred. No. 5.1e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 983 GCTGTAATATTCCTTCCTGTTATCGTTCAAAACATTGGGTACAGATTCAAG 1035
DB 83951 GCTGTAATATTCCTTCCTGTTATCGTTCAAAACATTGGGTACAGATTCAAG 839003

RESULT 24
AAV52393
ID AAV52393 standard; DNA; 492 BP.
XX
XX AAV52393;
AC
XX 19-JUL-1999 (first entry)
DT
XX
DE Streptococcus pneumoniae complement C3-degrading protease DNA.
XX
XX Human complement C3-degrading protease; vaccine; infection;
KM meningitis; pneumonia; xerograft transplantation; transplant rejection;
KW inflammation; ds.
XX
OS Streptococcus pneumoniae.

XX
XX W09915675-A1.
XX
XX 01-APR-1999.
ED
XX
XX 24-SEP-1998; 98WO-US20186.
XX
XX 24-SEP-1997; 97US-0059907.
PR
XX
XX (AMCY) AMERICAN CYANAMID CO.
PA (MINN) UNITV MINNESOTA.
XX
XX
PI Cheng Q, Finkel DJ, Green BA, Hostetter MK, Masi AW;
XX WPI; 1999-254719/21.
DR P-P.SDB; AAV05752.
XX
XX
PT New isolated human complement C3-degrading proteinase
XX
XX Claim 21; Page 49; 66pp; English.
XX
XX This DNA sequence encodes a 20 kDa protein (see AAV05752) of
CC Streptococcus pneumoniae serotype 3 that is capable of degrading
CC human complement protein C3 (HCP3). It was isolated from a
CC library of insertionally interrupted pneumococcal genes by
CC identifying those clones that had decreased C3 degrading activity
CC as compared to wild-type S. pneumoniae. Alignment of the sequence
CC with the S. pneumoniae (serotype 4) genome showed that the open
CC reading frame that codes for the 20 kDa protein may be part of a
CC larger open reading frame, i.e. a 2163 bp (see AAV5394) in the
CC serotype 4 genome, which encodes a protein of approximately 79
CC kDa (see AAV05753). Amino acids 1-58 and 90-132 of the 20 kDa
CC protein have substantial sequence identity with amino acids 170-227
CC and 258-300 of the 79 kDa protein. Proteins and peptides or
CC polypeptides containing these regions, and DNA sequences encoding
CC them (nucleotides 1-174 and 320-492 of the present sequence) are
CC claimed. HCP3 proteases and polypeptides can be used as immune
CC system stimulating compositions (claimed). They can produce an
CC immune response against S. pneumoniae to immunize or treat a
CC mammalian subject against infection or colonization (claimed).
CC They can produce a B cell response, a T cell response, an
CC epithelial cell response, or an endothelial cell response
CC (claimed). The expression of the proteins on the surface of an
CC organ of an animal used in xenotransplantation can be used to
CC inhibit C3-mediated inflammation and rejection.
XX
SQ Sequence 492 BP; 152 A; 119 C; 98 G; 123 T; 0 other;
XX
Query Match 2.1%; Score 50; DB 20; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 985 TCGTAATATTCCTTCCTGTTATCGTTCAAAACATTGGGTACAGATTCA 1034
DB 185 TCGTAATATTCCTTCCTGTTATCGTTCAAAACATTGGGTACAGATTCA 234

RESULT 25
AAV52488
ID AAV52488 standard; DNA; 973 BP.
XX
XX AAV52488;
AC
XX 23-OCT-1998 (first entry)
DT
XX
DE Streptococcus pneumoniae genome fragment SEQ ID NO:355.
XX
XX Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
KM computer readable medium; vaccine; pharmaceutical composition; ds.
XX
OS Streptococcus pneumoniae.
XX
PN W09818931-A2.

XX The present sequence represents a cloning primer used in an example from
 CC the present invention which describes proteins from Streptococcus
 CC pneumoniae. Nucleic acid sequence encoding Streptococcus pneumoniae
 CC proteins can be useful in vaccines for inducing protective antibodies
 CC against Streptococcus pneumoniae, for treatment or prevention of
 CC infection e.g. pneumonia, otitis media or meningitis. Probes based on
 CC the nucleic acids are used to detect Streptococcus infection (by usual
 CC hybridisation or amplification methods), also for isolating
 CC Streptococcus genes or their allelic variants. The proteins can be used
 CC similarly to detect specific antibodies in standard immunoassays,
 CC especially for diagnosing or monitoring infections. Antibodies which
 CC bind the proteins are used to detect corresponding antigens, to purify
 CC the proteins and for passive immunisation (optionally coupled to a
 CC toxin). Vaccines are administered, e.g. by injection, orally or through
 CC the skin, typically at 0.01-1000 (especially 10-300) µg/ml per dose.
 CC The cloning primers used in the present invention are given in AAV27437
 CC to AAV27562 and AAV39870 to AAV39969.
 CC XX
 SQ Sequence 40 BP; 10 A; 6 C; 7 G; 17 T; 0 other;
 Query Match 1.3%; Score 30; DB 19; Length 40;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2360 CCTTCATCTGTAAGTAAAGAAAAATAAAC 2389
 DB 40 CCTTCATCTGTAAGTAAAGAAAAATAAAC 11
 RESULT 28
 ID AAA47601/c
 AC AAA47601 standard; DNA; 40 BP.
 XX
 XX AAA47601;
 DT 20-OCT-2000 (first entry)
 XX
 DE Primer for amplifying Sp36 gene of S. pneumoniae.
 XX
 KW Streptococcus pneumoniae; infection; vaccine; coiled coil region;
 KW histidine triad residue; Sp36; antibody; otitis media;
 KW nasopharyngeal infection; bronchial infection; bronchitis; sepsis;
 KW meningitis; lobar pneumonia; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200037105-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 21-DEC-1999; 99WO-US30390.
 XX
 PR 21-DEC-1998; 98US-0113048.
 XX
 PA (MEDI-) MEDIMUNE INC.
 XX
 PI Johnson US, Koenig S, Adamou JE;
 XX
 DR WPI: 2000-452129/39.
 PT Vaccine useful for prophylaxis and treatment of pneumococcal infections
 PT such as otitis media, nasopharyngeal and bronchial infections,
 PT comprises Streptococcus pneumoniae proteins
 XX
 PS Example 1; Page 54; 70pp; English.
 XX
 CC Although a number of proteins have been suggested as being involved
 CC in the pathogenicity of Streptococcus pneumoniae, there still remains
 CC a need to identify polypeptides having epitopes in common from
 CC various strains of S. pneumoniae in order to utilise such
 CC polypeptides in vaccines to protect against a wide variety of
 CC S. pneumoniae. New vaccine compositions are described which comprise a

CC Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino
 CC acids in length that comprise at least one histidine triad residue
 CC (HxxHxxH) or a coiled-coil region, or an antibody directed against
 CC these features. The vaccine is useful in protecting against infection
 CC by Streptococcus pneumoniae. The vaccine composition comprising
 CC antibodies to is useful for passive immunization for treating
 CC pneumococcal infections which includes otitis media, nasopharyngeal
 CC and bronchial infections. Three primers (AAA47599-601) were designed
 CC that would amplify the Sp36 gene and allow its cloning into pGEM10
 CC and expression as a histidine tagged protein lacking the signal
 CC sequence for purification by nickel-affinity chromatography.
 CC XX
 SQ Sequence 40 BP; 10 A; 6 C; 7 G; 17 T; 0 other;
 Query Match 1.3%; Score 30; DB 21; Length 40;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2360 CCTTCATCTGTAAGTAAAGAAAAATAAAC 2389
 DB 40 CCTTCATCTGTAAGTAAAGAAAAATAAAC 11
 RESULT 29
 ID ABQ84960/c
 AC ABQ84960 standard; DNA; 40 BP.
 XX
 XX ABQ84960;
 DT 04-SEP-2002 (first entry)
 XX
 DE Streptococcus pneumoniae ORF cloning primer SEQ ID NO:282.
 XX
 KW Streptococcus pneumoniae; epitope; vaccine; antigenic protein;
 KW antibacterial; Streptococcal infection; detection; primer; ss.
 XX
 OS Synthetic.
 XX
 PN US2002061545-A1.
 XX
 PD 23-MAY-2002.
 XX
 PF 22-JAN-2001; 2001US-0765272.
 XX
 PR 30-OCT-1997; 97US-0961083.
 XX
 PA (CHOI/) CHOI G H.
 PA (KUNS/) KUNSCH C A.
 PA (BARA/) BARASH S C.
 PA (DILL/) DILLON P J.
 PA (DOUG/) DOUGHERTY B.
 PA (FANN/) FANNON M R.
 PA (ROSE/) ROSEN C A.
 XX
 PI Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR;
 PI Rosen CA;
 XX
 DR WPI: 2002-479261/51.
 PT New Streptococcus pneumoniae antigens, useful for detecting
 PT Streptococcus and for preventing or attenuating disease caused by
 PT Streptococcus infection -
 XX
 PS Example 1; Page 63; 70pp; English.
 XX
 CC ABQ84792 to ABQ84904 represents nucleic acids which encode the
 CC Streptococcus pneumoniae antigens given in ABP54557 to ABP54669.
 CC The S. pneumoniae antigens have antibacterial activity and can be
 CC used in vaccines. The S. pneumoniae antigens can also be used to
 CC prevent or attenuate a Streptococcal infection in an animal. The
 CC polynucleotides encoding the S. pneumoniae antigens can be used to
 CC detect Streptococcus nucleic acids. ABQ84905 to ABQ85130 represent

CC primers used in the cloning of *S. pneumoniae* ORFs (open reading frames)
 CC which are used in an example from the present invention.
 XX
 SQ Sequence 40 BP; 10 A; 6 C; 7 G; 17 T; 0 other;

Query Match 1.3%; Score 30; DB 24; Length 40;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2360 CCTCATCTGTAGTAAAGGAAAAATTAAC 2389
 Db 40 CCTCATCTGTAGTAAAGGAAAAATTAAC 11

RESULT 30
 ID AAA47599
 AC AAA47599 standard; DNA; 36 BP.

DT 20-OCT-2000 (first entry)

DE Primer for amplifying Sp36 gene of *S. pneumoniae*.

XX Streptococcus pneumoniae; infection; vaccine; coiled coil region;
 XX histidine triad residue; Sp36; antibody; otitis media;
 KW nasopharyngeal infection; bronchial infection; bronchitis; sepsis;
 KW meningitis; lobar pneumonia; primer; ss.

OS Synthetic.

PN WO200037105-A2.

PD 29-JUN-2000.

PF 21-DEC-1999; 99WO-US30390.

PR 21-DEC-1998; 98US-0113048.

PA (MEDI-) MEDIMUNE INC.

XX Johnson LS, Koenig S, Adamou JE;

DR WPI; 2000-452129/39.

PT Vaccine useful for prophylaxis and treatment of pneumococcal infections
 PT such as otitis media, nasopharyngeal and bronchial infections,
 PT comprises Streptococcus pneumoniae proteins
 XX
 PS Example 1; Page 53; 70pp; English.

CC Although a number of proteins have been suggested as being involved
 CC in the pathogenicity of Streptococcus pneumoniae, there still remains
 CC a need to identify polypeptides having epitopes in common from
 CC various strains of *S. pneumoniae* in order to utilize such
 CC polypeptides in vaccines to protect against a wide variety of
 CC *S. pneumoniae*. New vaccine compositions are described which comprise a
 CC Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino
 CC acids in length that comprise at least one histidine triad residue
 CC (HxxHxx) or a coiled-coil region, or an antibody directed against
 CC these features. The vaccine is useful in protecting against infection
 CC by Streptococcus pneumoniae. The vaccine composition comprising
 CC antibodies to its useful for passive immunization for treating
 CC pneumococcal infections which includes otitis media, nasopharyngeal
 CC and bronchial infections. Three primers (AAA47599-601) were designed
 CC that would amplify the Sp36 gene and allow its cloning into pOE10
 CC and expression as a histidine tagged protein lacking the signal
 CC sequence for purification by nickel-affinity chromatography.

XX Sequence 36 BP; 8 A; 8 C; 9 G; 11 T; 0 other;

Query Match 1.1%; Score 27; DB 21; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTAGAGTTGGAGCTGTATCAAGC 27
 Db 10 TTCTTAGAGTTGGAGCTGTATCAAGC 36

RESULT 31
 ID AAV27491
 AC AAV27491 standard; DNA; 37 BP.

DT 02-OCT-1998 (first entry)

DE Streptococcus pneumoniae ORF cloning primer SEQ ID NO:281.

XX Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
 KW detection; pneumonia; otitis media; meningitis; cloning primer; ss.

OS Synthetic.

PN Streptococcus pneumoniae.

PD WO9818930-A2.

PF 07-MAY-1998.

PR 30-OCT-1997; 97WO-US19422.

PA 31-OCT-1996; 96US-0029960.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Choi GH, Hromocky J A, Johnson LS, Kunsch CA;

DR WPI; 1998-272224/24.

PT Nucleic acid encoding antigenic peptide(s) from Streptococcus
 PT pneumoniae - or their epitope-containing fragments, useful in
 PT protective or therapeutic vaccines, and for diagnosis
 XX
 PS Example 1; Page, 106; 118pp; English.

CC The present sequence represents a cloning primer used in an example from
 CC the present invention which describes proteins from Streptococcus
 CC pneumoniae. Nucleic acid sequence encoding Streptococcus pneumoniae
 CC proteins can be useful in vaccines for inducing protective antibodies
 CC against Streptococcus pneumoniae, for treatment or prevention of
 CC infection e.g. pneumonia, otitis media or meningitis. Probes based on
 CC the nucleic acids are used to detect Streptococcus infection (by usual
 CC hybridisation or amplification methods), also for isolating
 CC Streptococcus genes or their allelic variants. The proteins can be used
 CC especially for detecting specific antibodies in standard immunoassays,
 CC bind the proteins are used to detect corresponding antigens, to purify
 CC the proteins and for passive immunisation (optionally coupled to a
 CC toxin). Vaccines are administered, e.g. by injection, orally or through
 CC the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.
 CC The cloning primers used in the present invention are given in AAV27437
 CC to AAV27562 and AAV29870 to AAV39969.

XX Sequence 37 BP; 8 A; 8 C; 10 G; 11 T; 0 other;

Query Match 1.1%; Score 27; DB 19; Length 37;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTAGAGTTGGAGCTGTATCAAGC 27
 Db 11 TTCTTAGAGTTGGAGCTGTATCAAGC 37

RESULT 32

AB084959
ID AB084959 standard; DNA; 37 BP.
AC AB084959;
XX
XX
DT 04-SEP-2002 (first entry)
XX
DE Streptococcus pneumoniae ORF cloning primer SEQ ID NO:281.
XX
XX Streptococcus pneumoniae; epitope; vaccine; antigenic protein;
KM antibacterial; Streptococcal infection; detection; primer; ss.
XX
OS Streptococcus pneumoniae.
XX Synthetic.
XX
XX US2002061545-A1.
XX
XX 23-MAY-2002.
XX
XX 22-JAN-2001; 2001US-0765272.
XX
XX 30-OCT-1997; 97US-0961083.
XX
XX (CHOI/) CHOI G H.
PA (KUNS/) KUNSCH C A.
PA (BARA/) BARASH S C.
PA (DILL/) DILLON P J.
PA (DOUG/) DOUGHERTY B.
PA (FANN/) FANNON M R.
PA (ROSE/) ROSEN C A.
XX
PI Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR;
PI Rosen CA;
XX
XX WPI: 2002-479261/51.
XX
XX New Streptococcus pneumoniae antigens, useful for detecting
PT Streptococcus and for preventing or attenuating disease caused by
PT Streptococcus infection -
XX
PS Example 1; Page 63; 70pp; English.
XX
XX AB084792 to AB084904 represents nucleic acids which encode the
CC Streptococcus pneumoniae antigens given in ABP54557 to ABP54669.
CC The S. pneumoniae antigens have antibacterial activity and can be
CC used in vaccines. The S. pneumoniae antigens can also be used to
CC prevent or attenuate a Streptococcal infection in an animal. The
CC polynucleotides encoding the S. pneumoniae antigens can be used to
CC detect Streptococcus nucleic acids. AB084905 to AB085130 represent
CC primers used in the cloning of S. pneumoniae ORFs (open reading frames)
CC which are used in an example from the present invention.
XX
XX Sequence 37 BP; 8 A; 8 C; 10 G; 11 T; 0 other;
SO

Query Match 1.1%; Score 27; DB 24; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTACGAGTTGGAGCTGTATCAAGC 27
DB 11 TTCTTACGAGTTGGAGCTGTATCAAGC 37

RESULT 33
AAA47600
ID AAA47600 standard; DNA; 35 BP.
XX
XX AAA47600;
XX
XX 20-OCT-2000 (first entry)
XX
XX Primer for amplifying Sp36 gene of S. pneumoniae.
DE
XX

KM Streptococcus pneumoniae; infection; vaccine; coiled coil region;
KM histidine triad residue; Sp36; antibody; otitis media;
KM nasopharyngeal infection; bronchial infection; bronchitis; sepsis;
KM meningitis; lobar pneumonia; primer; ss.
XX
OS Synthetic.
XX
XX WO200037105-A2.
XX
XX 29-JUN-2000.
XX
XX 21-DEC-1999; 99WO-US30390.
XX
XX 21-DEC-1998; 98US-0113048.
XX
XX (MEDI-) MEDIMUNE INC.
XX
XX Johnson LS, Koenig S, Adamou JE;
XX
XX WPI: 2000-452129/39.
XX
XX
XX Vaccine useful for prophylaxis and treatment of pneumococcal infections
PT such as otitis media, nasopharyngeal and bronchial infections,
PT comprises Streptococcus pneumoniae proteins
XX
XX Example 1; Page 53; 70pp; English.
XX
XX Although a number of proteins have been suggested as being involved
CC in the pathogenicity of Streptococcus pneumoniae, there still remains
CC a need to identify polypeptides having epitopes in common from
CC various strains of S. pneumoniae in order to utilize such
CC polypeptides in vaccines to protect against a wide variety of
CC S. pneumoniae. New vaccine compositions are described which comprise a
CC Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino
CC acids in length that comprise at least one histidine triad residue
CC (HxxHxH) or a coiled-coil region, or an antibody directed against
CC these features. The vaccine is useful in protecting against infection
CC by Streptococcus pneumoniae. The vaccine composition comprising
CC antibodies to is useful for passive immunization for treating
CC pneumococcal infections which includes otitis media, nasopharyngeal
CC and bronchial infections. Three primers (AAA47599-601) were designed
CC that would amplify the Sp36 gene and allow its cloning into pCR10
CC and expression as a histidine tagged protein lacking the signal
CC sequence for purification by nickel-affinity chromatography.
XX
XX Sequence 35 BP; 11 A; 7 C; 9 G; 8 T; 0 other;
SO

Query Match 1.1%; Score 26; DB 21; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ACTGTATCAAGCTAGAACGGTTAAGG 41
DB 10 ACTGTATCAAGCTAGAACGGTTAAGG 35

RESULT 34
AAA65762
ID AAA65762 standard; DNA; 33 BP.
XX
XX AAA65762;
XX
XX 21-NOV-2000 (first entry)
XX
XX Streptococcus pneumoniae BVH-11 PCR primer SEQ ID NO:37.
XX
XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KM prophylaxis; therapy; diagnosis; meningitis; bacteremia;
KM otitis media; pneumonia; immunisation; bactericidal; PCR primer; ss.
XX
XX Streptococcus pneumoniae.
OS
XX
XX WO200039299-A2.
XX
XX

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XX 06-JUL-2000.
PD
XX
XX 20-DEC-1999; 99WO-CA01218.
PF
XX
XX 23-DEC-1998; 98US-0113800.
PR
XX
XX (BIOC-) BIOCHEM PHARMA INC.
PA
XX
XX Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
PI
XX WPI; 2000-452397/39.
DR
XX
XX Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT
XX otitis media, bacteraemia and/or pneumonia -
PS
XX Example 8; Page 49; 106pp; English.
XX
XX The present invention describes nucleic acids (I) encoding protein
CC
XX antigens (II) from Streptococcus pneumoniae. The protein antigens
CC
XX have bactericidal activity. The nucleic acids, encoding the protein
CC
XX antigens, may be used for the recombinant production of the proteins
CC
XX they encode. The protein antigens may then be used as vaccines for the
CC
XX prevention and treatment of Streptococcal infections in mammals
CC
XX (especially humans) which result in, e.g. meningitis, otitis media,
CC
XX bacteraemia and/or pneumonia. The present sequence represents a PCR
CC
XX primer for a S. pneumoniae GAS BVH-71 protein antigen, which is used in
CC
XX an example from the present invention.
SQ
XX
XX Sequence 33 BP; 7 A; 9 C; 7 G; 10 T; 0 other;
SQ
XX
XX Query Match 1.0%; Score 25; DB 21; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 0.055;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 998 CTTGCTTATCGTTCAACCATTTGGG 1022
XX
XX 9 CTTGCTTATCGTTCAACCATTTGGG 33
XX
XX
XX RESULT 35
XX ABAK3684
XX ID ABAK3684 standard; DNA; 33 BP.
XX
XX ABAK3684;
XX
XX 08-MAY-2002 (first entry)
XX
XX S. pneumoniae BVH-11 gene, PCR primer HAMJ 282.
XX
XX BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
XX
XX pneumonia; Streptococcal bacterial infection; PCR; primer; ss.
XX
XX Streptococcus pneumoniae.
XX
XX WO200198334-A2.
XX
XX 27-DEC-2001.
XX
XX 19-JUN-2001; 2001WO-CA00908.
XX
XX 20-JUN-2000; 2000US-212683P.
XX
XX (SHIR-) SHIRE BIOCHEM INC.
XX
XX Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
XX
XX WPI; 2002-122272/16.
XX
XX New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
XX
XX epitope-bearing polypeptides, useful as vaccine components for treating
XX
XX or preventing streptococcal infections such as otitis media,
XX
XX meningitis, and bacteraemia

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```

XX
XX Example 1; Page 31; 113pp; English.
PS
XX
XX The invention describes an isolated polypeptide (I) with 70-90%
CC
XX identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC
XX BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC
XX comprising (I) is useful for therapeutic or prophylactic treatment of
CC
XX meningitis, otitis media, bacteraemia or pneumonia infection in an
CC
XX individual susceptible to these disorders. (II) is also useful for
CC
XX therapeutic or prophylactic treatment of any streptococcal bacterial
CC
XX infection (e.g., caused by Streptococcus pneumoniae, group A
CC
XX Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC
XX as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. novae or
CC
XX Staphylococcus aureus) in an individual susceptible to the infection.
CC
XX A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC
XX techniques. The Streptococcus polypeptides are useful in a diagnostic
CC
XX test for S. pneumoniae infection. (III) is useful for designing DNA
CC
XX probes for use in detecting the presence of Streptococcus in a biological
CC
XX sample suspected of containing the bacteria. The DNA probes may also be
CC
XX used for detecting circulating S. pneumonia nucleic acid in a sample for
CC
XX diagnosing streptococcal infections. This sequence represents a primer
CC
XX used for the isolation of S. pneumoniae genes from which the antigenic
CC
XX peptides of the invention are derived.
SQ
XX
XX Sequence 33 BP; 7 A; 9 C; 7 G; 10 T; 0 other;
SQ
XX
XX Query Match 1.0%; Score 25; DB 24; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 0.055;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 998 CTTGCTTATCGTTCAACCATTTGGG 1022
XX
XX 9 CTTGCTTATCGTTCAACCATTTGGG 33
XX
XX
XX RESULT 36
XX AAA65764
XX ID AAA65764 standard; DNA; 34 BP.
XX
XX AAA65764;
XX
XX 21-NOV-2000 (first entry)
XX
XX Streptococcus pneumoniae BVH-11 PCR primer SEQ ID NO:39.
XX
XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
XX
XX prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
XX
XX otitis media; pneumonia; immunisation; bactericidal; PCR primer; ss.
XX
XX Streptococcus pneumoniae.
XX
XX WO200039299-A2.
XX
XX 06-JUL-2000.
XX
XX 20-DEC-1999; 99WO-CA01218.
XX
XX 23-DEC-1998; 98US-0113800.
XX
XX (BIOC-) BIOCHEM PHARMA INC.
XX
XX Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
XX
XX WPI; 2000-452397/39.
XX
XX Streptococcal antigens useful for vaccinating against e.g. meningitis,
XX
XX otitis media, bacteraemia and/or pneumonia -
XX
XX Example 8; Page 49; 106pp; English.
XX
XX The present invention describes nucleic acids (I) encoding protein
CC
XX antigens (II) from Streptococcus pneumoniae. The protein antigens
CC
XX have bactericidal activity. The nucleic acids, encoding the protein
CC

```

CC antigens, may be used for the recombinant production of the proteins
CC they encode. The protein antigens may then be used as vaccines for the
CC prevention and treatment of Streptococcal infections in mammals
CC (especially humans) which result in, e.g. meningitis, otitis media,
CC bacteraemia and/or pneumonia. The present sequence represents a PCR
CC primer for a S. pneumoniae GAS BVH-71 protein antigen, which is used in
CC an example from the present invention.
XX
SQ Sequence 34 BP; 10 A; 8 C; 7 G; 9 T; 0 other;
OY 797 GACATTGATAGTCTTGAACAGC 821
DB 10 GACATTGATAGTCTTGAACAGC 34
Query Match 1.0%; Score 25; DB 21; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 37
ID ABR33686 standard; DNA; 34 BP.
XX ABR33686;
AC
XX ABR33686;
DT 08-MAY-2002 (first entry)
XX
DE S. pneumoniae BVH-11 gene, PCR primer HAMJ 284.
KW BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
KW pneumonia; streptococcal bacterial infection; PCR; primer; ss.
XX
OS Streptococcus pneumoniae.
XX
XX MO200198334-A2.
XX
XX 27-DEC-2001.
XX
XX 19-JUN-2001; 2001WO-CA00908.
XX
XX 20-JUN-2000; 2000US-212683P.
XX
XX (SHIR-) SHIRE BIOCHEM INC.
XX
XX Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
XX WPI; 2002-122272/16.
XX
XX New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
XX pt epitope-bearing polypeptides, useful as vaccine components for treating
XX pt or preventing streptococcal infections such as otitis media,
XX meningitis, and bacteraemia -
XX
XX Example 1; Page 31; 113pp; English.
XX
PS The invention describes an isolated polypeptide (I) with 70-90*
CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC comprising (I) is useful for therapeutic or prophylactic treatment of
CC meningitis, otitis media, bacteraemia or pneumonia infection in an
CC individual susceptible to these disorders. (II) is also useful for
CC therapeutic or prophylactic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. norcardia or
CC Streptococcus aureus) in an individual susceptible to the infection.
CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for S. pneumoniae infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating S. pneumonia nucleic acid in a sample for
CC diagnosing streptococcal infections. This sequence represents a primer

CC used for the isolation of S. pneumoniae genes from which the antigenic
CC peptides of the invention are derived.
XX
SQ Sequence 34 BP; 10 A; 8 C; 7 G; 9 T; 0 other;
OY 797 GACATTGATAGTCTTGAACAGC 821
DB 10 GACATTGATAGTCTTGAACAGC 34
Query Match 1.0%; Score 25; DB 24; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 38
ID ABR33719 standard; DNA; 35 BP.
XX ABR33719;
AC
XX ABR33719;
DT 08-MAY-2002 (first entry)
XX
DE S. pneumoniae BVH-11 gene, PCR primer HAMJ 403.
KW BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
KW pneumonia; streptococcal bacterial infection; PCR; primer; ss.
XX
OS Streptococcus pneumoniae.
XX
XX MO200198334-A2.
XX
XX 27-DEC-2001.
XX
XX 19-JUN-2001; 2001WO-CA00908.
XX
XX 20-JUN-2000; 2000US-212683P.
XX
XX (SHIR-) SHIRE BIOCHEM INC.
XX
XX Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
XX WPI; 2002-122272/16.
XX
XX New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
XX pt epitope-bearing polypeptides, useful as vaccine components for treating
XX pt or preventing streptococcal infections such as otitis media,
XX meningitis, and bacteraemia -
XX
XX Example 1; Page 33; 113pp; English.
XX
PS The invention describes an isolated polypeptide (I) with 70-90*
CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC comprising (I) is useful for therapeutic or prophylactic treatment of
CC meningitis, otitis media, bacteraemia or pneumonia infection in an
CC individual susceptible to these disorders. (II) is also useful for
CC therapeutic or prophylactic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. norcardia or
CC Streptococcus aureus) in an individual susceptible to the infection.
CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for S. pneumoniae infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating S. pneumonia nucleic acid in a sample for
CC diagnosing streptococcal infections. This sequence represents a primer
CC used for the isolation of S. pneumoniae genes from which the antigenic
CC peptides of the invention are derived.
XX
SQ Sequence 35 BP; 10 A; 8 C; 8 G; 9 T; 0 other;

Query Match 1.0%; Score 25; DB 24; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 797 GACATTGATAGTCTCTTGAACAGC 821
DB 11 GACATTGATAGTCTCTTGAACAGC 35

RESULT 39

AAV27414
ID AAV27414 standard; DNA; 1342 BP.

AC AAV27414;

DT 02-OCT-1998 (first entry)

DE Streptococcus pneumoniae SPI03 nucleotide.

KW Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
XX detection; pneumonia; otitis media; meningitis; ss.

OS Streptococcus pneumoniae.

XX Key Location/Qualifiers

FT CDS 2..1342

FT /tag= a

FT /product= "SPI03"

FT /note= "no stop codon given"

PN W09818930-A2.

PD 07-MAY-1998.

PF 30-OCT-1997; 97WO-US19422.

PR 31-OCT-1996; 96US-0023960.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Choi GH, Hromockyj A, Johnson LS, Kunsch CA;

DR WPI: 1998-272224/24.

DR P-PSDB; AAW61228.

XX Nucleic acid encoding antigenic peptide(s) from Streptococcus
PT pneumoniae - or their epitope-containing fragments, useful in
XX protective or therapeutic vaccines, and for diagnosis

PS Claim 1; Page 85; 118pp; English.

CC The present sequence encodes a protein from Streptococcus pneumoniae.
CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein
CC can be useful in vaccines for inducing protective antibodies against
CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.
CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid
CC are used to detect Streptococcus infection (by usual hybridisation or
CC amplification methods), also for isolating Streptococcus genes or their
CC allelic variants. The protein can be used similarly for detecting specific
CC antibodies in standard immunoassays, especially for diagnosing or
CC monitoring infections. Antibodies which bind the protein are used to
CC detect corresponding antigens, to purify the protein and for passive
CC immunisation (optionally coupled to a toxin). Vaccines are administered,
CC e.g. by injection, orally or through the skin, typically at 0.01-1000
CC (especially 10-300) μ g/ml per dose.

CC Sequence 1342 BP; 451 A; 270 C; 261 G; 360 T; 0 other;

QY Query Match 1.0%; Score 24; DB 19; Length 1342;

Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 546 ATGCTTATATCGTCTCCTCATGAG 569

DB 525 ATGCTTATATCGTCTCCTCATGAG 548

RESULT 40

ABQ84882
ID ABQ84882 standard; DNA; 1342 BP.

AC ABQ84882;

DT 04-SEP-2002 (first entry)

DE S. pneumoniae SPI03 nucleotide sequence SEQ ID NO:181.

KW Streptococcus pneumoniae; epitope; vaccine; antigenic protein;
XX antibacterial; Streptococcal infection; detection; gene; ds.

OS Streptococcus pneumoniae.

PN US2002061545-A1.

PD 23-MAY-2002.

PF 22-JAN-2001; 2001US-0765272.

PR 30-OCT-1997; 97US-0961083.

PA (CHOI/) CHOI G H.

PA (KUNS/) KUNSCH C A.

PA (BARA/) BARASH S C.

PA (DILL/) DILLON P J.

PA (DOUG/) DOUGHERTY B.

PA (FANN/) FANNON M R.

PA (ROSE/) ROSEN C A.

PI Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR;

PI Rosen CA;

DR WPI: 2002-479261/51.

DR P-PSDB; ABP54647.

XX New Streptococcus pneumoniae antigens, useful for detecting
PT Streptococcus and for preventing or attenuating disease caused by
PT Streptococcus infection -

PS Claim 1; Page 45; 70pp; English.

CC ABQ84792 to ABQ84904 represents nucleic acids which encode the
CC Streptococcus pneumoniae antigens given in ABP54557 to ABP54669.
CC The S. pneumoniae antigens have antibacterial activity and can be
CC used in vaccines. The S. pneumoniae antigens can also be used to
CC prevent or attenuate a Streptococcal infection in an animal. The
CC polynucleotides encoding the S. pneumoniae antigens can be used to
CC detect Streptococcus nucleic acids. ABQ84905 to ABQ85130 represent
CC primers used in the cloning of S. pneumoniae ORFs (open reading frames)
CC which are used in an example from the present invention.

CC Sequence 1342 BP; 451 A; 270 C; 261 G; 360 T; 0 other;

QY Query Match 1.0%; Score 24; DB 24; Length 1342;

Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 546 ATGCTTATATCGTCTCCTCATGAG 569

DB 525 ATGCTTATATCGTCTCCTCATGAG 548

RESULT 41

ABN66839
ID ABN66839 standard; DNA; 1398 BP.

XX AC ABN66839;

XX	01-JUL-2002	(first entry)
DT		
XX	Streptococcus polynucleotide SEQ ID NO 1591.	
DE		
XX	Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;	
XX	group A streptococcus; Streptococcus pyogenes; antibacterial; gene;	
KW	antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.	
KX		
XX	Streptococcus agalactiae.	
OS		
XX	WO200234771-A2.	
PN		
XX	02-MAY-2002.	
PD		
XX	29-OCT-2001; 2001WO-GB04789.	
PF		
XX	27-OCT-2000; 2000GB-0026333.	
PR	24-NOV-2000; 2000GB-0028727.	
XX	07-MAR-2001; 2001GB-0005640.	
PR		
XX	(CHIR-) CHIRON SPA.	
PA	(GENO-) INST GENOMIC RES.	
XX		
PI	Telford J, Maignani V, Margarit Ros YI, Grandi G, Fraser C;	
PL	Tetcellin H;	
XX	W21; 2002-352536/38.	
DR	P-PSDB; ABP26208.	
XX		
PT	New Streptococcus protein for the treatment or prevention of infection	
PT	or disease caused by Streptococcus bacteria, such as meningitis, and	
XX	for detecting a compound that binds to the protein -	
PS	Claim 7; Page 3309-3310; 4525pp; English.	
XX		
CC	The invention relates to a protein (ABP25413-ABP30895) from group B	
CC	Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS	
CC	(Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in	
CC	the specification. The proteins have antibacterial and antiinflammatory	
CC	activity. (i), nucleic acids encoding (i), ABN6004-ABN71526 and	
CC	antibodies that bind (i) are used in the manufacture of medicaments for	
CC	the treatment or prevention of infection or disease caused by	
CC	Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.	
CC	Nucleic acids encoding (i) are used to detect Streptococcus in a	
CC	biological sample. (i) is used to determine whether a compound binds to	
CC	(i). A composition comprising (i) or a nucleic acid encoding (i), may be	
CC	used as a vaccine or diagnostic composition. The disease caused by	
CC	Streptococcus that is prevented or treated may be meningitis. Nucleic	
CC	acid encoding (i) may be used to recombinantly produce (i) and may be	
CC	used in gene therapy. Antibodies to (i) are used for affinity	
CC	chromatography, immunoassays, and distinguishing/identifying	
CC	Streptococcus proteins.	
XX		
XX	Sequence 1398 BP; 502 A; 273 C; 271 G; 352 T; 0 other;	
QY		
Query Match	1.0%; Score 24; DB 24; Length 1398;	
Best Local Similarity	100.0%; Pred. No. 0.21;	
Matches	24; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
DB		
485	CGCTATCTACTACAGATGATGTTAT 508	
583	CGCTATCTACTACAGATGATGTTAT 606	
RESULT 42		
ID	AAA65733 standard; DNA; 1455 BP.	
XX	AAA65733;	
XX		
DT	21-NOV-2000 (first entry)	
XX		

DE	Streptococcus pneumoniae BVH-3A gene SEQ ID NO:7.
XX	
KM	Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW	prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
XX	otitis media; pneumonia; immunisation; bactericidal; ds.
OS	Streptococcus pneumoniae.
XX	
PN	WO200039289-A2.
PD	06-JUL-2000.
XX	
PE	20-DEC-1999; 99WO-CA01218.
XX	
PR	23-DEC-1998; 98US-0113800.
XX	
PA	(BIOC-) BIOCHEM PHARMA INC.
XX	
PI	Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
XX	
DR	WI; 2000-452397/39.
DR	P-PSDB; AAB12718.
PT	Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT	otitis media, bacteraemia and/or pneumonia -
XX	
PS	Disclosure; Fig 7; 106pp; English.
XX	
CC	The present invention describes nucleic acids (I) encoding protein
CC	antigens (II) from Streptococcus pneumoniae. The protein antigens
CC	have bactericidal activity. The nucleic acids, encoding the protein
CC	antigens, may be used for the recombinant production of the proteins
CC	they encode. The protein antigens may then be used as vaccines for the
CC	prevention and treatment of Streptococcal infections in mammals
CC	(especially humans) which result in, e.g. meningitis, otitis media,
CC	bacteraemia and/or pneumonia. The present sequence encodes the
XX	S. pneumoniae BVH-3A protein antigen.
QO	Sequence 1455 BP; 491 A; 286 C; 285 G; 393 T; 0 other;
Query Match	1.0%; Score 24; DB 21; Length 1455;
Best Local Similarity	100.0%; Pred. No. 0.21;
Matches	24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	546 ATGCTTATATGTTCTCATGAG 569 596 ATGCTTATATGTTCTCATGAG 619
Db	
RESULT 43	
AAAA47603	
ID	AAAA47603 standard; DNA; 1455 BP.
XX	
AC	AAA47603;
XX	
DT	20-OCT-2000 (first entry)
XX	
DE	Recombinant variant of Sp36 gene (Sp36E) of S. pneumoniae.
XX	
KM	Streptococcus pneumoniae; infection; vaccine; coiled coil region;
KW	histidine triad residue; Sp36; antibody; otitis media;
KW	nasopharyngeal infection; bronchial infection; bronchitis; sepsis;
XX	meningitis; lobar pneumonia; ds.
OS	Streptococcus pneumoniae.
XX	
FH	. Key Location/Qualifiers
CDS	1..1455
FT	/tag= a
ET	/product= sp36E polypeptide
XX	
PN	WO200037105-A2.
XX	

```

PD 29-JUN-2000.
XX
XX 21-DEC-1999; 99WO-US0390.
XX
XX 21-DEC-1998; 98US-0113048.
XX
XX (MEDI-) MEDIMUNE INC.
XX
XX Johnson LS, Koenig S, Adamou JE;
XX
XX MPI; 2000-452129/39.
XX
XX P-PSDB; AAB01467.
XX
XX Vaccine useful for prophylaxis and treatment of pneumococcal infections
XX such as otitis media, nasopharyngeal and bronchial infections,
XX comprises Streptococcus pneumoniae proteins
XX
XX Disclosure; Page 60-61; 70pp; English.
XX
XX Although a number of proteins have been suggested as being involved
XX in the pathogenicity of Streptococcus pneumoniae, there still remains
XX a need to identify polypeptides having epitopes in common from
XX various strains of S. pneumoniae in order to utilise such
XX polypeptides in vaccines to protect against a wide variety of
XX S. pneumoniae. New vaccine compositions are described which comprise a
XX Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino
XX acids in length that comprise at least one histidine triad residue
XX (HxxHxx) or a coiled-coil region, or an antibody directed against
XX these features. The vaccine is useful in protecting against infection
XX by Streptococcus pneumoniae. The vaccine composition comprising
XX antibodies to is useful for passive immunization for treating
XX pneumococcal infections which includes otitis media, nasopharyngeal
XX and bronchial infections.
XX
SQ Sequence 1455 BP; 491 A; 287 C; 285 G; 392 T; 0 other;

Query Match          1.0%; Score 24; DB 21; Length 1455;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 546 ATGCTTATATCGTTCTCATGAG 569
DB 596 ATGCTTATATCGTTCTCATGAG 619

RESULT 44
AAA05473
ID AAA05473 standard; DNA; 1455 BP.
XX
XX AAA05473;
XX
XX 24-MAY-2000 (first entry)
XX
XX Streptococcus pneumoniae type 4 nucleotide sequence 4138.1.
XX
XX Streptococcus pneumoniae; vaccine; screening; protein antigen;
XX antibacterial; antiinflammatory; meningitis; infection; diagnosis;
XX pneumococcal disease; ds.
XX
XX Streptococcus pneumoniae.
XX
XX WO200006737-A2.
XX
XX 10-FEB-2000.
XX
XX 27-JUL-1999; 99WO-GB02451.
XX
XX 27-JUL-1998; 98GB-0016337.
XX
XX 19-MAR-1999; 99US-0125164.
XX
XX (MICR-) MICROBIAL TECHNIQS LTD.
XX
XX Gilbert CFG, Hansbro PM;
XX
PI

```

```

XX
XX MPI; 2000-195300/17.
XX
XX New Streptococcal protein, useful as a vaccine, for diagnosis of
XX pneumococcal diseases and for screening agents capable of antagonizing
XX or inhibiting expression of the protein
XX
XX Claim 7; Page 41-42; 108pp; English.
XX
XX AA081501 to AA081679 represent specifically claimed protein sequences
XX isolated from Streptococcus pneumoniae. AA05407 to AA0590 represent
XX specifically claimed nucleotide sequences isolated from S. pneumoniae.
XX The sequences have antibacterial and antiinflammatory properties.
XX The protein sequences, and fragments of them, are useful as immunogens
XX and/or antigens. The nucleotide sequences can be used in vaccines and in
XX diagnostic assays. The proteins and nucleotides can be useful for the
XX detection and diagnosis of S. pneumoniae. The protein sequences are also
XX useful for screening an agent capable of antagonizing, inhibiting or
XX interfering with the function or expression of the proteins in which the
XX agent is useful for treatment or prophylaxis of S. pneumoniae infection
XX and meningitis. AA05591 to AA05614 represent primers used in the
XX exemplification of the present invention.
XX
SQ Sequence 1455 BP; 491 A; 287 C; 285 G; 392 T; 0 other;

Query Match          1.0%; Score 24; DB 21; Length 1455;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 546 ATGCTTATATCGTTCTCATGAG 569
DB 596 ATGCTTATATCGTTCTCATGAG 619

RESULT 45
AA091804
ID AA091804 standard; DNA; 1455 BP.
XX
XX AA091804;
XX
XX 02-JUN-2000 (first entry)
XX
XX Streptococcus pneumoniae DNA sequence ID128.
XX
XX Streptococcus pneumoniae infection; immunogen; antigen; diagnosis; AIDS;
XX bacterial pneumonia; asplenia; heart disease; lung disease; alcoholism;
XX kidney disease; diabetes; immunosuppressive disorder; otitis media;
XX pneumococcal septicaemia; sinusitis; meningitis; therapy; ss.
XX
XX Streptococcus pneumoniae.
XX
XX WO200006738-A2.
XX
XX 10-FEB-2000.
XX
XX 27-JUL-1999; 99WO-GB02452.
XX
XX 27-JUL-1998; 98GB-0016336.
XX
XX 19-MAR-1999; 99US-0125329.
XX
XX (MICR-) MICROBIAL TECHNIQS LTD.
XX
XX Le Page RWF, Wells JM, Hannify SB, Hansbro PM;
XX
XX MPI; 2000-195301/17.
XX
XX P-PSDB; AA081708.
XX
XX Streptococcal proteins and polynucleotides useful for diagnosis,
XX treatment and prophylaxis of bacterial infections
XX
XX Claim 1; Page 39; 76pp; English.
XX
XX This sequence encodes a Streptococcus pneumoniae protein of the
XX
XX

```

invention. The proteins (or their homologues, derivatives and/or fragments) are useful as immunogens or antigens. Immunogenic or antigenic compositions comprising the proteins are useful as vaccines and also in diagnostic assays. The sequences are useful for the detection or diagnosis of *S. pneumoniae* infection, by contacting a sample to be tested with them. Agents capable of antagonising, inhibiting or interfering with the function or expression of the protein or polypeptide are useful in medical compositions in the treatment or prophylaxis of *S. pneumoniae* infection. As the sequences can be used to treat *S. pneumoniae* infection, they can be used to treat bacterial pneumonia, which has high rates in young children, the elderly, and in patients with predisposing conditions such as asplenia, heart, lung and kidney disease, diabetes, alcoholism, or with immunosuppressive disorders, especially AIDS. They can also be used to treat pneumococcal septicaemia, otitis media, sinusitis, and meningitis.

Sequence 1455 BP; 491 A; 287 C; 285 G; 392 T; 0 other;

Query Match 1.0%; Score 24; DB 21; Length 1455;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 546 ATGCTTATATGTTCTCATGAG 569
DB 596 ATGCTTATATGTTCTCATGAG 619

RESULT 46
AAA65738
ID AAA65738 standard; DNA; 2528 BP.
AC AAA65738;
XX
XX 21-NOV-2000 (first entry)
DT
XX Streptococcus pneumoniae SP63 BVH-3 gene SEQ ID NO:15.
DE
XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KW otitis media; pneumonia; immunisation; bactericidal; ds.
XX Streptococcus pneumoniae.
OS
XX MO200039299-A2.
PN
XX 06-JUL-2000.
XX
XX 20-DEC-1999; 99WO-CA01218.
PF
XX 23-DEC-1998; 98US-0113800.
PR
XX (BIOC-) BIOCHEM PHARMA INC.
PA
XX Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
P1
XX MPI: 2000-452397/39.
DR
XX P-PSDB; AAB12721.
DR
XX Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT otitis media, bacteraemia and/or pneumonia -
PT
XX Example 6; Fig 18; 106pp; English.
PS
XX The present invention describes nucleic acids (I) encoding protein
CC antigens (II) from Streptococcus pneumoniae. The protein antigens
CC have bactericidal activity. The nucleic acids, encoding the protein
CC antigens, may be used for the recombinant production of the proteins
CC they encode. The protein antigens may then be used as vaccines for the
CC prevention and treatment of Streptococcal infections in mammals
CC (especially humans) which result in, e.g. meningitis, otitis media,
CC bacteraemia and/or pneumonia. The present sequence encodes the
CC *S. pneumoniae* SP63 BVH-3 protein antigen.
XX

Sequence 2528 BP; 960 A; 398 C; 505 G; 665 T; 0 other;

Query Match 1.0%; Score 24; DB 21; Length 2528;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 546 ATGCTTATATGTTCTCATGAG 569
DB 536 ATGCTTATATGTTCTCATGAG 559

RESULT 47
ABK15105
ID ABK15105 standard; cDNA; 2528 BP.
XX
XX ABK15105;
AC
XX 08-MAY-2002 (first entry)
DT
XX DNA encoding Streptococcus pneumoniae BVH-3 version #2.
DE
XX BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
KW pneumonia; streptococcal bacterial infection; gene; ss.
KM
XX Streptococcus pneumoniae.
XX
XX
XX Key Location/Qualifiers
FH 1.2523
FT /*tag= a
FT /product= "BVH-3"
FT
XX MO200198334-A2.
XX
XX 27-DEC-2001.
PD
XX 19-JUN-2001; 2001WO-CA00908.
PF
XX 20-JUN-2000; 2000US-212683P.
PR
XX (SHIR-) SHIRE BIOCHEM INC.
PA
XX Hamel J, Quellet C, Charland N, Martin D, Brodeur B;
P1
XX MPI: 2002-122272/16.
DR
XX P-PSDB; AAU76151.
DR
XX New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
PT epitope-bearing polypeptides, useful as vaccine components for treating
PT or preventing Streptococcal infections such as otitis media,
PT meningitis, and bacteraemia -
PT
XX Example 8; Fig 9; 113pp; English.
PS
XX The invention describes an isolated polypeptide (I) with 70-90%
CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC comprising (I) is useful for therapeutic or prophylactic
CC treatment of meningitis, otitis media, bacteraemia or pneumonia infection
CC in an individual susceptible to these disorders. (II) is also useful for
CC therapeutic or prophylactic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, *S. dysgalactiae*, *S. uberis*, *S. novarcia* or
CC *Streptococcus aureus*) in an individual susceptible to the infection.
CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for *S. pneumoniae* infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating *S. pneumonia* nucleic acid in a sample for
CC diagnosing streptococcal infections. This sequence encodes the
CC Streptococcus pneumoniae protein BVH-3, used to create the antigenic
CC peptides described in the method of the invention.
CC


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Db      596 ATGCTTATCGTTCCTCATGAG 619
|||||
RESULT 50
AAA65735
ID      AAA65735 standard; DNA; 5048 BP.
XX
XX      AAA65735;
AC
XX      21-NOV-2000 (first entry)
DT
XX      Streptococcus pneumoniae BVH-3 gene SEQ ID NO:11.
DE
XX      Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
XX      prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KW      otitis media; pneumonia; immunisation; bactericidal; ds.
XX
XX      Streptococcus pneumoniae.
OS
XX      WO200039299-A2.
XX      06-JUL-2000.
XX
XX      20-DEC-1999; 99WO-CA01218.
XX      23-DEC-1998; 98US-0113800.
XX      (BIOC-) BIOCHEM PHARMA INC.
PA
XX      Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
XX      WPI; 2000-452397/39.
XX      Streptococcal antigens useful for vaccinating against e.g. meningitis,
XX      otitis media, bacteraemia and/or pneumonia -
XX      Example 6; Fig 14; 106pp; English.
XX
XX      The present invention describes nucleic acids (I) encoding protein
XX      antigens (II) from Streptococcus pneumoniae. The protein antigens
XX      have bactericidal activity. The nucleic acids, encoding the protein
XX      antigens, may be used for the recombinant production of the proteins
XX      they encode. The protein antigens may then be used as vaccines for the
XX      prevention and treatment of streptococcal infections in mammals
XX      (especially humans) which result in, e.g. meningitis, otitis media,
XX      bacteraemia and/or pneumonia. The present sequence encodes the
XX      S. pneumoniae BVH-3 protein antigen.
XX
XX      Sequence 5048 BP; 1709 A; 907 C; 1104 G; 1328 T; 0 other;
SQ
Query Match      1.0%; Score 24; DB 21; Length 5048;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      546 ATGCTTATCGTTCCTCATGAG 569
Db      2372 ATGCTTATCGTTCCTCATGAG 2395
|||||
RESULT 51
ABK15101
ID      ABK15101 standard; DNA; 5048 BP.
XX
XX      ABK15101;
AC
XX      08-MAY-2002 (first entry)
DT
XX      DNA encoding Streptococcus pneumoniae BVH-3 version #1.
DE
XX      BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
KW      pneumonia; streptococcal bacterial infection; gene; ds.
XX

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```

OS      Streptococcus pneumoniae.
XX
XX      Location/Qualifiers
FH      Key      1777..4896
FT      CDS
FT
FT      /tag=a
FT      /product="BVH-3"
FT      /note="The gene is flanked by sequences from the
FT      vector Sp64, no information on which is
FT      given in the specification"
XX
XX      WO200198334-A2.
XX      27-DEC-2001.
XX
XX      19-JUN-2001; 2001WO-CA09098.
XX      20-JUN-2000; 2000US-212683P.
XX      (SHIR-) SHIRE BIOCHEM INC.
XX
XX      Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
XX      WPI; 2002-122272/16.
XX      P-PSDB; AAU75932.
XX
XX      New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
XX      epitope-bearing polypeptides, useful as vaccine components for treating
XX      or preventing streptococcal infections such as otitis media,
XX      meningitis, and bacteraemia -
XX      Example 3; Fig 2; 113pp; English.
XX
XX      The invention describes an isolated polypeptide (I) with 70-90%
XX      identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
XX      BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
XX      comprising (I) is useful for therapeutic or prophylactic treatment of
XX      meningitis, otitis media, bacteraemia or pneumonia infection in an
XX      individual susceptible to these disorders. (II) is also useful for
XX      therapeutic or prophylactic treatment of any streptococcal bacterial
XX      infection (e.g., caused by Streptococcus pneumoniae, group A
XX      Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
XX      as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. novacida or
XX      S. pharyngosus) in an individual susceptible to the infection.
XX      A polynucleotide (III) encoding (I) is useful in DNA immunisation
XX      techniques. The Streptococcus polypeptides are useful in a diagnostic
XX      test for S. pneumoniae infection. (III) is useful for designing DNA
XX      probes for use in detecting the presence of Streptococcus in a biological
XX      sample suspected of containing the bacteria. The DNA probes may also be
XX      used for detecting circulating S. pneumonia nucleic acid in a sample for
XX      diagnosing streptococcal infections. This sequence encodes the
XX      Streptococcus pneumoniae protein BVH-3, used to create the antigenic
XX      peptides described in the method of the invention.
XX
XX      Sequence 5048 BP; 1709 A; 907 C; 1104 G; 1328 T; 0 other;
SQ
Query Match      1.0%; Score 24; DB 24; Length 5048;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      546 ATGCTTATCGTTCCTCATGAG 569
Db      2372 ATGCTTATCGTTCCTCATGAG 2395
|||||
RESULT 52
AAV52325/C
ID      AAV52325 standard; DNA; 6867 BP.
XX
XX      AAV52325;
AC
XX      23-OCT-1998 (first entry)
DT
XX      Streptococcus pneumoniae genome fragment SEQ ID NO:192.
DE

```

XX Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
 KW computer readable medium; vaccine; pharmaceutical composition; ds.
 XX
 OS Streptococcus pneumoniae.

XX WO9818931-A2.

XX 07-MAY-1998.

XX 30-OCT-1997; 97WO-US19588.

XX 31-OCT-1996; 96US-0029960.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M,
 PI Kunsch CA, Rosen CA;
 XX WPI, 1998-272225/24.

PT Computer-readable medium with recorded Streptococcus pneumoniae
 PT polynucleotide sequences - useful in diagnostic kits and assays, and
 PT pharmaceutical compositions and vaccines for Streptococcus
 PS pneumoniae

Claim 1; Page 1157-1161; 1409pp; English.

XX The present invention describes a computer readable medium which has
 CC the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)
 CC recorded on it, or a representative fragment or a sequence at least 95%
 CC identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in
 CC SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
 CC Streptococcus pneumoniae. The present invention also describes an
 CC isolated nucleic acid molecule encoding a homologue of any of the
 CC fragments of the S. pneumoniae genome (SEQ ID NO:1 to 391) where the
 CC nucleic acid molecule is produced by a process comprising: (a) screening
 CC a genomic DNA library using as a probe a target sequence defined by any
 CC of the sequences in SEQ ID NO:1 to 391, identifying members of the
 CC library which contain sequences that hybridise to the target sequence and
 CC isolating the nucleic acid molecules from the members; or (b) isolating
 CC mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid
 CC molecules whose nucleotide sequence is homologous to amplification
 CC primers derived from the fragment of the S. pneumoniae genome to prime
 CC the amplification and isolating the amplified sequences. The computer
 CC readable medium can be used in a computer-based system for identifying
 CC fragments of the S. pneumoniae genome of commercial importance, or
 CC expression modulating fragments of the S. pneumoniae genome. Products
 CC from the present invention can be used in diagnosis kits and assays, and
 CC pharmaceutical compositions and vaccines for S. pneumoniae.

XX Sequence 6867 BP; 1896 A; 1325 C; 1212 G; 2433 T; 1 other;

Query Match 1.0%; Score 24; DB 19; Length 6867;
 Best Local Similarity 100.0%; Pred. No. 0.22;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 546 ATGCTTATATCGTCTCATGGAG 569

DB 6190 ATGCTTATATCGTCTCATGGAG 6167

RESULT 53

ABN71527/c

ID ABN71527 standard; DNA; 2155561 BP.

XX ABN71527;

DT 02-JUL-2002 (first entry)

XX Streptococcus polynucleotide SEQ ID NO 10967.

XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

KW group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
 KW anti-inflammatory; infection; vaccine; meningitis; gene therapy; ds.
 XX
 OS Streptococcus sp.

XX WO200234771-A2.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB04789.

XX 27-OCT-2000; 2000GB-0026333.

XX 24-NOV-2000; 2000GB-0028727.

XX 07-MAR-2001; 2001GB-0005640.

XX (CHIR-) CHIRON SPA.

XX (GENO-) INST GENOMIC RES.

XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettein H;
 XX WPI, 2002-352536/38.

PT New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -

Claim 8; Page 4196-4488; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B
 CC Streptococcus pyogenes (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and anti-inflammatory
 CC activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and
 CC antibodies that bind (1) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (1) are used to detect Streptococcus in a
 CC biological sample. (1) is used to determine whether a compound binds to
 CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (1) may be used to recombinantly produce (1) and may be
 CC used in gene therapy. Antibodies to (1) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

XX Sequence 2155561 BP; 695741 A; 385320 C; 382958 G; 691542 T; 0 other;

Query Match 1.0%; Score 24; DB 24; Length 2155561;

Best Local Similarity 100.0%; Pred. No. 0.27; Mismatches 0; Indels 0; Gaps 0;

OY 485 CGTATACAGATGATGTTAT 508

DB 1890709 CGTATACAGATGATGTTAT 1890686

RESULT 54

AAC37581

ID AAC37581 standard; DNA; 1547 BP.

XX AAC37581;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 17910.

XX Hybridisation assay; genetic mapping; gene expression control;

XX protein identification; signal transduction pathway;

XX metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX	EP1033405-A2.		PR	01-JUL-1999;	99US-0141842.
PN			PR	01-JUL-1999;	99US-0142154.
XX	06-SEP-2000.		PR	02-JUL-1999;	99US-0142055.
PD			PR	06-JUL-1999;	99US-0142390.
XX			PR	08-JUL-1999;	99US-0142803.
PF	25-FEB-2000; 2000EP-0301439.		PR	09-JUL-1999;	99US-0142920.
XX			PR	12-JUL-1999;	99US-0142977.
XX			PR	13-JUL-1999;	99US-0143542.
PR	25-FEB-1999;	99US-0121825.	PR	14-JUL-1999;	99US-0143624.
PR	05-MAR-1999;	99US-0123180.	PR	15-JUL-1999;	99US-0144005.
PR	09-MAR-1999;	99US-0123548.	PR	16-JUL-1999;	99US-0144085.
PR	23-MAR-1999;	99US-0125788.	PR	16-JUL-1999;	99US-0144085.
PR	25-MAR-1999;	99US-0126264.	PR	16-JUL-1999;	99US-0144086.
PR	29-MAR-1999;	99US-0126785.	PR	19-JUL-1999;	99US-0144325.
PR	01-APR-1999;	99US-0127462.	PR	19-JUL-1999;	99US-0144331.
PR	06-APR-1999;	99US-0128234.	PR	19-JUL-1999;	99US-0144332.
PR	08-APR-1999;	99US-0128714.	PR	19-JUL-1999;	99US-0144333.
PR	16-APR-1999;	99US-0129845.	PR	19-JUL-1999;	99US-0144334.
PR	19-APR-1999;	99US-0130077.	PR	19-JUL-1999;	99US-0144335.
PR	21-APR-1999;	99US-0130449.	PR	20-JUL-1999;	99US-0144352.
PR	23-APR-1999;	99US-0130510.	PR	20-JUL-1999;	99US-0144632.
PR	23-APR-1999;	99US-0130891.	PR	20-JUL-1999;	99US-0144884.
PR	28-APR-1999;	99US-0131449.	PR	21-JUL-1999;	99US-0144814.
PR	30-APR-1999;	99US-0132048.	PR	21-JUL-1999;	99US-0145086.
PR	30-APR-1999;	99US-0132407.	PR	21-JUL-1999;	99US-0145088.
PR	04-MAY-1999;	99US-0132484.	PR	22-JUL-1999;	99US-0145085.
PR	05-MAY-1999;	99US-0132485.	PR	22-JUL-1999;	99US-0145087.
PR	06-MAY-1999;	99US-0132486.	PR	22-JUL-1999;	99US-0145089.
PR	06-MAY-1999;	99US-0132487.	PR	22-JUL-1999;	99US-0145192.
PR	07-MAY-1999;	99US-0132863.	PR	23-JUL-1999;	99US-0145115.
PR	11-MAY-1999;	99US-0134256.	PR	23-JUL-1999;	99US-0145218.
PR	14-MAY-1999;	99US-0134218.	PR	23-JUL-1999;	99US-0145224.
PR	14-MAY-1999;	99US-0134219.	PR	26-JUL-1999;	99US-0145276.
PR	14-MAY-1999;	99US-0134321.	PR	27-JUL-1999;	99US-0145913.
PR	14-MAY-1999;	99US-0134370.	PR	27-JUL-1999;	99US-0145918.
PR	18-MAY-1999;	99US-0134768.	PR	27-JUL-1999;	99US-0145919.
PR	19-MAY-1999;	99US-0134941.	PR	28-JUL-1999;	99US-0145951.
PR	20-MAY-1999;	99US-0135124.	PR	02-AUG-1999;	99US-0146386.
PR	21-MAY-1999;	99US-0135353.	PR	02-AUG-1999;	99US-0146388.
PR	24-MAY-1999;	99US-0135629.	PR	02-AUG-1999;	99US-0146389.
PR	25-MAY-1999;	99US-0136021.	PR	03-AUG-1999;	99US-0147038.
PR	27-MAY-1999;	99US-0136392.	PR	04-AUG-1999;	99US-0147204.
PR	28-MAY-1999;	99US-0136782.	PR	04-AUG-1999;	99US-0147302.
PR	01-JUN-1999;	99US-0137222.	PR	05-AUG-1999;	99US-0147192.
PR	03-JUN-1999;	99US-0137528.	PR	05-AUG-1999;	99US-0147260.
PR	04-JUN-1999;	99US-0137502.	PR	06-AUG-1999;	99US-0147303.
PR	07-JUN-1999;	99US-0137724.	PR	06-AUG-1999;	99US-0147416.
PR	08-JUN-1999;	99US-0138094.	PR	09-AUG-1999;	99US-0147493.
PR	10-JUN-1999;	99US-0138540.	PR	09-AUG-1999;	99US-0147935.
PR	10-JUN-1999;	99US-0138847.	PR	10-AUG-1999;	99US-0148171.
PR	14-JUN-1999;	99US-0139119.	PR	11-AUG-1999;	99US-0148319.
PR	16-JUN-1999;	99US-0139452.	PR	12-AUG-1999;	99US-0148341.
PR	16-JUN-1999;	99US-0139453.	PR	13-AUG-1999;	99US-0148555.
PR	17-JUN-1999;	99US-0139492.	PR	13-AUG-1999;	99US-0148684.
PR	18-JUN-1999;	99US-0139454.	PR	16-AUG-1999;	99US-0149368.
PR	18-JUN-1999;	99US-0139455.	PR	17-AUG-1999;	99US-0149175.
PR	18-JUN-1999;	99US-0139456.	PR	18-AUG-1999;	99US-0149426.
PR	18-JUN-1999;	99US-0139457.	PR	20-AUG-1999;	99US-0149722.
PR	18-JUN-1999;	99US-0139458.	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	99US-0139459.	PR	20-AUG-1999;	99US-0149929.
PR	18-JUN-1999;	99US-0139460.	PR	23-AUG-1999;	99US-0149902.
PR	18-JUN-1999;	99US-0139461.	PR	23-AUG-1999;	99US-0149930.
PR	18-JUN-1999;	99US-0139462.	PR	25-AUG-1999;	99US-0150566.
PR	18-JUN-1999;	99US-0139463.	PR	26-AUG-1999;	99US-0150884.
PR	18-JUN-1999;	99US-0139750.	PR	27-AUG-1999;	99US-0151065.
PR	18-JUN-1999;	99US-0139763.	PR	27-AUG-1999;	99US-0151066.
PR	21-JUN-1999;	99US-0139817.	PR	27-AUG-1999;	99US-0151080.
PR	22-JUN-1999;	99US-0139899.	PR	30-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	31-AUG-1999;	99US-0151438.
PR	23-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151930.
PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152353.
PR	28-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0153070.
PR	29-JUN-1999;	99US-0140991.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.


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PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156658.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160880.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 0.9%; Score 22; DB 21; Length 1547;
 Best Local Similarity 100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;

Qy 2285 ACTCTTCAATTATGATACCA 2306
 |||||
 Db 447 ACTCTTCAATTATGATACCA 468

```

RESULT 55
ID AAA65761 standard; DNA; 29 BP.
XX
AC AAA65761;
XX
DT 21-NOV-2000 (first entry)
XX
DE Streptococcus pneumoniae BVH-11 PCR primer SEQ ID NO:36.
XX
KW Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
XX prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
XX otitis media; pneumonia; immunisation; bactericidal; PCR primer; ss.
OS Streptococcus pneumoniae.
XX
PN WO200039299-A2.
XX
PD 06-JUL-2000.
XX
PF 20-DEC-1999; 99WO-CA01218.
XX

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PR 23-DEC-1998; 98US-0113800.
XX
PA (BIOC-) BIOCHEM PHARMA INC.
XX
PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
XX WPI; 2000-452397/39.
XX
PT Streptococcal antigens useful for vaccinating against e.g. meningitis,
XX otitis media, bacteraemia and/or pneumonia
XX
PS Example 8; Page 49; 106pp; English.
XX
CC The present invention describes nucleic acids (I) encoding protein
CC antigens (II) from Streptococcus pneumoniae. The protein antigens
CC have bactericidal activity. The nucleic acids, encoding the protein
CC antigens, may be used for the recombinant production of the proteins
CC they encode. The protein antigens may then be used as vaccines for the
CC prevention and treatment of Streptococcal infections in mammals
CC (especially humans) which result in, e.g. meningitis, otitis media,
CC bacteraemia and/or pneumonia. The present sequence represents a PCR
CC primer for a S. pneumoniae GAS BVH-71 protein antigen, which is used in
CC an example from the present invention.
XX
SQ Sequence 29 BP; 7 A; 8 C; 6 G; 8 T; 0 other;
XX
Query Match 0.9%; Score 21; DB 21; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 621 CTGCAGAGCCTTCTATCTG 641
|||||
Db 9 CTGCAGAGCCTTCTATCTG 29

RESULT 56
ABK33683
ID ABK33683 standard; DNA; 29 BP.
XX
AC ABK33683;
XX
DT 08-MAY-2002 (first entry)
XX
DE S. pneumoniae BVH-11 gene, PCR primer HAMJ 264.
XX
KW BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
XX pneumonia; streptococcal bacterial infection; PCR; primer; ss.
OS Streptococcus pneumoniae.
XX
PN WO200198334-A2.
XX
PD 27-DEC-2001.
XX
PF 19-JUN-2001; 2001WO-CA00908.
XX
PR 20-JUN-2000; 2000US-212683P.
XX
PA (SHIR-) SHIRE BIOCHEM INC.
XX
PI Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
XX WPI; 2002-122272/16.
XX
DR New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
XX epitope-bearing polypeptides, useful as vaccine components for treating
XX or preventing streptococcal infections such as otitis media,
XX meningitis, and bacteraemia
XX
PS Example 1; Page 31; 113pp; English.
XX
CC The invention describes an isolated polypeptide (I) with 70-90%
XX identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of

```


CC diagnosis of Candida-mediated diseases (local or systemic infections);
 CC and (ii) to screen for agents that inhibit expression of hyphae-specific
 CC proteins, potential therapeutic agents. The products of the invention
 CC have fungicidal activity. (I), or related proteins and antibodies, are
 CC specific for the hyphal (virulent) form of Candida albicans, so allow
 CC differentiation between virulent and avirulent strains. This sequence
 CC encodes the Candida albicans hyphal-specific protein Cap18p isolated from
 CC contig4-2069.

XX Sequence 501 BP; 205 A; 59 C; 76 G; 161 T; 0 other;

XX Query Match 0.8%; Score 20; DB 24; Length 501;

XX Best Local Similarity 100.0%; Pred. No. 21;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1512 CAATTCTCAATTGAGTAT 1531

DB 450 CAATTCTCAATTGAGTAT 431

RESULT 59
 AAA05814

ID AAA05814 standard; DNA; 1146 BP.

XX AAA05814;

DT 30-MAY-2000 (first entry)

DE Group B Streptococcus protein encoding nucleotide sequence SEQ ID NO:12.

KW Group B Streptococcus; Streptococcus agalactiae; protein antigen;

KW vaccine; screening; immunogen; detection; diagnosis; infection;

KW antibody; affibody; antibacterial; ds.

OS Streptococcus agalactiae.

XX WO200006736-A2.

PD 10-FEB-2000.

XX 27-JUL-1999; 99WO-GB02444.

XX 27-JUL-1998; 98GB-0016335.

PR 19-MAR-1999; 99US-0125163.

PA (MICR-) MICROBIAL TECHNICS LTD.

PI Le Page RWF, Wells JM, Hanniffy SB;

DR WPI; 2000-195299/17.

DR P-PSDB; AAY91286.

PT New Group B Streptococcus protein, useful as vaccine, for diagnosis of

XX Streptococcal infections and for screening of antibodies or affibodies

XX Claim 4; Fig 1; 123pp; English.

XX AAA05803 to AAA05872 encode proteins, polypeptides and peptides (given

CC in AAY91275 to AAY91343) isolated from Group B Streptococcus (GBS), also

CC known as Streptococcus agalactiae. The GBS polynucleotides and

CC polypeptides have antibacterial activity. Immunogenic compositions

CC comprising GBS polynucleotides or polypeptides can be used as vaccines

CC and for the treatment or prophylaxis of GBS infection. The

CC polynucleotides and polypeptides can also be used in the detection of GBS

CC and for screening DNA encoding bacterial cell envelope associated or

CC secreted antigens in gram positive bacteria. AAA05873 to AAA05941

CC represent primers used in the exemplification of the present invention.

XX Sequence 1146 BP; 389 A; 229 C; 234 G; 294 T; 0 other;

XX Query Match 0.8%; Score 20; DB 21; Length 1146;

XX Best Local Similarity 100.0%; Pred. No. 22;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 479 CAGAGCGCTACTACTACAGA 498
 DB 571 CAGAGCGCTACTACTACAGA 590

RESULT 60
 ABN69535

ID ABN69535 standard; DNA; 2466 BP.

XX ABN69535;

DT 01-JUL-2002 (first entry)

DE Streptococcus polynucleotide SEQ ID NO 6983.

KW Streptococcus; GAS; GBS; Group B streptococcus; Streptococcus agalactiae;

KW group A streptococcus; Streptococcus pyogenes; antibacterial; gene;

KW antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.

OS Streptococcus agalactiae.

XX WO200234771-A2.

PD 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB04789.

XX 27-OCT-2000; 2000GB-0026333.

PR 24-NOV-2000; 2000GB-0028727.

PR 07-MAR-2001; 2001GB-0005640.

PA (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

PI Telford J, Masiagnani V, Margarit Ros YI, Grandi G, Fraser C;

PI Tettelein H;

DR WPI; 2002-352536/38.

DR P-PSDB; ABP28904.

PT New Streptococcus protein for the treatment or prevention of infection

XX or disease caused by Streptococcus bacteria, such as meningitis, and

XX for detecting a compound that binds to the protein -

XX Claim 7; Page 3860-3861; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B

CC streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS

CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in

CC the specification. The proteins have antibacterial and antiinflammatory

CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and

CC antibodies that bind (I) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by

CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

CC Nucleic acids encoding (I) are used to detect Streptococcus in a

CC biological sample. (I) is used to determine whether a compound binds to

CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be

CC used as a vaccine or diagnostic composition. The disease caused by

CC streptococcus that is prevented or treated may be meningitis. Nucleic

CC acid encoding (I) may be used to recombinantly produce (I) and may be

CC used in gene therapy. Antibodies to (I) are used for affinity

CC chromatography, immunoassays, and distinguishing/identifying

CC Streptococcus proteins.

XX Sequence 2466 BP; 841 A; 475 C; 513 G; 637 T; 0 other;

XX Query Match 0.8%; Score 20; DB 24; Length 2466;

XX Best Local Similarity 100.0%; Pred. No. 23;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 479 CAGAGCGCTACTACTACAGA 498

|||||

Db 571 CAAGACGCTACTACTACAGA 590

RESULT 61

ID ABN70334 standard; DNA; 2466 BP.

XX ABN70334;

XX 01-JUL-2002 (first entry)

XX Streptococcus polynucleotide SEQ ID NO 8581.

XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

KM group A streptococcus; Streptococcus pyogenes; antibacterial; gene;

XX antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.

XX Streptococcus agalactiae.

XX WO200234771-A2.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB04789.

XX 27-OCT-2000; 2000GB-0026333.

XX 24-NOV-2000; 2000GB-0028727.

XX 07-MAR-2001; 2001GB-0005640.

XX (CHIR-) CHIRON SPA.

XX (GENO-) INST GENOMIC RES.

XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;

XX Tettelein H;

XX WPI; 2002-352536/38.

XX P-PSDB; ABP29703.

XX New Streptococcus protein for the treatment or prevention of infection

PT or disease caused by Streptococcus bacteria, such as meningitis, and

PT for detecting a compound that binds to the protein.

XX Claim 7; Page 3969; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B

CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS

CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in

CC the specification. The proteins have antibacterial and antiinflammatory

CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and

CC antibodies that bind (I) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by

CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

CC Nucleic acids encoding (I) are used to detect Streptococcus in a

CC biological sample. (I) is used to determine whether a compound binds to

CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be

CC used as a vaccine or diagnostic composition. The disease caused by

CC Streptococcus that is prevented or treated may be meningitis. Nucleic

CC acid encoding (I) may be used to recombinantly produce (I) and may be

CC used in gene therapy. Antibodies to (I) are used for affinity

CC chromatography, immunoassays, and distinguishing/identifying

CC Streptococcus proteins.

XX Sequence 2466 BP; 841 A; 475 C; 513 G; 637 T; 0 other;

XX Query Match 0.8%; Score 20; DB 24; Length 2466;

XX Best Local Similarity 100.0%; Pred. No. 23;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 479 CAAGACGCTACTACTACAGA 498

Db 571 CAAGACGCTACTACTACAGA 590

RESULT 62

AAA65740

XX AAA65740 standard; DNA; 2469 BP.

XX AAA65740;

XX 21-NOV-2000 (first entry)

XX Streptococcus pneumoniae GBS BVH-71 gene SEQ ID NO:80.

XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;

KM prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;

XX otitis media; pneumonia; immunisation; bactericidal; ds.

XX Streptococcus pneumoniae.

XX WO200039299-A2.

XX 06-JUL-2000.

XX 20-DEC-1999; 99WO-CA01218.

XX 23-DEC-1998; 98US-0113800.

XX (BIOC-) BIOCHEM PHARMA INC.

XX Hanel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;

XX WPI; 2000-452397/39.

XX P-PSDB; AAB12746.

XX Streptococcal antigens useful for vaccinating against e.g. meningitis,

PT otitis media, bacteraemia and/or pneumonia -

XX Example 13; Fig 45; 106pp; English.

XX The present invention describes nucleic acids (I) encoding protein

CC antigens (II) from Streptococcus pneumoniae. The protein antigens

CC have bactericidal activity. The nucleic acids, encoding the proteins

CC antigens, may be used for the recombinant production of the proteins

CC they encode. The protein antigens may then be used as vaccines for the

CC prevention and treatment of Streptococcal infections in mammals

CC (especially humans) which result in, e.g. meningitis, otitis media,

CC bacteraemia and/or pneumonia. The present sequence encodes the

CC S. pneumoniae GBS BVH-71 protein antigen.

XX Sequence 2469 BP; 842 A; 481 C; 519 G; 627 T; 0 other;

XX Query Match 0.8%; Score 20; DB 21; Length 2469;

XX Best Local Similarity 100.0%; Pred. No. 23;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 479 CAAGACGCTACTACTACAGA 498

Db 571 CAAGACGCTACTACTACAGA 590

XX Streptococcus agalactiae.

PN WO200006736-A2.
 XX
 PD 10-FEB-2000.
 XX
 PF 27-JUL-1999; 99WO-GB02444.
 XX
 PR 27-JUL-1998; 98GB-0016335.
 XX
 PR 19-MAR-1999; 99US-0125163.
 XX
 PA (MICR-) MICROBIAL TECHNIKS LTD.
 XX
 PI Le Page RMF, Wells JM, Hanniffy SB;
 XX
 DR WPI; 2000-195299/17.
 XX
 DR P-PSDB; AA91283.
 XX
 PT New Group B Streptococcus protein, useful as vaccine, for diagnosis of
 XX Streptococcal infections and for screening of antibodies or affibodies
 XX
 PS Claim 4; Fig 1; 123pp; English.
 XX
 CC AAA05803 to AAA05872 encode proteases, polypeptides and peptides (given
 CC in AA91275 to AA91343) isolated from Group B Streptococcus (GBS), also
 CC known as Streptococcus agalactiae. The GBS polynucleotides and
 CC polypeptides have antibacterial activity. Immunogenic compositions
 CC comprising GBS polynucleotides or polypeptides can be used as vaccines
 CC and for the treatment or prophylaxis of GBS infection. The
 CC polynucleotides and polypeptides can also be used in the detection of GBS
 CC and for screening DNA encoding bacterial cell envelope associated or
 CC secreted antigens in gram positive bacteria. AA05873 to AA05941
 CC represent primers used in the exemplification of the present invention.
 SQ Sequence 2469 BP; 842 A; 477 C; 514 G; 636 T; 0 other;

Query Match 0.8%; Score 20; DB 21; Length 2469;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 479 CAAGGACGCTATCTACAGA 498
 DB 571 CAAGGACGCTATCTACAGA 590

RESULT 64

ID AAS00038 standard; DNA; 2469 BP.
 XX
 AC AAS00038;

DT 11-MAY-2001 (first entry)
 XX
 DE Streptococcus agalactiae DNA encoding GBS36.

KW Group B streptococci protein 36; GBS36; immunogen; vaccine;
 KW antibody; necrotising fasciitis; scarlet fever; sepsis; impetigo;
 KW bacterial meningitis; otitis media; community-acquired pneumonia; ds.

OS Streptococcus agalactiae.

FH Key Location/Qualifiers
 FT CDS 1..2469
 FT /*tag= a
 FT /product= "GBS36"

PN WO200114421-A1.

PD 01-MAR-2001.

PF 25-AUG-2000; 2000WO-US23417.

PR 25-AUG-1999; 99US-0150750.

PA (MEDI-) MEDIMUNE INC.

XX
 PI Koenig S, Heinrichs J, Johnson LS, Adamou JB;
 XX
 DR WPI; 2001-211305/21
 XX
 DR P-PSDB; AAU00028, AAU00030.
 XX
 PT New polypeptides obtained from group A or B streptococci, especially
 XX Streptococcus aureus homologous to Sp36 protein of Streptococcus
 PT pneumoniae useful as antibacterial vaccines
 XX
 PS Claim 10; Page 53-54; 62pp; English.

CC The sequence encodes Streptococcus agalactiae Group B Streptococci
 CC protein 36, GBS36. A recombinant cell producing GBS36, GBS36(2) or
 CC GBS36 is useful as a vaccine for vaccinating an animal, preferably a
 CC human against infection by a bacterial organism such as a streptococcal
 CC or staphylococcal bacteria, and for treating a disease caused by group A
 CC streptococci, group B streptococci or Staphylococcus aureus in an animal
 CC preferably a human. Vaccines and antibodies against the proteins of the
 CC invention are useful in prophylaxis and/or treatment of diseases such as
 CC necrotising fasciitis, scarlet fever, sepsis, impetigo, bacterial
 CC meningitis, otitis media, community-acquired pneumonia and many diseases
 CC of newborns. The proteins are also used as immunogens to stimulate the
 CC production of antibodies for use in passive immunotherapy, for use as
 CC diagnostic reagents and for use as reagents in other processes such as
 CC affinity chromatography.

SQ Sequence 2469 BP; 844 A; 477 C; 514 G; 634 T; 0 other;

Query Match 0.8%; Score 20; DB 22; Length 2469;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 479 CAAGGACGCTATCTACAGA 498
 DB 571 CAAGGACGCTATCTACAGA 590

RESULT 65

ID AAA65741 standard; DNA; 2472 BP.
 XX
 AC AAA65741;

DT 21-NOV-2000 (first entry)

DE Streptococcus pneumoniae GAS BVH-71 gene SEQ ID NO:82.

KW Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
 KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
 KW otitis media; pneumonia; immunisation; bactericidal; ds.

OS Streptococcus pneumoniae.

PN WO200039299-A2.

PD 06-JUL-2000.

PF 20-DEC-1999; 99WO-CA01218.

PR 23-DEC-1998; 98US-0113800.

PA (BIOC-) BIOCHEM PHARMA INC.

PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;

DR WPI; 2000-452397/39.

DR P-PSDB; AAB12747.

PT Streptococcal antigens useful for vaccinating against e.g. meningitis,

PT otitis media, bacteraemia and/or pneumonia

XX

PS

Example 13; Fig 47; 106pp; English.

XX The present invention describes nucleic acids (I) encoding protein
 CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein
 CC antigens, may be used for the recombinant production of the protein
 CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals
 CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence encodes the
 CC S. pneumoniae GAS BVH-71 protein antigen.

XX
 SQ Sequence 2472 BP, 846 A, 480 C, 514 G, 632 T, 0 other;

Query Match 0.8%; Score 20; DB 21; Length 2472;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 479 CAAGAGCGCTACTACTACAGA 498
 |||||
 Db 571 CAAGAGCGCTACTACTACAGA 590

RESULT 66
 ABN66838 standard; DNA, 2475 BP.

XX
 AC ABN66838;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE Streptococcus polynucleotide SEQ ID NO 1589.
 XX
 KM Streptococcus GAS; group B streptococcus; Streptococcus agalactiae;
 KM group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
 KM antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
 XX
 OS Streptococcus pyogenes.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB04789.
 XX
 PR 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Massignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tectelin H;
 XX
 DR WPI: 2002-352536/38.
 DR P-PSDB; ABP26207.
 XX
 PT New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 XX
 PS Claim 7; Page 3309; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B
 CC Streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to

CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

XX
 SQ Sequence 2475 BP, 844 A, 486 C, 518 G, 627 T, 0 other;

Query Match 0.8%; Score 20; DB 24; Length 2475;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 479 CAAGAGCGCTACTACTACAGA 498
 |||||
 Db 571 CAAGAGCGCTACTACTACAGA 590

RESULT 67
 AAS00036 standard; DNA, 2478 BP.

XX
 AC AAS00036;
 XX
 DT 11-MAY-2001 (first entry)
 XX
 DE Streptococcus pyogenes DNA encoding GAS36.
 XX
 KM Group A streptococci protein 36; GAS36; immunogen; vaccine;
 KM antibody; necrotising fasciitis; scarlet fever; sepsis; impetigo;
 KM bacterial meningitis; otitis media; community-acquired pneumonia; ds.
 XX
 OS Streptococcus pyogenes.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2478
 FT /*tag= a
 FT /*product= "GAS36"
 XX
 PN WO200114421-A1.
 XX
 PD 01-MAR-2001.
 XX
 PF 25-AUG-2000; 2000WO-US23417.
 XX
 PR 25-AUG-1999; 99US-0150750.
 XX
 PA (MEDI-) MEDIMMUNE INC.
 XX
 PI Koenig S, Heinrichs J, Johnson LS, Adamou JE;
 PI WPI: 2001-211305/21.
 DR P-PSDB; AAU00026, AAU00029.
 XX
 PT New polypeptides obtained from group A or B streptococci, especially
 PT Streptococcus aureus homologous to Sp36 protein of Streptococcus
 PT pneumoniae useful as antibacterial vaccines -
 XX
 PS Claim 10; Page 46-47; 62pp; English.

XX The sequence encodes Streptococcus pyogenes Group A Streptococci
 CC protein 36, GAS36. A recombinant cell producing GAS36, GAS36(2) or
 CC GAS36 is useful as a vaccine for vaccinating an animal, preferably a
 CC human against infection by a bacterial organism such as a streptococcal
 CC or staphylococcal bacteria, and for treating a disease caused by group A
 CC streptococci, group B streptococci or staphylococcus aureus in an animal
 CC preferably a human. Vaccines and antibodies against the proteins of the
 CC invention are useful in prophylaxis and/or treatment of diseases such as
 CC necrotising fasciitis, scarlet fever, sepsis, impetigo, bacterial
 CC meningitis, otitis media, community-acquired pneumonia and many diseases
 CC of newborns. The proteins are also used as immunogens to stimulate the
 CC production of antibodies for use in passive immunotherapy, for use as

CC diagnostic reagents and for use as reagents in other processes such as
CC affinity chromatography.

XX Sequence 2478 BP; 846 A; 486 C; 518 G; 628 T; 0 other;

XX Query Match 0.8%; Score 20; DB 22; Length 2478;
XX Best Local Similarity 100.0%; Pred. No. 23;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 479 CAAGACGCTATCTACAGA 498
DB 571 CAAGACGCTATCTACAGA 590

RESULT 68
AA169348/c
ID AA169348 standard; DNA; 5158 BP.

XX AA169348;

XX 18-FEB-2002 (first entry)

XX C. albicans contig4-2069 DNA containing hyphal-specific proteins.

XX Hyphal-specific protein; biochip; diagnosis; infection; Cap18p; Cap19p;
XX screening; fungicide; virulent; ds.

XX Candida albicans.

XX WO200185989-A2.

XX 15-NOV-2001.

XX 10-MAY-2001; 2001WO-EP05363.

XX 11-MAY-2000; 2000DE-1023130.

XX (FRAU) FRAUNHOFER GBS FOERDERUNG ANGEWANDTEN.

XX Rupp S, Johannes F, Sohn K;

XX WPI; 2002-062252/08.

XX Nucleotide chip for specific detection of the hyphal, virulent, form of
XX Candida albicans, comprises a solid support carrying a nucleotide
XX sequence for identifying and transcribing genes that encode
XX hyphae-specific proteins

XX Disclosure; Page 60-61; 65pp; German.

XX This invention describes a novel nucleotide chip which comprises a
XX solid support carrying a nucleotide sequence for identifying and
XX transcribing genes that encode hyphal-specific proteins. The chip of the
XX invention, and related protein and antibody chips, are used: (i) for
XX diagnosis of Candida-mediated diseases (local or systemic infections);
XX and (ii) to screen for agents that inhibit expression of hyphae-specific
XX proteins, potential therapeutic agents. The products of the invention
XX have fungicidal activity, (i), or related proteins and antibodies, are
XX specific for the hyphal (virulent) form of Candida albicans, so allow
XX differentiation between virulent and avirulent strains. This sequence
XX represents the Candida albicans derived contig4-2069 DNA which encodes
XX the Cap18p and Cap19p hyphal-specific protein described in the method
XX of the invention.

XX Sequence 5158 BP; 1762 A; 768 C; 781 G; 1847 T; 0 other;

XX Query Match 0.8%; Score 20; DB 24; Length 5158;
XX Best Local Similarity 100.0%; Pred. No. 23;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1512 CAATTTCTCAATTCAGTAT 1531
DB 4215 CAATTTCTCAATTCAGTAT 4196

RESULT 69

AA91105
ID AA91105 standard; DNA; 5215 BP.

XX AA91105;

XX 15-NOV-1999 (first entry)

XX Group B Streptococcus (GBS) antigens encoding DNA (clone 3).

XX Group B Streptococcus; GBS; antigen; vaccine; Streptococcus infection;
XX sepsis; meningitis; pneumonia; immunocompromise; diabetes; liver disease;
XX cancer; veterinary; mastitis; ss.

XX Streptococcus sp.

XX Key Location/Qualifiers

XX CDS 3..125

XX /tag= a

XX /note= "see AAY27346"

XX CDS 133..2514

XX /tag= b

XX /note= "see AAY27347"

XX CDS 367..2514

XX /tag= c

XX /note= "see AAY27348"

XX CDS complement (2716..2946)

XX /tag= d

XX /note= "see AAY27349"

XX CDS complement (2995..3252)

XX /tag= e

XX /note= "see AAY27350"

XX CDS complement (3299..3676)

XX /tag= f

XX /note= "see AAY27351"

XX CDS complement (3837..4124)

XX /tag= g

XX /note= "see AAY27352"

XX CDS complement (4351..5214)

XX /tag= h

XX /note= "see AAY27353"

XX MO9942588-A2.

XX 26-AUG-1999.

XX 17-FEB-1999; 99WO-CA00114.

XX 20-FEB-1998; 98US-0075425.

XX (BIOC-) BIOCHEM VACCINS INC.

XX Royer M, Brodeur BR, Charlebois I, Hamel J, Martin D;
XX Bionix C;

XX WPI; 1999-540309/45.
XX P-PDB; AAY27346, AAY27347, AAY27348, AAY27349, AAY27350, AAY27351,
XX AAY27352, AAY27353.

XX Novel group B Streptococcus antigens - useful as vaccine
XX compositions for prophylaxis or therapy of Streptococcus infections

XX Claim 10; Fig 3A; 154pp; English.

XX The invention provides Group B Streptococcus (GBS) antigens
XX (AAY27336-370) and nucleic acids (AAY91103-X91111) encoding the antigens.
XX The GBS antigens can be recombinantly expressed using standard
XX recombinant methodology. The GBS antigens of the invention can be used as
XX vaccine components for the treatment or prophylaxis of diseases and
XX symptoms mediated by Streptococcus infection, especially group A
XX Streptococcus (S. pyogenes), GBS or S. agalactiae, S. dysgalactiae, S.

CC uberis, *S. nodocardia*, as well as *Staphylococcus aureus*. The vaccines are
 CC administered to those individuals at risk of GBS infection, particularly
 CC pregnant women and infants for sepsis, meningitis, and pneumonia, as well
 CC as immunocompromised individuals, such as those with diabetes, liver
 CC disease or cancer. The vaccines also have veterinary applications, such as
 CC for the treatment of mastitis in cattle. The present sequence represents
 CC a DNA encoding 8 GBS antigens of the invention.
 XX
 SQ Sequence 5215 BP; 1631 A; 957 C; 1038 G; 1589 T; 0 other;
 Query Match 0.8%; Score 20; DB 20; Length 5215;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 479 CAAGGACGCTATCTACAGCA 498
 Db 616 CAAGGACGCTATCTACAGCA 635
 RESULT 70
 ID ABX54820 standard; cDNA; 164 BP.
 AC ABX54820;
 XX
 DT 26-FEB-2003 (first entry)
 XX
 DE Bovine EST associated with lactation/muscle/fat deposition #4749.
 XX
 KW Bovine; ss; EST; expressed sequence tag; lactation; LMPD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX
 OS Bos Taurus.
 XX
 PN US2002137160-A1.
 XX
 PD 26-SEP-2002.
 XX
 PE 26-OCT-2001; 2001US-0983965.
 XX
 PR 17-DEC-1998; 98US-113678P.
 PR 15-DEC-1999; 99US-0465231.
 XX
 PA (BYATT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX
 PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX
 DR WPI: 2003-102386/09.
 XX
 PT Purified nucleic acid molecules, useful for genome mapping, gene
 PT identification and analysis, cattle breeding or preparation of
 PT constructs for cattle gene expression and genetically improved cattle -
 XX
 XX Claim 2; SEQ ID No 4749; 38pp; English.
 PS
 XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMPD), derived
 CC from cattle, and the LMPD nucleic acid can specifically hybridise to a
 CC second nucleic acid molecule comprising any of 5912 nucleotide
 CC sequences, appearing as ABX50072-ABX55983, or complements of them.
 CC Also included are: (1) a transformed cell having a nucleic acid
 CC comprising an LMPD nucleic acid linked to a promoter and a 3' non-
 CC translated sequence that functions in the cell to cause termination of
 CC transcription and addition of polyadenylated ribonucleotides to a 3' end
 CC of the mRNA molecule; and (2) determining a level or pattern of a
 CC molecule in a bovine cell or tissue comprising: (a) incubating a marker
 CC nucleic acid (comprising any of the 5912 nucleic acid sequences or its
 CC complement or fragment) with a complementary nucleic acid molecule
 CC obtained from the bovine cell or tissue, where hybridisation between the

CC marker nucleic acid and the complementary nucleic acid permits the
 CC detection of the molecule; and (b) detecting the level or pattern of the
 CC complementary nucleic acid, where the detection of the complementary
 CC nucleic acid is predictive of the level or pattern of the molecule.
 CC The LMPD nucleic acid is used for determining a level or pattern
 CC of a molecule in a bovine cell or tissue. It is useful for genome
 CC mapping, gene identification and analysis, cattle breeding, preparation
 CC of constructs for use in cattle gene expression, or for genetically
 CC improving cattle. The present sequence is one of the 5912 bovine
 CC LMPD EST (expressed sequence tag) nucleic acids.
 CC Note: The present sequence was not shown in the specification but
 CC was obtained in electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?docid=20020137160.
 XX
 SQ Sequence 164 BP; 60 A; 41 C; 34 G; 29 T; 0 other;
 Query Match 0.8%; Score 19; DB 25; Length 164;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1112 TCAATCTCTTGTGTTA 1130
 Db 83 TCAATCTCTTGTGTTA 65
 RESULT 71
 ID ABV02215 standard; cDNA; 426 BP.
 AC ABV02215;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 2206.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PE 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI: 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 XX Claim 1; Page 432; 11750pp; English.
 PS
 XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer

Query Match	Best Local Similarity	Score 19	DB 23	Length 426
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0	100.0%; Pred. No. 68;			
Oy	1224 TTTAAATCTTGAAAGCAA	1242		
Db	164 TTTAAATCTTGAAAGCAA	146		
RESULT 72				
AAS30789				
ID	AAS30789 standard; cDNA; 427 BP.			
XX	AAS30789;			
XX	04-DEC-2001 (first entry)			
DT	Human CDNA encoding G protein-coupled receptor ngPCR-2341.			
DE				
XX	Human; G protein-coupled receptor; ngPCR-X; ss; antiviral; analgesic; cytosolic; cardiac; antidiabetic; anorectic; hypotensive; hypertensive; antiparkinsonian; nootropic; neuroprotective; antidepressant; viral infection; HIV-1; human immunodeficiency virus; HIV-2; pain; cancer; metabolic disease; cardiovascular disease; type 2 diabetes; obesity; anorexia; hypotension; hypertension; myocardial infarction; atherosclerosis; Parkinson's disease; psychosis; neurological disorder; schizophrenia; migraine; major depression; anxiety; mental disorder; manic depression; dyskinesia; Huntington's disease; Tourette's Syndrome.			
XX	Homo sapiens.			
OS	WO20016750-A2.			
PN	13-SEP-2001.			
XX				
PD	08-MAR-2001; 2001WO-US07322.			
XX				
PF	08-MAR-2000; 2000US-0187581.			
PR	08-MAR-2000; 2000US-0187582.			
PR	08-MAR-2000; 2000US-0187714.			
PR	08-MAR-2000; 2000US-0187715.			
PR	08-MAR-2000; 2000US-0187825.			
PR	08-MAR-2000; 2000US-0187828.			
PR	08-MAR-2000; 2000US-0187829.			
PR	08-MAR-2000; 2000US-0187830.			
PR	08-MAR-2000; 2000US-0187833.			
PR	08-MAR-2000; 2000US-0187874.			
PR	08-MAR-2000; 2000US-0187930.			
PR	08-MAR-2000; 2000US-0188049.			
PR	08-MAR-2000; 2000US-0188294.			
PR	08-MAR-2000; 2000US-0189292.			
PR	08-MAR-2000; 2000US-0187928.			
XX				
XX	(PHAA) PHARMACIA & UPJOHN CO.			
PA				
XX				
XX	Vogeli G, Wood LS;			
XX				
DR	WPI; 2001-536778/59.			
DR	P-PSDB; AAU19220.			
XX				
PT	Isolated nucleic acid molecules encoding G protein-coupled receptors			
PT	termed ngPCR-X, useful in the treatment and diagnosis of viral			
PT	infections, cancers and mental disorders (e.g. Parkinson's disease and			

PT	schizophrenia) -
XX	
PS	Claim 4, Page 204; 336pp; English.
CC	
CC	The invention relates to novel isolated nucleic acid molecules encoding
CC	G protein-coupled receptors termed ngPCR-x, ngPCR-x polynucleotides,
CC	polypeptides, and modulators may be used in the treatment of diseases and
CC	conditions such as infections, such as viral infections caused by HIV-1
CC	(human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and
CC	cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity,
CC	anorexia, hypertension, hypertension, myocardial infarction,
CC	atherosclerosis), Parkinson's disease, and psychotic and
CC	neurological disorders, including schizophrenia, migraine, major
CC	depression, anxiety, mental disorder, manic depression, and
CC	dyskinesias, such as Huntington's disease or Tourette's Syndrome
CC	and many other diseases and syndromes listed in the specification.
CC	ngPCR-x polynucleotides and polypeptides, as well as ngPCR-x
CC	modulators, may also be used in diagnostic assays for such diseases or
CC	conditions.
CC	The present sequence encodes a G protein-coupled
CC	receptor of the invention.
SQ	
XX	
XX	Sequence 427 BP, 194 A; 67 C; 64 G; 102 T; 0 other;
XX	
XX	Query March 0.8%; Score 19; DB 22; Length 427;
XX	Best Local Similarity 100.0%; Pred. No. 68;
XX	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	
Db	1224 TTAATAATCTGAAGCAA 1242
	154 TTAATAATCTGAAGCAA 172
RESULT 73	
ID	ABV11384/c
XX	ABV11384 standard; cDNA; 468 BP.
AC	
XX	ABV11384;
DT	
XX	13-SEP-2002 (first entry)
DE	
XX	Human prostate expression marker cDNA 11375.
KW	
XX	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX	pharmacogenomic marker; gene; ss.
OS	
XX	Homo sapiens.
XX	
XX	WO200160860-A2.
XX	
XX	23-AUG-2001.
XX	
XX	20-FEB-2001; 2001WO-US05171.
XX	
XX	17-FEB-2000; 2000US-183319P.
XX	16-MAR-2000; 2000US-189862P.
XX	25-MAY-2000; 2000US-207454P.
XX	09-JUN-2000; 2000US-211314P.
XX	18-JUL-2000; 2000US-219007P.
XX	13-DEC-2000; 2000US-255281P.
XX	
XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX	
XX	Schlegel R, Endege WO, Monahan JE;
XX	
XX	WPI; 2001-662795/76.
XX	
XX	Novel isolated nucleic acid molecule associated with cancerous state of
XX	prostate cells and correlating with presence of prostate cancer, useful
XX	for detecting presence of prostate cancer, stage of prostate cancer -
XX	
XX	Claim 1; Page 1852; 11750pp; English.
XX	
XX	The invention relates to an isolated nucleic acid molecule (I) comprising
CC	

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SO Sequence 468 BP; 95 A; 78 C; 74 G; 220 T; 1 other;
Query Match 0.8%; Score 19; DB 23; Length 468;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1224 TTTAAATCTGAAAGCAA 1242
DB 136 TTTAAATCTGAAAGCAA 118
RESULT 74
ABV32529/C
ID ABV32529 standard; cDNA; 481 BP.
XX
AC ABV32529;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 32520.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 6937; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SO Sequence 481 BP; 101 A; 81 C; 85 G; 213 T; 1 other;
Query Match 0.8%; Score 19; DB 23; Length 481;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1224 TTTAAATCTGAAAGCAA 1242
DB 181 TTTAAATCTGAAAGCAA 163
RESULT 75
ABV41454/C
ID ABV41454 standard; cDNA; 481 BP.
XX
AC ABV41454;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 41445.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 8330; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a

CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 481 BP; 101 A; 81 C; 85 G; 213 T; 1 other;

Query Match 0.8%; Score 19; DB 23; Length 481;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1224 TTTAAATCTGAAAGCAA 1242
 Db 181 TTTAAATCTGAAAGCAA 163

RESULT 76
 AB089355/C
 ID AB089355 standard; cDNA; 693 BP.

XX AB089355;

DT 27-SEP-2002 (first entry)

XX Human prostate expressed polynucleotide SEQ ID NO 611.

XX Human; prostate; cytostatic; tumour; cancer; vaccine; gene therapy;

KW gene; ss.

XX Homo sapiens.

XX WO200255700-A2.

XX 18-JUL-2002.

XX 07-DEC-2001; 2001WO-US47349.

XX 07-DEC-2000; 2000US-254648P.

PR 13-MAR-2001; 2001US-275688P.

XX (CHIR) CHIRON CORP.

PA (HYSE-) HYSEQ INC.

PI Escobedo J, Garcia PD, Kaasam A, Lamson G, Drmanac R;

PI Ckrnenjakov R, Dickson M, Drmanac S, Labat I, Leshkowitz D;

PI Kita D, Garcia V, Jones WL, Stache-Grain B, Scott EM;

XX WPI; 2002-557824/59.

PT New genes and gene products isolated from human prostate, useful for
 PT treating or diagnosing tumor or cancer (e.g. prostate cancer or breast
 PT cancer), or as vaccines for treating or preventing these diseases -

PS Claim 1, SEQ ID NO 611; 186pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide comprising any of
 CC 1477 sequences or its fragment, degenerate variant, antisense or
 CC complement. The polynucleotides and gene products are useful for treating
 CC lung cancer or medullary carcinoma (e.g. prostate cancer, breast cancer,
 CC cat, rabbit or horse or human). The polynucleotides and polypeptides are
 CC also useful as vaccines for treating or preventing these diseases. The
 CC polynucleotides are useful for gene therapy. The present sequence is that
 CC of one of a group of polynucleotides (AB088745-AB090015) disclosed
 CC electronically as sequences of the invention. However only 1271
 CC polynucleotide sequences are given, whereas 1477 polynucleotides and 91
 CC proteins are claimed.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence.

XX Sequence 693 BP; 239 A; 88 C; 115 G; 235 T; 16 other;

Query Match 0.8%; Score 19; DB 24; Length 693;
 Best Local Similarity 100.0%; Pred. No. 69;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 TCTTACCTCCATCTCCAGA 1752
 Db 155 TCTTACCTCCATCTCCAGA 137

RESULT 77
 ABV21401
 ID ABV21401 standard; cDNA; 1203 BP.

XX ABV21401;

DT 13-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 21392.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KW pharmacogenomic marker; gene; ss.

XX Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US05171.

XX 17-FEB-2000; 2000US-18319P.

PR 16-MAR-2000; 2000US-189862P.

PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -

PS Claim 1; Page 3561; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 1203 BP; 545 A; 170 C; 185 G; 302 T; 1 other;

Query Match 0.8%; Score 19; DB 23; Length 1203;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1224 TTTAAATCTGAAAGCAA 1242
 Db 557 TTTAAATCTGAAAGCAA 575

RESULT 78
 ABV27219
 ID ABV27219 standard; cDNA; 1205 BP.
 XX
 AC ABV27219;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker CDNA 27210.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200160860-A2.
 PD 23-AUG-2001.
 XX
 PE 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-18319P.
 PR 16-MAR-2000; 2000US-18962P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-21907P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 WPI; 2001-662795/76.
 XX
 DR Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 BS Claim 1; Page 5523; 11750P; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SO Sequence 1205 BP; 547 A; 170 C; 185 G; 302 T; 1 other;
 XX
 Query Match 0.8%; Score 19; DB 23; Length 1205;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1224 TTTAAATCTTCAGAACAA 1242
 DB 559 TTTAAATCTTCAGAACAA 577
 XX
 RESULT 79
 AAA05838
 ID AAA05838 standard; DNA; 1455 BP.
 XX
 AC AAA05838;

XX
 DT 30-MAY-2000 (first entry)
 XX
 DE Group B Streptococcus protein encoding nucleotide³ sequence SEQ ID NO:38.
 XX
 KW Group B Streptococcus; Streptococcus agalactiae; protein antigen;
 KW vaccine; screening; immunogen; detection; diagnosis; infection;
 KW antibody; affibody; antibacterial; ds.
 XX
 OS Streptococcus agalactiae.
 XX
 FN WO200006736-A2.
 PD 10-FEB-2000.
 XX
 PE 27-JUL-1999; 99WO-GB02444.
 XX
 PR 27-JUL-1998; 98GB-0016335.
 PR 19-MAR-1999; 99US-0125163.
 XX
 PA (MICR-) MICROBIAL TECHNIQS LTD.
 XX
 PI Le Page RWF, Wells JM, Hamifly SB;
 XX
 WPI; 2000-195299/17.
 DR P-PSDB; AAY91310.
 XX
 PT New Group B Streptococcus protein, useful as vaccine, for diagnosis of
 PT Streptococcal infections and for screening of antibodies or affibodies
 XX
 PS Claim 4; Fig 1; 123P; English.
 XX
 CC AAA05803 to AAA05872 encode proteins, polypeptides and peptides (given
 CC in AAY91275 to AAY91343) isolated from Group B streptococcus (GBS), also
 CC known as Streptococcus agalactiae. The GBS polynucleotides and
 CC polypeptides have antibacterial activity. Immunogenic compositions
 CC comprising GBS polynucleotides or polypeptides can be used as vaccines
 CC and for the treatment or prophylaxis of GBS infection. The
 CC polynucleotides and polypeptides can also be used in the detection of GBS
 CC and for screening DNA encoding bacterial cell envelope associated or
 CC secreted antigens in gram positive bacteria. AAA05873 to AAA05941
 CC represent primers used in the exemplification of the present invention.
 XX
 SO Sequence 1455 BP; 584 A; 237 C; 271 G; 363 T; 0 other;
 XX
 Query Match 0.8%; Score 19; DB 21; Length 1455;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1583 GATGTTACATTTTGGATG 1601
 DB 343 GATGTTACATTTTGGATG 361
 XX
 RESULT 80
 AAA70231/C
 ID AAA70231 standard; DNA; 1650 BP.
 XX
 AC AAA70231;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:364.
 XX
 KW Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine;
 KW antimalarial; malaria; protozoacide; infection; insecticide; ds.
 XX
 OS Plasmodium falciparum.
 XX
 FN WO200025728-A2.
 PD 11-MAY-2000.
 XX


```

PR 15-NOV-1994; 94WO-US13200.
XX
XX (UYEM-) UNIV EMORY.
XX
XX Loliar JS, Runge MS;
XX
XX WPI; 1998-271107/24.
XX
XX P-PSDB; AAW53485.
XX
XX Hybrid of human and animal factor VIII - containing porcine and
XX murine amino acid sequences is useful in the treatment of
XX haemophilia
XX
XX Disclosure; Column 65-72; 48bp; English.
XX
XX The present sequence encodes murine factor VIII used in the present
XX invention. The present invention describes a new procoagulant hybrid
XX factor VIII (I) comprising human factor VIII and has amino acid
XX sequences substituted from the group of A2 domain fragments consisting
XX of amino acids 373-540, 373-508, 445-508, 484-508, 489-508
XX and 484-489 from the human 2332 amino acid A2 domain sequence (II) as
XX given in the specification (see AAW53483). The substitution is from
XX corresponding non-human mammalian factor VIII sequences. Also described
XX is a method for treating factor VIII deficiency comprising administering
XX a therapeutically effective dose of (I) in a pharmaceutical carrier.
XX (II), prepared from reconstitution of purified molecules or recombinant
XX techniques, is useful in the treatment of haemophiliacs who have factor
XX VIII deficiencies and whose blood is not normally able to clot after
XX internal or external bleeding. (I) compared to native human factor VIII
XX is more stable at physiological conditions and has a higher specific
XX clotting activity.
XX
XX SQ Sequence 7493 BP; 2487 A; 1503 C; 1436 G; 2067 T; 0 other;
XX
XX Query Match 0.8%; Score 19; DB 19; Length 7493;
XX Best Local Similarity 100.0%; Pred. No. 76;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 2347 AAAGAGTATACCTTCA 2365
XX ||||||||||||||||
XX Db 206 AAAGAGTATACCTTCA 224
XX
XX RESULT 83
XX ID AAV12115 standard; cDNA to mRNA; 7493 BP.
XX
XX AC AAV12115;
XX
XX DT 17-JUN-1998 (first entry)
XX
XX DE Mus musculus factor VIII coding region.
XX
XX KW factor VIII; recombinant; modified; haemophilia; treatment; ds.
XX
XX OS Mus musculus.
XX
XX Key Location/Qualifiers
XX FH 5'UTR 1..407
XX FT /*tag= a
XX FT 7368..7493
XX FT /*tag= b
XX FT polyA_signal 7471..7476
XX FT /*tag= c
XX FT CDS 408..7367
XX FT /*tag= d
XX FT /product= factor VIII
XX
XX MO9749725-A1.
XX
XX 31-DEC-1997.
XX
XX 26-JUN-1997; 97WO-US11155.

```

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XX
XX 26-JUN-1996; 96US-0670707.
XX
XX (UYEM-) UNIV EMORY.
XX
XX Loliar JS;
XX
XX WPI; 1998-077108/07.
XX
XX P-PSDB; AAW44135.
XX
XX New modified factor VIII molecules - having reducing immunogenicity
XX
XX Disclosure; Pages 74-77; 126pp; English.
XX
XX The sequence is that encoding murine factor VIII. It can be used in
XX the production of modified factor VIII. The factor VIII molecules
XX have coagulant activity and can be used for treating factor VIII
XX deficiency, particularly for treating patients with haemophilia.
XX The products can also be used in detection and diagnosis. This
XX modified factor VIII has less immunoreactivity with naturally
XX occurring inhibitory antibodies to factor VIII and may be less apt
XX to elicit the production of antibodies to factor VIII than human
XX factor VIII. Some of the hybrid factor VIII molecules have specific
XX activity greater than that of human factor VIII and equal to or greater
XX than that of porcine factor VIII.
XX
XX SQ Sequence 7493 BP; 2487 A; 1503 C; 1436 G; 2067 T; 0 other;
XX
XX Query Match 0.8%; Score 19; DB 19; Length 7493;
XX Best Local Similarity 100.0%; Pred. No. 76;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 2347 AAAGAGTATACCTTCA 2365
XX ||||||||||||||||
XX Db 206 AAAGAGTATACCTTCA 224
XX
XX RESULT 84
XX ID AAX91164 standard; cDNA to mRNA; 7493 BP.
XX
XX AC AAX91164;
XX
XX DT 26-NOV-1999 (first entry)
XX
XX DE Mouse factor VIII protein encoding nucleotide sequence.
XX
XX KW Factor VIII protein; hybrid protein; porcine; mouse; immunogenicity;
XX antigenic; procoagulant; factor X activation; haemophilia; human; ds.
XX
XX OS Mus musculus.
XX
XX FN MO9946274-A1.
XX
XX PD 16-SEP-1999.
XX
XX PE 10-MAR-1999; 99WO-US05193.
XX
XX PR 10-MAR-1998; 98US-0037601.
XX
XX (UYEM-) UNIV EMORY.
XX
XX Loliar JS;
XX
XX WPI; 1999-551355/46.
XX
XX P-PSDB; AAY31596.
XX
XX New porcine and modified human factor VIII proteins for treating
XX haemophilia -
XX
XX Examples; Page 131-136; 187pp; English.
XX
XX The invention provides DNA encoding porcine factor VIII, hybrid porcine
XX

```

CC /human factor VIII, or modified human factor VIII having reduced
CC immunogenicity. Active factor VIII increases catalytic efficiency of
CC factor IXa towards factor X activation. The factor VIII proteins of the
CC invention can be produced by standard recombinant methodology and have
CC less antigenic activity, or greater procoagulant activity, than prior art
CC factor VIII. The invention is used to treat haemophilia. The present
CC sequence represents the nucleotide sequence encoding the A and C domains
CC of mouse factor VIII protein.
SQ Sequence 7493 BP; 2487 A; 1503 C; 1436 G; 2067 T; 0 other;
Query Match 0.8%; Score 19; DB 20; Length 7493;
Best Local Similarity 100.0%; Pred. NO. 76;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2347 AAAGAGTAATCCTCA 2365
Db 206 AAAGAGTAATCCTCA 224
RESULT 85
ABK49586/C
ID ABK49586 standard; DNA; 143306 BP.
XX
AC ABK49586;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human transporter protein gene.
XX
XX Human; ds; gene; transporter; transgenic; transporter mediated disease;
KW drug screening; pharmacogenomic analysis; chromosome 18; SNP;
KW single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 3000..140308 /tag= a
FT FT /product= "Transporter"
FT FT 3000..3051
FT FT /tag= b
FT FT /number= 1
FT FT 3052..62251
FT FT /tag= c
FT FT /number= 1
FT FT 62251..62601
FT FT /tag= d
FT FT /number= 2
FT FT 62602..84982
FT FT /tag= e
FT FT /number= 2
FT FT 84983..85100
FT FT /tag= f
FT FT /number= 3
FT FT 85101..98275
FT FT /tag= g
FT FT /number= 3
FT FT 98276..98436
FT FT /tag= h
FT FT /number= 4
FT FT 98437..133431
FT FT /tag= i
FT FT /number= 4
FT FT 133432..133618
FT FT /tag= j
FT FT /number= 5
FT FT 133619..137732
FT FT /tag= k
FT FT /number= 5
FT FT 137733..137875
FT FT /tag= l
FT FT /number= 6

FT intron 137876..139687
FT /tag= m
FT /number= 6
FT 139688..140305
FT /tag= n
FT /number= 7
FT replace (981,C)
FT /tag= o
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (1012,T)
FT /tag= p
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (1390,G)
FT /tag= q
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (3432,T)
FT /tag= r
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (4658,C)
FT /tag= s
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (4772,A)
FT /tag= t
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (7738,C)
FT /tag= u
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (9118,A)
FT /tag= v
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (9192,G)
FT /tag= w
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (9222,A)
FT /tag= x
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (9734,T)
FT /tag= y
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (9795,G)
FT /tag= z
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (9853,C)
FT /tag= aa
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (10397,A)
FT /tag= ab
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (11198,T)
FT /tag= ac
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (11470,T)
FT /tag= ad
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (11534,C)
FT /tag= ae
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (11557,G)
FT /tag= af
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (11540,G)
FT /tag= ag
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (11708,C)
FT /tag= ah
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (11953,T)
FT /tag= ai
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (1167,C)
FT /tag= aj
FT /standard_name= "Single-nucleotide polymorphism"
FT replace (12172,C)
FT variation

```

FT      /*tag= ak
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I2188,A)
FT      /*tag= al
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I3471..13472,TTT)
FT      /*tag= am
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I3781,C)
FT      /*tag= an
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I4031,G)
FT      /*tag= ao
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I4110,C)
FT      /*tag= ap
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I4248,G or T)
FT      /*tag= aq
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I4676,C or A)
FT      /*tag= ar
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I4981,T)
FT      /*tag= as
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I6365,G)
FT      /*tag= at
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I6827,A)
FT      /*tag= au
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I7599,T)
FT      /*tag= av
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I8093,G)
FT      /*tag= aw
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I8226,C)
FT      /*tag= ax
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I8467..18468,GTT or GGT)
FT      /*tag= ay
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I8511..18512,TAC or TTC)
FT      /*tag= az
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I9107,A)
FT      /*tag= ba
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I9223,G)
FT      /*tag= bb
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I20102,C)
FT      /*tag= bc
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I21946,T)
FT      /*tag= bd
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I2240,C)
FT      /*tag= be
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I22679,G)
FT      /*tag= bf
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I23178,C or G)
FT      /*tag= bg
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I23370,G)
FT      /*tag= bh
FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I23583,G)
FT      /*tag= bi

```

```

FT      /standard name="Single-nucleotide polymorphism"
FT      replace (I24159,A)
FT      /*tag= bj
FT      Query Match
FT      Best Local Similarity 100.0%; Score 19; DB 24; Length 143306;
FT      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      321 TCAAGTAGATGCAAAATA 339
DB      18852 TCAAGTAGATGCAAAATA 18834
RESULT 86
AAA77296/c
ID AAA77296 standard; cDNA; 51 BP.
XX
AC AAA77296;
XX
DT 16-NOV-2000 (first entry)
XX
DE Human clone cg43997710 polymorphic site, SEQ ID NO:979.
XX
KW Human; single nucleotide polymorphism; SNP;
KW detection; identification; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace (26,A)
FT /*tag= a
XX
PN MO200029623-A2.
XX
PD 25-MAY-2000.
XX
PF 17-NOV-1999; 99WO-US27293.
XX
PR 17-NOV-1998; 98US-0109024.
PR 16-NOV-1999; 99US-0109024.
XX
PA (CURA-) CURAGEN CORP.
PI Shinketsu RA, Leach MD;
XX
WP: 2000-387826/33.
XX
DR Human nucleic acids containing single nucleotide polymorphisms, useful
PT for treating a subject suffering, or at risk from a pathology due to
PT the presence of a sequence polymorphism -
XX
PS Claim 1; Page 453; 543pp; English.
XX
CC Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC 1112 (AAA76318-A77429) are consecutive pairs of nucleotides which
CC contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are
CC consecutive pairs of nucleotides containing SNPs which result in changes
CC in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC in non-conservative changes. The SNPs in sequences 1187 to 1192
CC (AAA77504-A77509) generate frameshift mutations. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic
CC proteins/peptides using the antibodies. The nucleic acids are useful for
CC gene therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the
CC wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals.

```


XX Sequence 51 BP; 19 A; 6 C; 13 G; 13 T; 0 other;
 SQ Query Match 0.8%; Score 18; DB 21; Length 51;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1914 ATATATTAATTTGCTT 1931
 |||||
 41 ATATATTAATTTGCTT 24
 Db
 RESULT 87
 ABX55959/c
 ID ABX55959 standard; cDNA; 324 BP.
 XX
 XX ABX55959;
 AC
 XX 26-FEB-2003 (first entry)
 DT
 XX Bovine EST associated with lactation/muscle/fat deposition #5888.
 DE
 XX Bovine; ss; EST; expressed sequence tag; lactation; LMPD;
 KM muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX
 XX Bos Taurus.
 OS
 XX US200217160-A1.
 PN
 XX 26-SEP-2002.
 PD
 XX 26-OCT-2001; 2001US-0983965.
 PF
 XX 17-DEC-1998; 98US-113678P.
 PR 15-DEC-1999; 99US-0465231.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX
 PI Byatt JC; Mathialagan N; Tao N; Warren WC;
 DR WPI; 2003-102386/09.
 XX
 PT Purified nucleic acid molecules, useful for genome mapping, gene
 PT identification and analysis, cattle breeding or preparation of
 PT constructs for cattle gene expression and genetically improved cattle -
 XX
 XX Claim 2; SEQ ID No 5888; 38pp; English.
 PS
 CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMPD), derived
 CC from cattle, and the LMPD nucleic acid can specifically hybridize to a
 CC second nucleic acid molecule comprising any of 5912 nucleotide
 CC sequences, appearing as ABX50072-ABX55983, or complements of them.
 CC Also included are; (1) a transformed cell having a nucleic acid
 CC comprising an LMPD nucleic acid linked to a promoter and a 3' non-
 CC translated sequence and that functions in the cell to cause termination of
 CC transcription and addition of polyadenylated ribonucleotides to a 3' end
 CC of the mRNA molecule; and (2) determining a level or pattern of a
 CC molecule in a bovine cell or tissue comprising: (a) incubating a marker
 CC nucleic acid (comprising any of the 5912 nucleic acid sequences or its
 CC complement or fragment) with a complementary nucleic acid molecule
 CC obtained from the bovine cell or tissue, where hybridisation between the
 CC marker nucleic acid and the complementary nucleic acid permits the
 CC detection of the molecule; and (b) detecting the level or pattern of the
 CC complementary nucleic acid, where the detection of the complementary
 CC nucleic acid is predictive of the level or pattern of the molecule.
 CC The LMPD nucleic acid is used for determining a level or pattern
 CC of a molecule in a bovine cell or tissue. It is useful for genome
 CC mapping, gene identification and analysis, cattle breeding, preparation

CC of constructs for use in cattle gene expression, or for genetically
 CC improving cattle. The present sequence is one of the 5912 bovine
 CC LMPD EST (expressed sequence tag) nucleic acids.
 CC Note: The present sequence was not shown in the specification but
 CC was obtained in electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?docid=20020137160.
 XX
 SQ Sequence 324 BP; 113 A; 62 C; 49 G; 100 T; 0 other;
 Query Match 0.8%; Score 18; DB 25; Length 324;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1101 TTTAAATAGACTCAAAATT 1118
 |||||
 108 TTTAAATAGACTCAAAATT 91
 Db
 RESULT 88
 AAC05686/c
 ID AAC05686 standard; cDNA; 327 BP.
 XX
 XX AAC05686;
 AC
 XX 06-OCT-2000 (first entry)
 DT
 XX Human secreted protein 5' EST, SEQ ID NO: 9761.
 DE
 XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KM gene therapy; chromosome mapping; ss.
 KW
 XX Homo sapiens.
 OS
 XX EP1033401-A2.
 PN
 XX 06-SEP-2000.
 PD
 XX 21-FEB-2000; 2000EP-0200610.
 PF
 XX 26-FEB-1999; 99US-0122487.
 PR
 XX (GEST) GENSET.
 XX
 PA Dumas Milne Edwards J; Duclert A; Giordano J;
 PA
 XX
 PI WPI; 2000-500381/45.
 DR
 XX
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 XX Claim 1; SEQ ID 9761; 71pp + CD-ROM; English.
 PS
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC cDNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX
 SQ Sequence 327 BP; 79 A; 72 C; 70 G; 106 T; 0 other;
 Query Match 0.8%; Score 18; DB 21; Length 327;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 739 TACAATATAACACAG 756
| | | | | | | | | |
Db 173 TACAATATAACACAG 156

RESULT 89
AAFI7998
ID AAFI7998 standard; DNA; 372 BP.
XX
AC AAFI7998;
XX
DT 14-MAR-2001 (first entry)
XX
DE Lung cancer associated polynucleotide sequence SEQ ID 17.
XX
KM Human; lung cancer associated protein; neuroprotective; cytostatic;
KM cardioactive; immunomodulatory; muscular active; vulnery;
KM gastrointestinal; nephrotropic; antiinfective; gynecological;
KM antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KM proliferative disorder; wound healing; infectious disease; ds.
XX
OS Homo sapiens.
XX
PN WO200055180-A2.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05918.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE-) ROSEN C A.
XX
PI Ruben SM;
XX
DR WPI; 2000-587514/55.
XX
P-PSDB; AAB58122.
XX
PT Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer -
XX
PS Claim 1; Page 502; 1425pp; English.
XX
CC polynucleotide sequences AAFI7982 - AAFI8424 encode human lung cancer
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC antagonists may have neuroprotective; cytostatic; cardioactive;
CC immunomodulatory; muscular active; general; vulnery; gastrointestinal
CC general; nephrotropic; antiinfective; gynecological; or antibacterial
CC activity. The invention also includes antibodies specific for the
CC protein or polynucleotide sequences. The lung cancer associated
CC polynucleotide sequences may be used for detection of lung cancer,
CC chromosome identification, as chromosome markers, and for numerous other
CC diagnostic or research purposes. The proteins may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders. The proteins may also be used in the treatment of wounds and
CC infectious diseases. Polynucleotide sequences AAFI8425 - AAFI8433 and
CC peptide AAB58549 are used in the course of the invention for the
CC identification and characterisation of the polynucleotide and protein
CC sequences.
XX
SQ Sequence 372 BP; 91 A; 83 C; 113 G; 81 T; 4 other;

Query Match 0.8%; Score 18; DB 21; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2195 AAAGAAGCAGAGTTTGG 2212
| | | | | | | | | |

Db 99 AAAGAAGCAGAGTTTGG 116

RESULT 90
ABV94637
ID ABV94637 standard; cDNA; 372 BP.
XX
AC ABV94637;
XX
DT 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 10.
XX
KM Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KM cytostatic; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US02781.
XX
PR 30-JAN-2001; 2001US-265305P.
XX
PR 31-JAN-2001; 2001US-265682P.
XX
PR 09-FEB-2001; 2001US-267568P.
XX
PR 21-MAR-2001; 2001US-278651P.
XX
PR 28-APR-2001; 2001US-287112P.
XX
PR 16-MAY-2001; 2001US-291631P.
XX
PR 12-JUL-2001; 2001US-305484P.
XX
PR 20-AUG-2001; 2001US-313999P.
XX
PR 27-NOV-2001; 2001US-333626P.
XX
PA (CORI-) CORIAX CORP.
XX
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX
XX
DR WPI; 2002-627435/67.
XX
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful
PT for diagnosing, preventing and/or treating cancer, particularly
PT pancreatic cancer -
XX
PS Claim 1; SEQ ID NO 10; 300pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145);
CC (b) complements of (a); (c) sequences consisting of at least 20
CC contiguous residues of (a); (d) sequences that hybridize to (a), under
CC moderately stringent conditions; (e) sequences having at least 75% or 90%
CC identity to (a); or (f) degenerate variants of (a). Polypeptides
CC (ABV68596-ABV68637) encoded by (I) and oligonucleotide can be used to
CC detect cancer in a patient and compositions comprising polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations and
CC antigen presenting cells expressing the polypeptide are useful in
CC treating pancreatic cancer and stimulating an immune response. The
CC polynucleotides can be used as probes or primers for nucleic acid
CC hybridisation, in the design and preparation of ribozyme molecules for
CC inhibiting expression of the tumour polypeptides and proteins in the
CC tumour cells, in vaccines and for gene therapy.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 372 BP; 127 A; 48 C; 68 G; 129 T; 0 other;

Query Match 0.8%; Score 18; DB 24; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 232 TATCATCAGTGAGAAATT 249
| | | | | | | | | |

Db 228 TATCATCAGTGAGAAATT 245

RESULT 91
AA184590
ID AA184590 standard; cDNA; 379 BP.
XX
XX AA184590;
XX
XX
DT 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 4650.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
XX Homo sapiens.
OS
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US04927.
XX
XX 28-FEB-2000; 2000US-0515126.
XX 18-MAY-2000; 2000US-0577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
PI
XX
XX WPI: 2001-514838/56.
XX
XX P-PSDB; AA004659.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
XX Claim 1; SEQ ID NO 4650; 1359pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibit activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 379 BP; 160 A; 65 C; 68 G; 86 T; 0 other;

Query Match 0.8%; Score 18; DB 22; Length 379;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 751 CACAGCAACAAACAGCAA 768
DB 74 CACAGCAACAAACAGCAA 91

RESULT 92
AAC00113
ID AAC00113 standard; cDNA; 423 BP.
XX
XX AAC00113;

XX
XX 06-OCT-2000 (first entry)
DT
XX
XX Human secreted protein 5' EST, SEQ ID NO: 111.
DE
XX
XX Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
XX Homo sapiens.
OS
XX EP1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-0200610.
XX
XX 26-FEB-1999; 990US-0122487.
XX
XX (GSEST) GENSEST.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI
XX
XX WPI: 2000-500381/45.
XX
XX P-PSDB; AAG00107.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 1; SEQ ID 111; 71pp + CD-ROM; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC derived from 30 different tissues. EST sequences usually correspond
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC well suited for isolating cDNA sequences derived from the 5' ends of
CC mRNAs and even in those cases where longer cDNA sequences have been
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC mRNAs with intact 5' ends and can therefore be used to obtain full length
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
CC vectors.
XX
XX Sequence 423 BP; 108 A; 91 C; 133 G; 89 T; 2 other;

Query Match 0.8%; Score 18; DB 21; Length 423;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2195 AAAGAGCGAAGATTGG 2212
DB 130 AAAGAGCGAAGATTGG 147

RESULT 93
AAC77174
ID AAC77174 standard; cDNA; 448 BP.
XX
XX AAC77174;
AC
XX
XX 08-FEB-2001 (first entry)
XX
XX Human ORF2729 polynucleotide sequence SEQ ID NO:5457.
XX
XX Human; open reading frame; ORF; detection; cytosolic; hepatotropic;
KW vulnery; antiporatic; antiparkinsonian; nocotropic; neuroprotective;
KW anticonvulsant; osteopahic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antineoplastic;
KW antiviral; antibacterial; antifungal; antineumatic; antithyroid;

KW anti-nausea; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; anti-inflammatory disease; coagulation;
 KW thrombosis; contraceptive; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200058473-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000WO-US08621.
 XX
 PR 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI: 2000-602362/57.
 DR P-PSDB; AAB42965.
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 PS Claim 5, Page 4639; 5507pp; English.
 XX
 CC AACT4446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatocytic; vulnery;
 CC antiproliferative; antiparkinsonian; nootropic; neuroprotective;
 CC osteoprotic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiac; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatologic; immunosuppressive;
 CC anti-inflammatory; antibacterial; antiviral; antifungal; antineoplastic;
 CC antithyroid; and anti-nausea. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, anti-inflammatory disease, to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX
 SQ Sequence 448 BP; 111 A; 106 C; 129 G; 102 T; 0 other;
 Query Match 0.8%; Score 18; DB 21; Length 448;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1914 ATATATTTAAATTTGCTT 1931
 Db 308 ATATATTTAAATTTGCTT 325
 RESULT 94
 AABN5206/C
 ID AABN5206 standard; cDNA; 495 BP.
 XX
 AC AABN5206;

XX
 DT 28-JUN-2002 (first entry)
 XX
 DE Human cancer related polynucleotide SEQ ID NO 5173.
 XX
 KW Human; cytostatic; gene expression; gene mapping; tissue profiling;
 KW gene therapy; cancer; tumour; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO20024500-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 16-AUG-2001; 2001WO-US25840.
 XX
 PR 16-AUG-2000; 2000US-226326P.
 XX
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 XX
 PI Escobedo J, Garcia PD, Sudduth-Klinger J, Reinhard C, Randazzo F,
 PI Lamson G, Scott EM, Zhang G, Kassam A, Pot D, Labat I;
 XX
 DR WPI: 2002-241905/29.
 XX
 PT New nucleic acid for producing a polypeptide, detecting differentially
 PT expressed genes correlated with a cancerous state of a mammalian cell,
 PT and inhibiting tumor growth -
 XX
 PS Claim 1; SEQ ID NO 5173; 883pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (ABN27253-ABN33262)
 CC with cytostatic activity. The polynucleotide is used to produce a
 CC polypeptide, to detect differentially expressed genes correlated with a
 CC cancerous state of a mammalian cell and to inhibit tumour growth. The
 CC polynucleotide is used as a probe in mapping and tissue profiling. The
 CC encoded polypeptide and antibodies to the polypeptide can also be used
 CC for therapeutic and diagnostic purposes. The polynucleotide is useful for
 CC gene therapy.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 495 BP; 157 A; 83 C; 87 G; 168 T; 0 other;
 Query Match 0.8%; Score 18; DB 24; Length 495;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 789 AAAGTAATGACATGATA 806
 Db 312 AAAGTAATGACATGATA 295
 RESULT 95
 AAC57418/C
 ID AAC57418 standard; DNA; 499 BP.
 XX
 AC AAC57418;
 XX
 DT 25-JAN-2001 (first entry)
 XX
 DE Archidonic acid metabolism related genomic biallelic marker #52.
 XX
 KW Human; biallelic marker; archidonic acid metabolism; genotyping;
 KW detection; hybridisation; phenotype; haplotype; SNP; polymorphic base;
 KW single nucleotide polymorphism; hybridisation assay; sequencing assay;
 KW specific amplification assay; identification; ERM; 12-LO-RBM;
 KW eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds.
 XX
 OS Homo sapiens.
 XX

PN WO200047771-A2.
 XX
 PD 17-AUG-2000.
 XX
 PF 11-FEB-2000; 2000WO-IB00184.
 XX
 PR 12-FEB-1999; 99US-0119917.
 PR 23-MAR-1999; 99US-0275267.
 PR 07-MAY-1999; 99US-0133200.
 XX
 PA (GEST) GENSET.
 XX
 PI Blumenfeld M, Bougueleret L, Chumakov I;
 PI WPI; 2000-571881/53.
 DR
 XX
 PT Novel biallelic markers useful for detecting conditions and genotypes
 PT associated with arachidonic acid metabolism -
 PS
 PS Claim 13; Page 274; 802pp; English.
 XX
 CC The present invention describes polynucleotides including biallelic
 CC markers derived from genes involved in arachidonic acid metabolism and
 CC from genomic regions flanking those genes. Methods from the present
 CC invention may be used to select individuals for clinical trials and
 CC predict responses to treatment with drugs. The polynucleotides may be
 CC used in hybridisation assays, sequencing assays and specific
 CC amplification assays for identifying an eicosanoid-related biallelic
 CC marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a
 CC segment of nucleotide containing an ERBM. The polynucleotides are
 CC useful in diagnostic kits. The markers may be used to detect conditions
 CC and genotypes associated with arachidonic acid metabolism. AAC57367 to
 CC AAC58018 and AAB24019 and AAB24020 represent sequences used in the
 CC exemplification of the present invention.
 CC N.B. Polymorphic bases (single nucleotide polymorphisms also known as
 CC SNPs) in the polynucleotide sequences from the present invention have
 CC been given as their corresponding degenerate bases e.g. a polymorphic
 CC base of C or T has been given as Y.
 CC
 SQ Sequence 499 BP; 123 A; 61 C; 86 G; 227 T; 2 other;
 QY
 Query Match 0.8%; Score 18; DB 21; Length 499;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 751 CACAGCAACACACAGCAA 768
 76 CACAGCAACACACAGCAA 59
 RESULT 96
 AAC57938/c
 ID AAC57938 standard; DNA; 499 BP.
 AC
 AC AAC57938;
 XX
 DT 25-JAN-2001 (first entry)
 XX
 DE Arachidonic acid metabolism related genomic biallelic marker #572.
 XX
 KW Human; biallelic marker; arachidonic acid metabolism; genotyping;
 KW detection; hybridisation; phenotype; SNP; polymorphic base;
 KW single nucleotide polymorphism; hybridisation assay; sequencing assay;
 KW specific amplification assay; identification; ERBM; 12-LO-RBM;
 KW eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200047771-A2.
 PD 17-AUG-2000.
 XX
 PF 11-FEB-2000; 2000WO-IB00184.

XX
 PR 12-FEB-1999; 99US-0119917.
 PR 23-MAR-1999; 99US-0275267.
 PR 07-MAY-1999; 99US-0133200.
 XX
 PA (GEST) GENSET.
 XX
 PI Blumenfeld M, Bougueleret L, Chumakov I;
 PI WPI; 2000-571881/53.
 DR
 XX
 PT Novel biallelic markers useful for detecting conditions and genotypes
 PT associated with arachidonic acid metabolism -
 PS
 PS Claim 13; Page 709; 802pp; English.
 XX
 CC The present invention describes polynucleotides including biallelic
 CC markers derived from genes involved in arachidonic acid metabolism and
 CC from genomic regions flanking those genes. Methods from the present
 CC invention may be used to select individuals for clinical trials and
 CC predict responses to treatment with drugs. The polynucleotides may be
 CC used in hybridisation assays, sequencing assays and specific
 CC amplification assays for identifying an eicosanoid-related biallelic
 CC marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a
 CC segment of nucleotides containing an ERBM. The polynucleotides are
 CC useful in diagnostic kits. The markers may be used to detect conditions
 CC and genotypes associated with arachidonic acid metabolism. AAC57367 to
 CC AAC58018 and AAB24019 and AAB24020 represent sequences used in the
 CC exemplification of the present invention.
 CC N.B. Polymorphic bases (single nucleotide polymorphisms also known as
 CC SNPs) in the polynucleotide sequences from the present invention have
 CC been given as their corresponding degenerate bases e.g. a polymorphic
 CC base of C or T has been given as Y.
 CC
 SQ Sequence 499 BP; 123 A; 61 C; 86 G; 228 T; 1 other;
 QY
 Query Match 0.8%; Score 18; DB 21; Length 499;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 751 CACAGCAACACACAGCAA 768
 76 CACAGCAACACACAGCAA 59
 RESULT 97
 AAL45031
 ID AAL45031 standard; CDNA; 914 BP.
 AC
 AC AAL45031;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE A thaliana AMP deaminase coding sequence fragment EST.
 XX
 KW AMP deaminase; adenosine monophosphate; transgenic plant; EST;
 KW herbicide resistance; herbicide; inhibitor; expressed sequence tag; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 FT CDS 2..880
 FT /*tag= a
 FT /product= "AMP deaminase fragment"
 PN WO200206319-A2.
 PD 24-JAN-2002.
 XX
 XX 06-JUL-2001; 2001WO-EP07767.
 PF 17-JUL-2000; 2000DE-1035084.
 XX

PA (AVET) AVENTIS CROPS SCIENCE GMBH.
 XX
 PS
 PI Schulz A, Streiber W, Hanke C, Schmidt F, Schubel A;
 XX
 DR WPI, 2002-195802/25.
 XX
 DR P-PSDB; AA016944.
 XX
 PT New nucleic acid for plant adenosine monophosphate deaminase, useful in
 XX screening for herbicides and preparing herbicide-resistant plants -
 PS Example 2; Page 23; 51pp; German.
 XX
 CC The present invention provides the protein and coding sequences of the
 CC Arabidopsis thaliana adenosine monophosphate (AMP) deaminase. The coding
 CC sequence can be used to transform prokaryotic or eukaryotic cells,
 CC especially to produce transgenic plants (e.g. barley, rice, soya etc.)
 CC resistant to herbicidal inhibitors of AMP-deaminase, for recombinant
 CC production of proteins with AMP-deaminase activity, and to identify
 CC related genes in other organisms. The protein can be used for
 CC identification and biochemical/structural characterisation of new
 CC AMP-deaminase inhibitors and potential herbicides. The present sequence
 CC is an EST encoding a fragment of the protein of the invention.
 XX
 SQ Sequence 914 BP; 250 A; 215 C; 196 G; 253 T; 0 other;
 XX
 Query Match 0.8%; Score 18; DB 24; Length 914;
 Best Local Similarity 100.0%; Pred. No. 2,3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1661 CACTGATTGGAAGAAGAT 1678
 DB 716 CACTGATTGGAAGAAGAT 733
 RESULT 98
 AAS56173/c
 ID AAS56173 standard; DNA; 924 BP.
 XX
 AC AAS56173;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Salmonella typhi DNA for cellular proliferation protein #206.
 XX
 KW Antisense; ds; prokaryotic cellular proliferation gene;
 XX antibiotic; antibacterial; drug design.
 XX
 OS Salmonella typhi.
 XX
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 XX
 PR 23-MAY-2000; 2000US-206848P.
 XX
 PR 26-MAY-2000; 2000US-207727P.
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 PR 23-OCT-2000; 2000US-242578P.
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 PR 27-NOV-2000; 2000US-253625P.
 XX
 PR 22-DEC-2000; 2000US-257931P.
 XX
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
 XX Yamamoto RT, Xu HH;
 XX
 DR WPI: 2001-611495/70.
 XX
 DR P-PSDB; AAU38314.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -

XX
 PS Claim 27; Seq ID No 9810; 51pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence encodes an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pcr_sequences.
 XX
 SQ Sequence 924 BP; 241 A; 213 C; 269 G; 200 T; 1 other;
 XX
 Query Match 0.8%; Score 18; DB 23; Length 924;
 Best Local Similarity 100.0%; Pred. No. 2,3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2106 ACTTCAAGCGGATGAAG 2123
 DB 854 ACTTCAAGCGGATGAAG 837
 RESULT 99
 ABL12667/c
 ID ABL12667 standard; CDNA; 1038 BP.
 XX
 AC ABL12667;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32483.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 XX
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 XX
 DR P-PSDB; ABB68564.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS Claim 1; SEQ ID NO 32483; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB01840-AB16175) and the encoded proteins
CC (AB057737-AB072072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1038 BP; 295 A; 238 C; 222 G; 283 T; 0 other;

Query Match 0.8%; Score 18; DB 23; Length 1038;
Best Local Similarity 100.0%; Pred.No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1882 TAATTGATTATTCCTCA 1899
Db 788 TAATTGATTATTCCTCA 771

RESULT 100
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ID AAC44226 standard; DNA; 1077 BP.
XX
AC AAC44226;
XX
DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 42087.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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 PR 26-OCT-1999; 99US-0161361.

PR 28-OCT-1999; 99US-0161920.
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Query Match 0.8%; Score 18; DB 21; Length 1077;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Job time : 683 secs

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OM nucleic - nucleic search, using sw model

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and is derived by analysis of the total score distribution.

SUMMARIES

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18	21	0.9	935	13	BU273390	603531527	BU273390 603531527
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20	20	0.8	228	28	AZ502341	1M0341023	AZ502341 1M0341023
21	20	0.8	233	28	AZ769909	1M0571001	AZ769909 1M0571001
22	20	0.8	267	28	AZ943045	2M0203306	AZ943045 2M0203306
23	20	0.8	371	10	BB803034	BB803034	BB803034 BB803034
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68	19	0.8	175	10	BE505229	dc19g09.x	BE505229 dc19g09.x
69	19	0.8	186	28	BH867080	hg93b06.y	BH867080 hg93b06.y
70	19	0.8	220	9	AV236691	AV236691	AV236691 AV236691
71	19	0.8	257	28	AO948125	Sheared D	AO948125 Sheared D
72	19	0.8	271	10	BA402033	BA402033	BA402033 BA402033
73	19	0.8	296	14	CD265572	PSM011XC	CD265572 PSM011XC
74	19	0.8	303	10	AM880404	QVO-OT03	AM880404 QVO-OT03
75	19	0.8	303	12	BM248898	K0824E07-	BM248898 K0824E07-
76	19	0.8	304	10	BB290438	BB290438	BB290438 BB290438
77	19	0.8	304	10	BB367558	BB367558	BB367558 BB367558

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78      19      0.8      309      29      B2244064      B2244064      CH230-362
79      19      0.8      317      10      B1138766      B1138766      B1138766
80      19      0.8      319      10      BB463922      BB463922      BB463922
81      19      0.8      324      9      AV046714      AV046714      AV046714
82      19      0.8      333      28      BH294683      BH294683      CH230-122
83      19      0.8      335      28      AA558478      AA558478      nk39d05.s
84      19      0.8      340      28      A0825612      A0825612      HS_5437_B
85      19      0.8      364      28      A0910031      A0910031      G5STC0640
86      19      0.8      370      10      BF374552      BF374552      MR1-TN004
87      19      0.8      375      10      BF376477      BF376477      MR1-TN004
88      19      0.8      377      9      A1883328      A1883328      fc60e02.y
89      19      0.8      386      13      BY649148      BY649148      BY649148
90      19      0.8      396      10      BF376465      BF376465      MR1-TN004
91      19      0.8      401      10      BE002498      BE002498      PM3-BN008
92      19      0.8      401      29      B2941299      B2941299      CH240_91P
93      19      0.8      402      10      BF885054      BF885054      MR1-TN004
94      19      0.8      409      10      BF554284      BF554284      UT-R-C1-K
95      19      0.8      412      13      BY605266      BY605266      BY605266
96      19      0.8      414      9      AL961018      AL961018      AL961018
97      19      0.8      415      12      BM248963      BM248963      K0825607-
98      19      0.8      417      10      BE505361      BE505361      dc23a08.x
99      19      0.8      418      13      BY457007      BY457007      BY457007
100     19      0.8      434      28      A0207842      A0207842      HS_3028_A
101     19      0.8      434      29      CC029019      CC029019      3591.1.10
102     19      0.8      440      10      BE635488      BE635488      SHBSTA06
103     19      0.8      440      28      A0188923      A0188923      HS_3192_B
104     19      0.8      448      9      AM046397      AM046397      UT-M-BH1-
105     19      0.8      457      28      BS6992      BS6992      C1T-HSP-200
106     19      0.8      457      28      AU081605      AU081605      AU081605
107     19      0.8      462      28      A0393398      A0393398      CIRBI-E1-
108     19      0.8      467      13      A1502258      A1502258      UT-R-C1-K
109     19      0.8      479      13      BY492908      BY492908      BY492908
110     19      0.8      485      10      BF942976      BF942976      QVO-NN114
111     19      0.8      491      28      A0944295      A0944295      Sheared D
112     19      0.8      495      9      AL867799      AL867799      AL867799
113     19      0.8      499      13      BU663360      BU663360      C1100a05.
114     19      0.8      501      28      A2481176      A2481176      IM0303F14
115     19      0.8      514      10      BF025045      BF025045      dc83e03.x
116     19      0.8      517      28      BH788839      BH788839      f2mb021f0
117     19      0.8      524      9      AL651149      AL651149      AL651149
118     19      0.8      525      9      AM743009      AM743009      up55c01.x
119     19      0.8      536      9      AL644915      AL644915      AL644915
120     19      0.8      536      28      A2364035      A2364035      IM0110L01
121     19      0.8      537      10      BE098306      BE098306      UT-R-B11-
122     19      0.8      539      14      CB829845      CB829845      r106a09.y
123     19      0.8      541      9      A1009609      A1009609      EST204060
124     19      0.8      546      29      CC172145      CC172145      1176b05.G
125     19      0.8      547      9      AL598888      AL598888      DKFZP313A
126     19      0.8      553      28      A2396203      A2396203      A1639919
127     19      0.8      557      9      AL639919      AL639919      AL639919
128     19      0.8      560      29      B2821447      B2821447      FUGDV21TD
129     19      0.8      561      28      A2494994      A2494994      IM0330B11
130     19      0.8      566      28      A2231630      A2231630      RPCI-23-6
131     19      0.8      573      28      A0489684      A0489684      RPCI-11-2
132     19      0.8      576      14      CB867995      CB867995      HC02K10w
133     19      0.8      577      28      BH786618      BH786618      f2mb014f0
134     19      0.8      578      10      BF007111      BF007111      1477049.A
135     19      0.8      582      28      BH398547      BH398547      AG-ND-148
136     19      0.8      583      28      A2338047      A2338047      IM0068B19
137     19      0.8      590      28      BS9270      BS9270      C1T-HSP-201
138     19      0.8      595      13      BQ286841      BQ286841      1161b10.x
139     19      0.8      597      9      AU100630      AU100630      AU100630
140     19      0.8      597      12      BM491868      BM491868      P9D2n.PK0
141     19      0.8      609      13      BU479735      BU479735      BU479735
142     19      0.8      615      28      BS5701      BS5701      C1T-HSP-200
143     19      0.8      620      9      A1574440      A1574440      uk21c01.y
144     19      0.8      620      9      AL647248      AL647248      AL647248
145     19      0.8      629      9      AL792122      AL792122      AL792122
146     19      0.8      630      9      AL874461      AL874461      AL874461
147     19      0.8      631      9      AL627924      AL627924      AL627924
148     19      0.8      634      9      AL891387      AL891387      AL891387
149     19      0.8      636      9      AL642283      AL642283      AL642283

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151     19      0.8      636      28      A2411549      A2411549      IM0184H11
152     19      0.8      640      9      AL873932      AL873932      AL873932
153     19      0.8      642      10      BB467078      BB467078      BB467078
154     19      0.8      643      9      AL954908      AL954908      AL954908
155     19      0.8      643      9      AM391405      AM391405      QV4-ST021
156     19      0.8      648      13      BQ859663      BQ859663      QGC13K13.
157     19      0.8      649      9      AL861345      AL861345      AL861345
158     19      0.8      651      9      AL893908      AL893908      AL893908
159     19      0.8      652      9      AL888054      AL888054      AL888054
160     19      0.8      652      13      BQ397518      BQ397518      NISC.RG28
161     19      0.8      652      14      CA814289      CA814289      CA814289
162     19      0.8      656      9      AL973266      AL973266      AL973266
163     19      0.8      657      29      CC445648      CC445648      PUKM64TD
164     19      0.8      658      14      CD213529      CD213529      HSI_41.GO
165     19      0.8      661      13      BU269133      BU269133      603507891
166     19      0.8      662      9      AL857690      AL857690      AL857690
167     19      0.8      664      28      A2154788      A2154788      SP_0019_A
168     19      0.8      668      9      AL886201      AL886201      AL886201
169     19      0.8      672      29      B2530407      B2530407      B2530407
170     19      0.8      673      14      CB670071      CB670071      OCAK66TM
171     19      0.8      675      28      BH942657      BH942657      odg51e01
172     19      0.8      675      29      AG041704      AG041704      Pan.trog1
173     19      0.8      678      29      AG093187      AG093187      Pan.trog1
174     19      0.8      682      29      AG103329      AG103329      Pan.trog1
175     19      0.8      689      13      BU466818      BU466818      603372113
176     19      0.8      689      28      A2356122      A2356122      IM0097P01
177     19      0.8      690      13      BU467071      BU467071      603373366
178     19      0.8      696      12      BM436991      BM436991      VVA012D07
179     19      0.8      696      29      CNS0105C      CNS0105C      AL155680
180     19      0.8      701      29      B2786641      B2786641      AL962927
181     19      0.8      701      28      AZ104118      AZ104118      RPCI-23-2
182     19      0.8      711      13      BU004246      BU004246      OCG3f03.Y
183     19      0.8      711      14      CA750429      CA750429      UT-M-PY0-
184     19      0.8      711      13      BU450047      BU450047      603217196
185     19      0.8      716      10      BB340597      BB340597      BB340597
186     19      0.8      716      13      BU285148      BU285148      603603039
187     19      0.8      719      9      AL632000      AL632000      AL632000
188     19      0.8      721      13      BQ868729      BQ868729      OGD1D06.Y
189     19      0.8      726      14      CB667006      CB667006      OSGNEB14C
190     19      0.8      726      28      BH931736      BH931736      odg92f07.
191     19      0.8      727      28      B2057551      B2057551      1K975b04.
192     19      0.8      728      13      BU481748      BU481748      603469336
193     19      0.8      732      28      BH028155      BH028155      RPCI-24-3
194     19      0.8      734      13      BU752729      BU752729      SJWCMB10
195     19      0.8      737      14      CB527334      CB527334      UT-M-PY0-
196     19      0.8      739      14      CB650155      CB650155      OSGNEB14H
197     19      0.8      749      29      AG075433      AG075433      Pan.trog1
198     19      0.8      750      14      CB655195      CB655195      OSGNEC08F
199     19      0.8      753      13      BU329419      BU329419      603494601
200     19      0.8

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ALIGNMENTS

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RESULT 1      261 bp      mRNA      linear      EST 19-MAR-2001
LOCUS      BE528097
DEFINITION      Arabidopsis developing seed Arabidopsis thaliana cDNA
ACCESSION      BE528097
VERSION      BE528097.1
KEYWORDS      GI:9786075
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
1 (bases 1 to 261)
White,J.A., Todd,J., Newman,T., Focks,N., Gire,T., Martinez de
Iiarduya,O., Jaworski,J.G., Ohlrogge,J. and Bennett,C.
A new set of Arabidopsis expressed sequence tags from developing
seeds. The metabolic pathway from carbohydrates to seed oil

```

JOURNAL Plant Physiol. 124 (4), 1582-1594 (2000)
MEDLINE 20567808
PUBMED 1115876
COMMENT Contact: Benning, C

BASE COUNT	80 a	52 c	55 g
ORIGIN			

	Query Match	Score	DB	Length
Best Local Similarity	100.0%	22	10	261
Matches	22	Conservative	0	Mismatches
			Indels	Gaps
Qy	2285	ACTCTTCAATTATGGATPACA	2306	
Db	200	ACTCTTCAATTATGGATPACA	221	

FEATURES	details.	Location/Qualifiers
source		1. .618

BASE COUNT	171 a	152 c	110 g	182 f	3 others
ORIGIN					

	Query Match	0.9%;	Score 22;	DB 9;	Length 618;
	Best Local Similarity	100.0%;	Pred. No. 27;		
Matches	22; Conservative	0;	Mismatches	0;	Gaps 0;
Oy	2285 ACTCTTCAATTAAGATAACA	2306			
Dab	481 ACTCTTCAATTAAGATAACA	502			

BASE COUNT	210 a	107 c	135 g	229 t	1 others
ORIGIN					

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Query Match      0.9%; Score 22; DB 28; Length 682;
Best Local Similarity 100.0%; Pxd. No. 29;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ox    1811 AAAGGGAAAAACGAATTCAC 1832
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        |||||
Db     44 AAAGGGAAAAACGAATTCAC 23

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RESULT 4
LOCUS BU473013/c 411 bp mRNA linear EST 30-NOV-2002
DEFINITION 603365019r1 CSEQRBN21 Gallus gallus cDNA clone CHEST262f5 5', mRNA
sequence.
ACCESSION BU473013
VERSION BU473013.1 GI:25966590
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianine; Gallus.
REFERENCE 1 (bases 1 to 411)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.,
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
JOURNAL MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
FEATURES
source
1..411
Location/Qualifiers
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="CHEST262f5"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="CSEQRBN21"
/note="Organ: ovary; Vector: pluescript II KS(+); Site 1:
EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pbluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996) 791, except that a significantly longer
reannealing hybridization was used."
BASE COUNT 105 a 65 c 94 g 146 t 1 others
ORIGIN
Query Match 0.9%; Score 21; DB 13; Length 411;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2190 AACTCAAGAGCAGAGCTT 2210
|||||
Db 273 AACTCAAGAGCAGAGCTT 253
|||||
RESULT 5
LOCUS B1544663 499 bp mRNA linear EST 05-SEP-2001
DEFINITION 603242619r1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5284997 5',
mRNA sequence.
ACCESSION B1544663
COMMENT B1544663

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VERSION B1544663.1 GI:15431975
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 499)
NIH-MGC http://imgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
JOURNAL Contact: Robert Strausberg, Ph.D.
Email: cgapds-rc@mail.nih.gov
Tissue Procurement: Miklos Palokvits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: L14M11720 row: f column: 06
High quality sequence stop: 299.
FEATURES
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1..499
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5284997"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_id="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescript (modified
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); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.5 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 122 a 142 c 165 g 70 t
ORIGIN
Query Match 0.9%; Score 21; DB 12; Length 499;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 389 GAGGAATCAATCGACAAA 409
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Db 414 GAGGAATCAATCGACAAA 434
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RESULT 6
LOCUS AM932212 549 bp mRNA linear EST 18-MAY-2001
DEFINITION EST358055 tomato fruit mature green, TMU Lycopersicon esculentum
cDNA clone CLEF471J3 5', mRNA sequence.
ACCESSION AM932212
VERSION AM932212.1 GI:8107613
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 549)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F.,
Upson, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Roming, C.M.,
Paez, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato fruit tissue
Unpublished
JOURNAL Contact: CUGI
COMMENT Clemson University Genomics Institute

```

FEATURES
source
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

Location/Qualifiers
1. 549
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA96"
/db_xref="taxon:4081"
/clone="cLEF4713"
/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
/clone_lib="tomato fruit mature green, TAMU"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI, cLEF- Fruit were tagged at the 1cm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the pericarp"
BASE COUNT 166 a 97 c 124 g 161 t 1 others
ORIGIN

Query Match 0.9%; Score 21; DB 10; Length 549;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 AGGCTGATATGTTATCAAG 326
DB 135 AGGCTGATATGTTATCAAG 155

RESULT 7
BU397983/c 581 bp mRNA linear EST 27-NOV-2002
LOCUS 603534550F1 CSBQCHN58 Gallus gallus cDNA CHEST494c13 5', mRNA
DEFINITION sequence.
ACCESSION BU397983
VERSION BU397983.1 GI:25767039
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 581)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickler, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken CDNA
Curr. Biol. 12 (22), 1965-1969 (2002)
COMMENT
PUBLISHED 22335534
12445392
CONTACT: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk

FEATURES
source
Location/Qualifiers
1. 581
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST494c13"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSBQCHN58"
/note="Organ: small intestine; Vector: pBluescript II KS(+

); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adaptors, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
BASE COUNT 156 a 98 c 119 g 208 t
ORIGIN

Query Match 0.9%; Score 21; DB 13; Length 581;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2190 AACTCAAGACGACGAGTTT 2210
DB 368 AACTCAAGACGACGAGTTT 348

RESULT 8
AZ391393/c 640 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0153A03R Mouse 10kb plasmid UUGCim library Mus musculus genomic
DEFINITION clone UUGC1M0153A03 R, genomic survey sequence.
ACCESSION AZ391393
VERSION AZ391393.1 GI:10506436
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 640)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE Unpublished
JOURNAL
COMMENT
CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0153 row: A column: 03
Seq primer: CACACAGAAACAGCTATGACC
Class: Plasmid ends
High quality sequence stop: 640.
Location/Qualifiers
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/strain="C57BL/6J"
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/clone="UUGC1M0153A03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCim library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 215 a 139 c 183 g 102 t 1 others
ORIGIN

Query Match 0.9%; Score 21; DB 28; Length 640;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1539 ACGAAGTTCGATTCCTCAAT 1559
Db 332 ACGAAGTTCGATTCCTCAAT 312

RESULT 9
LOCUS BU345704 664 bp mRNA linear EST 28-NOV-2002
DEFINITION 60417083991 CSEQCHN68 Gallus gallus cDNA clone CHEST1033m10 5',
mRNA sequence.
ACCESSION BU345704
VERSION BU345704.1 GI:25853705
KEYWORDS EST
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 664)
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
TITLE A Comprehensive Collection of Chicken CDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392

COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES

source

1..664
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST1033m10"
/sex="Female"
/tissue_type="cerebellum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHN68"
/note="Organ: brain; Vector: pluscript II KS(+); Site 1:
EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adaptors, digested with EcoRI

, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

BASE COUNT 186 a 97 c 144 g 237 t
ORIGIN

Query Match 0.9%; Score 21; DB 13; Length 664;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2190 AACTCAAGAGCAGAGTTT 2210
Db 295 AACTCAAGAGCAGAGTTT 275

RESULT 10
LOCUS AG084591 681 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-082604.F, genomic survey sequence.
ACCESSION AG084591
VERSION AG084591.1 GI:1636393
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE 1
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Torok, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of library PTB
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 681)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Torok, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission

COMMENT Submitted (02-AUG-2001) Aao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanzee@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13

LIBRARY

Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers

FEATURES

source

1..681
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-082604.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 125 a 213 c 191 g 152 t
ORIGIN

Query Match 0.9%; Score 21; DB 29; Length 681;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1755 CAGATGTTAAAGCAATCCAA 1775
Db 142 CAGATGTTAAAGCAATCCAA 122

RESULT 11
 LOCUS BU549886
 DEFINITION BU549886 K. Sato unpublished cDNA library, cv. Haruna Nijo
 accession Bg935c04 3', mRNA sequence.
 VERSION BU549886
 KEYWORDS EST.
 SOURCE BU549886.1 GI:24968336
 ORGANISM Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 690)
 Sato, K., Saitoh, D. and Takeda, K.
 Barley EST sequencing project in NIG and Okayama Univ
 Unpublished
 Contact: Tadao Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 1..690
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Haruna Nijo"
 /db_xref="taxon:112509"
 /clone="bg935c04"
 /tissue_type="shoots"
 /dev_stage="germination"
 /clone_lib="K. Sato unpublished cDNA library, cv. Haruna
 Nijo germination shoots"
 Nijo germination shoots"

BASE COUNT 239 a 154 c 134 g 163 t
 ORIGIN

Query Match 0.9%; Score 21; DB 12; Length 690;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 AGGCCGCACTGCACCAA 1098
 ||||||||||||||||||
 Db 76 AGGCCGCACTGCACCAA 96

RESULT 12
 LOCUS BU403931
 DEFINITION BU403931 731 bp mRNA linear EST 27-NOV-2002
 accession BU403931
 VERSION BU403931
 KEYWORDS EST.
 SOURCE BU403931.1 GI:25772987
 ORGANISM Gallus gallus (chicken)
 Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianidae; Gallus.
 1 (bases 1 to 731)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 12445392
 Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)

PO Box 89, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 1..731
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hixex"
 /db_xref="taxon:9831"
 /clone="CHEST974d2"
 /dev_stage="36"
 /lab_host="DH10B"
 /clone_lib="CSECHN59"
 /note="Organ: limbs; Vector: pluescript II KS(+); Site_1:
 EcoRI, Site_2: NotI. This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with EcoRI
 , size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

BASE COUNT 200 a 121 c 157 g 252 t
 ORIGIN

Query Match 0.9%; Score 21; DB 13; Length 731;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2190 AACTCAAGAGACAGAGTTT 2210
 ||||||||||||||||||
 Db 531 AACTCAAGAGACAGAGTTT 511

RESULT 13
 LOCUS BU283494
 DEFINITION BU283494 742 bp mRNA linear EST 27-NOV-2002
 accession BU283494
 VERSION BU283494
 KEYWORDS EST.
 SOURCE BU283494.1 GI:25732950
 ORGANISM Gallus gallus (chicken)
 Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianidae; Gallus.
 1 (bases 1 to 742)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 12445392
 Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)

PO Box 89, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 1..742
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton Line 151"

BASE COUNT
ORIGIN

201 a 124 c 159 g 258 t

/db_xref="taxon:9031"
/clone="CHEST675K20"
/sex="Female"
/tissue_type="not cerebrum or cerebellum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_idb="CSEOCHN54"
/note="Organ: brain; Vector: plbusscript II KS(+); Site_1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was bluntend, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the plbusscript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

Query Match	Score 21;	DB 13;	Length 742;
Best Local Similarity	100.0%;	Pred. No. 90;	
Matches	21;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	2190	AACCTCAAGAACGACGACGTTT	2210
Db	359	AACCTCAAGAACGACGACGTTT	339

RESULT 14	
BU15421/c	
LOCUS	BU15421
DEFINITION	BU15421 754 bp mRNA linear EST 25-NOV-2002
ACCESSION	603140883f1 CSECHL15 Gallus gallus CDNA clone Chsrtl322 5', mRNA sequence.
VERSION	BU15421
KEYWORDS	BU15421.1 GI:25321521
SOURCE	EST.
ORGANISM	Gallus gallus (chicken)
	Gallus gallus

REFERENCE

AUTHORS

TITLE

MEDLINE

COMMENT

FEATURES
source

```

/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHBST132e22"
/sex="Female"
/tissue_type="cerebrum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="CSEQOCHL15"

```

```

/note="Organ: brain; Vector: pBluescript II KS(+); Site 1:
EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
1-climmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3',
end DNA sequencing by Glenn Fu, et al., U.S. Patent # 6,387
,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BglI and
BamHI sites (5'ggcgccgtcgaaccccgagtcgaataaag)
[5'aattcttttcgcagccgggtgcagc]"

```

Query	March	0.9%	Score 21;	DB 13;	Length 754;
Best Local Similarity	100.0%;	Pred. No. 90;			
Matches	21;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	2190	AACCTAAGAAGCGAAGCTT	2210		
	667	AACCTAAGAAGCGAAGCTT	647		

RESULT 15	
LOCUS	BU211482
DEFINITION	BU211482 769 bp mRNA linear EST 25-NOV-2002 604156363f1 CSECHNO3 Gallus gallus cDNA clone CHEST1013e10 5', mRNA sequence.
ACCESSION	BU211482
VERSION	BU211482.1 GI:25385632
KEYWORDS	EST.
SOURCE	Gallus gallus (chicken)
ORGANISM	Gallus gallus

REFERENCE	1 (bases 1 to 769)
AUTHORS	Boardman, P. E., Sans-Ezquerro, J., Overton, I. M., Burt, D. W., Bosch, E., Fong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.
TITLE	A Comprehensive Collection of Chicken CDNA
JOURNAL	Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE	23355534
PUBMED	12445392
COMMENT	Contact: Simon Hubbard

P0 Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Email: Simon.Hubbard@umist.ac.uk.

source	1. .769
--------	---------

methylnated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adaptors, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS 1989, 86:9192-9196 and Bonaldo et al., Genome Research 6:

BASE COUNT 257 a 177 c 147 g 188 t
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

Query Match 0.9%; Score 21; DB 13; Length 769;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2190 AACTCAAGACGACGAGTTT 2210
 |||||
 Db 389 AACTCAAGACGACGAGTTT 409

RESULT 16
 BU308927/c 799 bp mRNA linear EST 26-NOV-2002
 LOCUS 603538542F1 CSEQCHN60 Gallus gallus cDNA clone CHEST504c11 5', mRNA
 DEFINITION sequence.

ACCESSION BU308927
 VERSION BU308927.1 GI:25816928
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 TITLE A Comprehensive Collection of Chicken CDNAS
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22335534
 PUBMED 12445392

COMMENT

Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612260409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

1. 799
 Location/Qualifiers
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton Line 151"
 /db_xref="taxon:9031"
 /clone="CHEST504c11"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1lb="CSEQCHN60"
 /note="Organ: heart; Vector: pBluescript II KS(+); Site_1:
 EcoRI; Site_2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with EcoRI
 , size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

BASE COUNT 221 a 134 c 176 g 268 t

Query Match 0.9%; Score 21; DB 13; Length 799;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2190 AACTCAAGACGACGAGTTT 2210
 |||||
 Db 465 AACTCAAGACGACGAGTTT 445

RESULT 17
 CC088871 870 bp DNA linear GSS 16-APR-2003
 LOCUS CSU-K33r.8E23.SP6 CSU-K33r Aedes aegypti genomic clone
 DEFINITION CSU-K33r.8E23, genomic survey sequence.
 ACCESSION CC088871
 VERSION CC088871.1 GI:29944500
 KEYWORDS GSS.
 SOURCE Aedes aegypti (yellow fever mosquito)
 ORGANISM Aedes aegypti

REFERENCE
 AUTHORS Loftus, B., Shetty, J., Severson, D., Brown, S. and Knudson, D.
 TITLE End sequencing of Aedes aegypti BACS
 JOURNAL Unpublished
 COMMENT Other_GSSs: CSU-K33r.8E23.T7
 Contact: Brendan Loftus
 Department of Eukaryotic Genomics
 TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: ente@tigr.org
 Library was provided by Susan Brown and Dennis Knudson at Colorado
 State University.
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source Location/Qualifiers

1. 870
 /organism="Aedes aegypti"
 /mol_type="genomic DNA"
 /strain="Rockville"
 /db_xref="taxon:7159"
 /clone="CSU-K33r.8E23"
 /clone_1lb="CSU-K33r"
 /note="Vector: pBlotBAC11; Site_1: HindIII"

BASE COUNT 276 a 161 c 161 g 272 t

Query Match 0.9%; Score 21; DB 29; Length 870;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1222 TGTAAATCTTGAAGCA 1242
 |||||
 Db 91 TGTAAATCTTGAAGCA 111

RESULT 18
 BU273390/c 935 bp mRNA linear EST 26-NOV-2002
 LOCUS 60353127F1 CSEQCHN53 Gallus gallus cDNA clone CHEST486f8 5', mRNA
 DEFINITION sequence.

ACCESSION BU273390
 VERSION BU273390.1 GI:25544340
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 TITLE A Comprehensive Collection of Chicken CDNAS
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)

MEDLINE 22335534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
 PO Box 88, Manchester, M60 10D, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 1..935
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton Line 151"
 /db_xref="taxon:9031"
 /clone="CHSST486f8"
 /sex="Female"
 /tissue_type="cerebrum"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSROCHN53"
 /note="Organ: Brain; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. CDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded CDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1996) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
 BASE COUNT 247 a 184 c 205 g 299 t
 ORIGIN
 Query Match .0.9%; Score 21; DB 13; Length 935;
 Best Local Similarity 100.0%; Pred.No. 94;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2190 AACTCAAGACGACGAGTTT 2210
 |||||
 500 AACTCAAGACGACGAGTTT 480
 RESULT 19
 BB538572 175 bp mRNA linear EST 31-JUL-2000
 LOCUS BB538572 RIKEN full-length enriched, 0 day neonate eyeball Mus
 DEFINITION musculus CDNA clone E130012112 3', mRNA sequence.
 ACCESSION BB538572
 VERSION BB538572.1 GI:9594072
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 175)
 Komno.H., Aizawa.K., Akahira.S., Akiyama.J., Arakawa.T., Carninci.
 P., Endo.T., Fukuda.S., Fukunishi.Y., Hara.A., Hayatsu.N.,
 Hirozane.T., Hori.F., Ishii.Y., Ishikawa.J., Ishikawa.T., Itoh.M.,
 Izawa.M., Kadoya.K., Kagawa.I., Kai.C., Kawai.J., Kikuchi.N.,
 Kiyosawa.H., Kojima.Y., Kondo.S., Koya.S., Kurihara.C., Kusakabe.M.,
 Matsuyama.T., Miki.R., Mizuno.Y., Nakamura.M., Oda.H., Okazaki.Y.,
 Ono.T., Owa.C., Saito.H., Sakai.C., Sato.K., Shibata.Y., Shibata.Y.,
 Shigemoto.Y., Shinagawa.A., Shiraki.T., Sogabe.Y., Sugihara.Y.,
 Suzuki.H., Suzuki.H., Tagawa.A., Takahashi.F., Tomiwa.N., Toya.
 T., Tsunoda.Y., Watanabe.S., Yamamuta.T., Yamashita.I.,
 Yano.R., Yasunishi.A., Yokota.T., Yoshida.K., Yoshiki.A., Yoshino.
 M., Muramatsu.M. and Hayashizaki.Y.

TITLE RIKEN Mouse ESTs (Komno.H., et al.)
 JOURNAL Unpublished
 COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsunumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci.P., Nishiyama.Y., Westover.A., Itoh.M., Nagaoka.S., Sasaki.
 N., Okazaki.Y., Muramatsu.M. and Hayashizaki.Y.
 Thermostabilization and thermocycling of the molalable enzymes by
 trehalose and its application for the synthesis of full length
 CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (12), 520-524 (1998)
 Itoh.M., Katsunai.T., Akiyama.J., Shibata.K., Izawa.M., Kawai.J.,
 Tomaru.Y., Carninci.P., Shibata.Y., Ozawa.Y., Muramatsu.M., Okazaki.
 Y. and Hayashizaki.Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci.P. and Hayashizaki.Y.
 High-efficiency full-length CDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.
 Location/Qualifiers
 1..175
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="E130012112"
 /tissue_type="eyeball"
 /dev_stage="0 day neonate"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 0 day neonate
 eyeball"
 /note="Site 1: SalI; Site 2: BamHI; CDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand CDNA was
 primed with a primer [5'
 GAGAGAGAGAGCGCGCCGACGCTTTTCTTTTCTTTT 3']. CDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand CDNA was prepared with the
 primer adapter of sequence [5'
 GAGAGAGAGATTCGAGTTAATTAATTAATCCCCCCCCCC 3']. CDNA
 was cleaved with BamHI and XhoI. Vector: a modified
 pBluescript KS(+) after bulk excision from Lambda FLX I."
 BASE COUNT 45 a 52 c 31 g 47 t
 ORIGIN
 Query Match 0.8%; Score 20; DB 10; Length 175;
 Best Local Similarity 100.0%; Pred.No. 2.2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 54 TTTCCTATATGATGAAAA 73
 |||||
 Db 140 TTTCCTATATGATGAAAA 159
 RESULT 20
 A2502341/C 228 bp DNA linear GSS 05-OCT-2000
 LOCUS A2502341 Mouse 10kb plasmid UUC1M library Mus musculus genomic
 DEFINITION clone UUC1M0341023 F, genomic survey sequence.
 ACCESSION A2502341
 VERSION A2502341.1 GI:10683573
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 228)

REFERENCE 1 (bases 1 to 228)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 1000 Std Error: 0.00
Plate: 0341 row: O column: 23
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 228.

FEATURES
source
1..228
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0341023"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 55 a 54 c 46 g 73 t

ORIGIN

Query Match 0.8%; Score 20; DB 28; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 TTTCCTATATAGATGGAAGA 73
|||||
Db 220 TTTCCTATATAGATGGAAGA 201

RESULT 21 233 bp DNA linear GSS 16-FEB-2001
AZ769909
LOCUS
DEFINITION IM0571001F Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0571001 F, genomic survey sequence.
ACCESSION AZ769909
VERSION AZ769909.1 GI:12890543
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 233)

REFERENCE 1 (bases 1 to 233)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 1000 Std Error: 0.00
Plate: 0571 row: J column: 01
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 233.

FEATURES
source
1..233
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0571J01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 57 a 48 c 44 g 84 t

ORIGIN

Query Match 0.8%; Score 20; DB 28; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 TTATCAAGGTAGATGGAAGA 337
|||||
Db 73 TTATCAAGGTAGATGGAAGA 92

RESULT 22 267 bp DNA linear GSS 26-APR-2001
AZ943045
LOCUS
DEFINITION ZM0203006R Mouse 10kb plasmid UUCG2M library Mus musculus genomic clone UUCG2M0203006 R, genomic survey sequence.
ACCESSION AZ943045
VERSION AZ943045.1 GI:13806817
KEYWORDS GSS.

KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)

REFERENCE
 1 (bases 1 to 267)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.,
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE
 Unpublished

JOURNAL
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0203 row: 0 column: 06
 Seq primer: CACACGAGAAACAGCTATGACAC
 Class: plasmid ends

FEATURES
 High quality sequence stop: 267.
 Location/Qualifiers
 1..267
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M020J06"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT
 87 a 68 c 56 g 56 t

ORIGIN
 Query Match 0.8%; Score 20; DB 28; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1711 AGCCTACTTAAGAAAAAG 1730
 |||||
 71 AGCCTACTTAAGAAAAAG 90

RESULT 23
 BB803034 371 bp mRNA linear EST 19-NOV-2001
 LOCUS BB803034 RIKEN full-length enriched, 16 days neonate male
 diencephalon Mus musculus cDNA clone G630051N24 3', mRNA sequence.
 ACCESSION BB803034

VERSION
 BB803034.1 GI:16975663
KEYWORDS
SOURCE EST.
ORGANISM Mus musculus (house mouse)

REFERENCE
 1 (bases 1 to 371)
 Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
 Hayatsu, M., Hiramoto, K., Hirooka, T., Hirozane, T., Imotani, K., Ishii,
 Y., Ito, M., Kawai, J., Kojima, Y., Komno, H., Kouda, M., Matsuyama, T.,
 Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, T., Okido, T.,
 Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
 Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa,
 A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
 Watanishi, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
 RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
 2001)

TITLE
 Unpublished

JOURNAL
 Contact: Yoshinori Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-resgsc.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh,
 M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwata, M., Ohara, E.,
 Watanishi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura,
 S., Kawai, D., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and
 Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Komno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,
 Y., and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 e mouse tissues.

FEATURES
 Location/Qualifiers
 1..371
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="G630051N24"
 /sex="male"
 /tissue_type="dienecephalon"
 /dev_stage="16 days neonate"
 /clone_id="RIKEN full-length enriched, 16 days neonate
 male diencephalon"

BASE COUNT
 97 a 88 c 87 g 99 t

ORIGIN
 Query Match 0.8%; Score 20; DB 10; Length 371;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 54 TTTCCTATATGATGAAAA 73
 |||||
 200 TTTCCTATATGATGAAAA 219

RESULT 24
 AA046037/c

LOCUS AQ046037 406 bp DNA linear GSS 14-APR-1999
 DEFINITION RPCI11-36019.TK RPCI-11 Homo sapiens genomic clone RPCI-11-36019,
 genomic survey sequence.
 ACCESSION AQ046037
 VERSION AQ046037.1 GI:3314964
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 406)
 Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
 Venter,J.C.
 Use of BAC End Sequences for Sequence-Ready Map Building (1998)
 TITLE Unpublished
 JOURNAL Other_GSSs: RPCI11-36019.TJ
 COMMENT Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genetics (info@resgen.com). BAC end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
 Class: BAC ends.

FEATURES
 source
 1..406
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:7513794"
 /db_xref="taxon:9606"
 /clone="RPCI-11-36019"
 /sex="Male"
 /cell_type="lymphocytes"
 /clone_11b="RPCI-11"
 /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
 RPCI11 Human Male BAC Library"

BASE COUNT 113 a 64 c 63 g 166 t
 ORIGIN

Query Match 0.8%; Score 20; DB 28; Length 406;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1214 TCTGAACGTCTAAATCT 1233
 ||||||||||||||||
 Db 199 TCTGAACGTCTAAATCT 180

RESULT 25
 LOCUS AQ216823 471 bp DNA linear GSS 19-SEP-1998
 DEFINITION HS_3253_B1_C01.T7 CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=3253 Col=1 Row=F, genomic survey
 sequence.
 ACCESSION AQ216823
 VERSION AQ216823.1 GI:3632143
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 471)
 Mahairas,G.G., Wallace,U.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and

JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 99380589
 10449764
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3253 row: F column: 1
 Class: BAC ends
 High quality sequence strop: 471.

FEATURES
 source
 1..471
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=3253 Col=1 Row=F"
 /sex="male"
 /clone_11b="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
 E-Coli DH10B"

BASE COUNT 143 a 103 c 85 g 139 t 1 others
 ORIGIN

Query Match 0.8%; Score 20; DB 28; Length 471;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 310 TGGATATCTTATCAAGTAG 329
 ||||||||||||||||
 Db 448 TGGATATCTTATCAAGTAG 429

RESULT 26
 LOCUS BZ685217 496 bp DNA linear GSS 05-FEB-2003
 DEFINITION PUBCP45TD.ZM.0.6.1.0.KB Zea mays genomic clone ZMWBTA024H18,
 genomic survey sequence.
 ACCESSION BZ685217
 VERSION BZ685217.1 GI:28244313
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 496)
 WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Resnick
 A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
 Maize Genomics Consortium
 Unpublished
 Contact: Cathy WhiteLaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whiteLaw@tigr.org
 Seq primer: TF
 Class: sheared ends.

FEATURES
 source
 1..496
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMWBTA024H18"
 /clone_11b="ZM.0.6.1.0.KB"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
 COT selected genomic DNA library"

BASE COUNT 137 a 81 c 82 g 196 t
 ORIGIN

Query Match 0.8%; Score 20; DB 29; Length 496;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1308 ACCAAGATTTATGATATAA 1327
 |||||
 Db 33 ACCAAGATTTATGATATAA 14

RESULT 27
 AM239782 540 bp mRNA linear EST 27-APR-2000
 LOCUS ptlic.pk002.h12 chicken MDV infected T cell cDNA library Gallus
 DEFINITION gallus cDNA clone ptlic.pk002.h12 5' similar to (AB023214) KIAA0997
 protein [Homo sapiens], mRNA sequence.
 AM239782
 VERSION AM239782.1 GI:6579522
 KEYWORDS EST
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 540)
 REFERENCE Morgan, R.
 CHICKEN ESTs from MDV infected T cells
 TITLE Unpublished
 JOURNAL
 COMMENT Contact: Robin Morgan
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1341
 Fax: 302-831-2822
 Email: morganudel.edu
 Clones can be ordered online at http://www.chickest.udel.edu.
 FEATURES
 source
 Location/Qualifiers
 1..540
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /clone="ptlic.pk002.h12"
 /sex="Male and Female"
 /cell_type="MDV infected splenic T cell"
 /lab_host="B.coli DHS alpha"
 /clone_lib="chicken MDV infected T cell cDNA library"
 /note="Vector: pBA2ADP"
 BASE COUNT 172 a 120 c 101 g 146 t 1 others
 ORIGIN

Query Match 0.8%; Score 20; DB 9; Length 540;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 751 CACAAGCAACACGACACA 770
 |||||
 Db 85 CACAAGCAACACGACACA 104

RESULT 28
 BH369198 584 bp DNA linear GSS 10-DEC-2001
 LOCUS BH369198/c
 DEFINITION AG-ND-139K6.TF ND-TM Anopheles gambiae genomic clone AG-ND-139K6,
 genomic survey sequence.
 ACCESSION BH369198
 VERSION BH369198.1 GI:17315299
 KEYWORDS GSS.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.

REFERENCE 1 (bases 1 to 584)
 AUTHORS Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J., Ren, C., Huff, E.R., Carlile, J.L., Black, K., Zhang, H.-B., Gardner, M.J. and Collins, F.H.
 TITLE Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the African malaria mosquito *Anopheles gambiae*
 JOURNAL Malaria Genet. Genomics 268 (6), 720-728 (2003)
 MEDLINE 22542063
 PUBMED 12553398
 COMMENT Other_GSSs: AG-ND-139K6.TF
 Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: bjoftus@igf.org
 This clone is from an A. gambiae BAC library (ND-TM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
 Seg primer: M13 For
 Class: BAC ends.
 FEATURES
 source
 Location/Qualifiers
 1..584
 /organism="Anopheles gambiae"
 /mol_type="genomic DNA"
 /strain="PEST"
 /db_xref="taxon:7165"
 /clone="AG-ND-139K6"
 /clone_lib="ND-TM"
 /note="Vector: pECBAC1; Site_1: HindIII"
 BASE COUNT 152 a 159 c 147 g 126 t
 ORIGIN

Query Match 0.8%; Score 20; DB 28; Length 584;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2141 CCTGCTGAGCCGAGATGCC 2160
 |||||
 Db 581 CCTGCTGAGCCGAGATGCC 562

RESULT 29
 BH766941/c 588 bp DNA linear GSS 20-MAR-2002
 LOCUS BH766941
 DEFINITION BMBACJ45E09T7_P5U Brugia malayi genomic BAC library 3 Brugia malayi
 genomic survey sequence.
 ACCESSION BH766941
 VERSION BH766941.1 GI:19564705
 KEYWORDS GSS.
 SOURCE Brugia malayi
 ORGANISM Brugia malayi
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 Onchocercidae; Brugia.
 1 (bases 1 to 588)
 REFERENCE Whitton, C., Daub, J., Ware, J., Quail, M., Hall, N., Barrell, B., Foster, J., Giuliano, D., Slatko, B. and Blaxter, M.
 TITLE Genome survey sequences from the human parasitic nematode *Brugia malayi*
 JOURNAL Unpublished
 COMMENT Contact: Blaxter ML
 Institute of Cell, Animal and Population Biology
 University of Edinburgh
 Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9 3JT, UK

Tel: +44 131 650 6760
 Fax: +44 131 670 5450
 Email: mark.blaxter@ed.ac.uk
 Sequenced from the Brugia malayi BAC library constructed by Claire Whitton and Dr Mike Quail. The sequence was generated by The Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in collaboration with Mark Blaxter, ICAPB, University of Edinburgh, Edinburgh, UK.
 Seg primer: T7 (TAATACACTCACTATAGG)
 Class: BAC ends.

FEATURES

source

Location/Qualifiers
 1. 588
 /organism="Brugia malayi"
 /mol_type="genomic DNA"
 /strain="T8S"
 /db_xref="taxon:6279"
 /sex="Mixed (male and female)"
 /tissue_type="whole parasite"
 /dev_stage="microfilaria (L1)"
 /clone_lib="Brugia malayi Genomic BAC Library 3"
 /note="Vector: pBACe3.6; Site 1: BamH I; Brugia malayi genomic DNA was partially cleaved with Sau3A I and size fractionated. 7,392 clones were generated with mean insert size ~48 kbp. The library was constructed by Claire Whitton, Blaxter Nematode Genetics Lab, University of Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing Unit, The Sanger Centre, Cambridge, UK."

BASE COUNT 190 a 88 c 95 g 214 t 1 others

ORIGIN

Query Match 0.8%; Score 20; DB 28; Length 588;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1276 AACTGCTAAAAAGAAAATG 1295
 |||
 347 AACTGCTAAAAAGAAAATG 328

DB

347 AACTGCTAAAAAGAAAATG 328

RESULT 30

CA370410

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

COMMENT

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CA370410 595 bp mRNA linear EST 06-NOV-2002
 650577 NCCGWA 1RT Oncorhynchus mykiss cDNA clone 1RT22U21_B_E11 5', mRNA sequence.
 CA370410
 CA370410.1 GI:24683000
 EST.
 Oncorhynchus mykiss (rainbow trout)
 Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. 1 (bases 1 to 595)
 Rexroad, C.E. and Keele, J.W.
 Sequence analysis of a rainbow trout normalized cDNA library
 Unpublished
 Contact: Rexroad CE
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leetown Road, Kearneysville, WV 25430, USA
 Tel: 304 724 8340 x2129
 Fax: 304 725 0351
 Email: crexroad@nccgwa.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified by cross_match v0.990329.
 Seg primer: AGCGATTAACAATTTCACACAGCA.
 Location/Qualifiers
 1. 595
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /clone="1RT22U21_B_E11"
 /tissue_type="pooled"

/lab_host="DH10B"
 /clone_lib="NCCGWA 1RT"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 library made from pooled tissue from brain, gill, liver, spleen, muscle, and kidney."
 BASE COUNT 178 a 198 c 135 g 84 t

ORIGIN

Query Match 0.8%; Score 20; DB 14; Length 595;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

757 CACCAACGCAACACTAACA 776
 |||
 96 CACCAACGCAACACTAACA 115

DB

96 CACCAACGCAACACTAACA 115

RESULT 31

BM282910

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

COMMENT

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BM282910 603 bp mRNA linear EST 11-NOV-2002
 BM282910 Nori Satoh unpublished cDNA library, gonad cDNA
 intestinalis cDNA clone cigd020g09 5', mRNA sequence.
 BM282910
 BM282910.1 GI:24863521
 EST.
 Ciona intestinalis
 Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.
 1 (bases 1 to 603)
 Satou, Y., Shin, I. T., Kohara, Y. and Satoh, N.
 Expressed genes in Ciona intestinalis (2002c)
 Unpublished
 Contact: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-Ku, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satoh@ascidian.zool.kyoto-u.ac.jp.
 Location/Qualifiers
 1. 603
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="cigd020g09"
 /tissue_type="gonad"
 /clone_lib="Nori Satoh unpublished cDNA library, gonad"

BASE COUNT

204 a 92 c 130 g 177 t

ORIGIN

Query Match 0.8%; Score 20; DB 13; Length 603;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2312 ATCATGCGACGACGAGAA 2331
 |||
 234 ATCATGCGACGACGAGAA 253

DB

234 ATCATGCGACGACGAGAA 253

RESULT 32

AZ524614

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

COMMENT

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ524614 622 bp DNA linear GSS 07-MAY-2001
 234BDD06 Pb MEN #21 Plasmodium berghei genomic 3', genomic survey
 sequence.
 AZ524614
 AZ524614.1 GI:13964669
 GSS.
 Plasmodium berghei
 Plasmodium berghei
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 1 (bases 1 to 622)
 Carlton, J.M.-R. and Dame, J.B.

TITLE The Plasmodium vivax and P. berghei gene sequence tag projects
JOURNAL Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
COMMENT Contact: Dame JB
Dept. of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
Tel: 352 392 4700
Fax: 352 392 9704
Email: damejb@mail.ufl.edu
Seq primer: M13(-20) forward
Class: shotgun.

FEATURES
SOURCE Location/Qualifiers

1..622
/organism="Plasmodium berghei"
/mol_type="genomic DNA"
/strain="ANKA clone 15cyl (clone of the ANKA 8417 clone)"
/db_xref="taxon:5821"
/dev_stage="asexual blood forms"
/lab_host="Mus musculus"
/clone_1fb="Pb MBN #21"
/note="Vector: pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP; Site_1: EcoRV; Site_2: EcoRV; genomic DNA was prepared from asynchronous blood stage forms of the cloned ANKA isolate of P. berghei grown in laboratory Swiss white mice. The DNA was purified from ultracentrifugation and precipitated. Purified DNA was digested with mung bean nuclease in the presence of 36-38% formamide at 50 C, as described (Verlick, K.D., Imbercki, R.B., and McCutchan, T.F. 1988. Nucleic Acids Research 16:6883-6896). The ends of the digestion fragments were polished using T4 DNA polymerase, and the fragments size selected in the range 500-2000 bp. These were ligated into the EcoRV-cleaved and dephosphorylated pBluescript SK(+) vector. Recombinant plasmids were used to transform E. coli XL10-Gold host cells."

BASE COUNT 269 a 45 c 71 g 237 t
ORIGIN

Query Match 0.8%; Score 20; DB 28; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1594 TTTGATGACATGATATTA 1613
|||||
125 TTTGATGACATGATATTA 144

RESULT 33
LOCUS AQ412913 630 bp DNA linear GSS 23-MAR-1999
DEFINITION RPCT-11-194P5.TV RPCT-11 Homo sapiens genomic clone RPCT-11-194P5,
genomic survey sequence.
ACCESSION AQ412913
VERSION AQ412913.1 GI:4472401
KEYWORDS GSS.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 630)
AUTHORS Zhao, S., Adams, M.D., Niernan, W., Malik, J., de Jong, P. and Venter, J.C.

TITLE Use of BAC End Sequences from Library RPCT-11 for Sequence-Ready
Map Building
JOURNAL Unpublished
COMMENT Contact: Shaying Zhao, William Niernan, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org

Clones are derived from the human BAC library RPCT-11. For BAC library availability, please contact Pieter de Jong (pieter@dong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genet cs (http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html).
Seq primer: SP6
Class: BAC ends.

FEATURES
SOURCE Location/Qualifiers

1..630
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7574476"
/db_xref="taxon:9606"
/clone="RPCT-11-194P5"
/sex="Male"
/cell_type="Lymphocytes"
/clone_1fb="RPCT-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCT11 Human Male BAC Library"

BASE COUNT 123 a 94 c 108 g 305 t
ORIGIN

Query Match 0.8%; Score 20; DB 28; Length 630;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2087 AGTGAAGTCCAAATAGAA 2106
|||||
DB 254 AGTGAAGTCCAAATAGAA 235

RESULT 34
LOCUS BH765160 636 bp DNA linear GSS 20-MAR-2002
DEFINITION BMBAC354A03SF6.PSU Brugia malayi Genomic BAC Library 3 Brugia
malayi genomic, genomic survey sequence.
ACCESSION BH765160
VERSION BH765160.1 GI:19562924
KEYWORDS GSS.

SOURCE Brugia malayi
ORGANISM Brugia malayi

REFERENCE 1 (bases 1 to 636)
AUTHORS Whitton, C., Daub, J., Ware, J., Quail, M., Hall, N., Barrell, B., Foster, J., Guillano, D., Slacko, B. and Blaxter, M.

TITLE Genome survey sequences from the human parasitic nematode Brugia
malayi
JOURNAL Unpublished
COMMENT Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
3JT, UK
Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk

Sequenced from the Brugia malayi BAC library constructed by Claire Whitton and Dr Mike Quail. The sequence was generated by The Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in collaboration with Mark Blaxter, ICAAP, University of Edinburgh, Edinburgh, UK.
Seq primer: SP6 (ATTAGGTACACTATAG)
Class: BAC ends.

FEATURES
SOURCE Location/Qualifiers

1..636
/organism="Brugia malayi"
/mol_type="genomic DNA"
/strain="IRS"
/db_xref="taxon:6279"
/sex="Mixed (male and female)"
/tissue_type="whole parasite"


```
/dev_stage="microfilaria (L1)"
/clone_lib="Brugia malayi Genomic Bac Library 3"
/notes="Vector: pBACE3.6; Site 1: BamH I; Brugia malayi
genomic DNA was partially cleaved with Sau3A I and size
fractionated. 7,392 clones were generated with mean insert
size ~48 kbp. The library was constructed by Claire
Whitton, Blaxter Nematode Genetics Lab, University of
Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
Unit, The Sanger Centre, Cambridge, UK."
```

BASE COUNT 226 a 90 c 96 g 224 t

ORIGIN

Query Match 0.8%; Score 20; DB 28; Length 636;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1741 TCCATCTCCAGACGAGATG 1760
|||||
520 TCCATCTCCAGACGAGATG 501

Db

RESULT 35
BWL12810/c 643 bp mRNA linear EST 24-OCT-2002
LOCUS BWL12810 Nori Satoh unpublished cDNA library, tailbud embryo Clona
DEFINITION intestinalis cDNA clone rc1b062j14 3', mRNA sequence.
ACCESSION BWL12810
VERSION BWL12810.1 GI:24359467
KEYWORDS EST.
SOURCE Clona intestinalis
ORGANISM Clona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Clona.
REFERENCE 1 (bases 1 to 643)
AUTHORS Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
TITLE Expressed genes in Clona intestinalis (2002c)
JOURNAL Unpublished
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
1..643
/organism="Clona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rc1b062j14"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud
embryo"

BASE COUNT 178 a 145 c 100 g 220 t

ORIGIN

Query Match 0.8%; Score 20; DB 13; Length 643;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2312 ATCATGCGAGAGAGAAAA 2331
|||||
597 ATCATGCGAGAGAGAAAA 578

Db

RESULT 36
BWL243771 649 bp mRNA linear EST 09-NOV-2002
LOCUS BWL243771 Nori Satoh unpublished cDNA library, tailbud embryo Clona
DEFINITION intestinalis cDNA clone clb062j14 5', mRNA sequence.
ACCESSION BWL243771
VERSION BWL243771.1 GI:24823689

KEYWORDS EST.
SOURCE Clona intestinalis
ORGANISM Clona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Clona.
REFERENCE 1 (bases 1 to 649)
AUTHORS Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
TITLE Expressed genes in Clona intestinalis (2002c)
JOURNAL Unpublished
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
1..649
/organism="Clona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="clb062j14"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud
embryo"

BASE COUNT 222 a 101 c 144 g 182 t

ORIGIN

Query Match 0.8%; Score 20; DB 13; Length 649;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2312 ATCATGCGAGAGAGAAAA 2331
|||||
37 ATCATGCGAGAGAGAAAA 56

Db

RESULT 37
BG698682 651 bp mRNA linear EST 07-MAY-2001
LOCUS BG698682 602703065P1 NC1_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4800280 5',
DEFINITION mRNA sequence.
ACCESSION BG698682
VERSION BG698682.1 GI:13966243
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 651)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10691 row: a column: 17
High quality sequence start: 3
High quality sequence stop: 606.
Location/Qualifiers
1..651
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4800280"
/lab_host="DH10B (TI phage-resistant)"

```

/clone_lib="NCI CGAP Skn3"
/note="Organ: skin; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      192 a      158 c      126 g      175 t
ORIGIN

Query Match      0.8%; Score 20; DB 10; Length 651;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1274 TTAAGTCTAAAGAGAGAAA 1293
      |||||
      178 TTAAGTCTAAAGAGAGAAA 197

RESULT 38
LOCUS      BF296373              656 bp      mRNA      linear      EST 04-MAY-2001
DEFINITION Plasmodium berghei Pb cDNA #17, Tommaso Pace, Marta Ponzi, and Clara Frontali
ACCESSION  BF296373
VERSION     BF296373.1  GI:13947326
KEYWORDS   EST.
SOURCE     Plasmodium berghei
ORGANISM   Plasmodium berghei
REFERENCE  1 (bases 1 to 656)
AUTHORS   Carlton, J.M., R. and Dame, J.B.
TITLE     The Plasmodium vivax and P. berghei gene sequence tag projects
JOURNAL   Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
COMMENT   Contact: Dame JB
          Department of Pathobiology, College of Veterinary Medicine
          University of Florida
          2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611-0880, USA
          Tel: 352 392 4700
          Fax: 352 392 9704
          Email: damej@mail.ufl.edu
          Seq primer: 73.
FEATURES
    source
        location/Qualifiers
            1..656
            /organism="Plasmodium berghei"
            /mol_type="mRNA"
            /strain="ANKA clone HP (gametocyte producer)"
            /db_xref="taxon:5821"
            /dev_stage="asynchronous blood stage"
            /lab_host="Wistar rats"
            /clone_lib="Pb cDNA #17, Tommaso Pace, Marta Ponzi, and
            Clara Frontali"
            /note="Vector: pBluescript II vector DNA, excised from
            Lambda ZAP II.; Site_1: EcoRI; Site_2: XhoI; Total RNA was
            extracted from asynchronous blood stage forms of the
            cloned ANKA isolate of P. berghei, grown in Wistar rats to
            30% parasitemia and 2-5% gametocytemia. Contaminating host
            white cells had previously been removed and final host
            cell contamination estimated to be approximately 5%.
            PolyA+ RNA was extracted and reverse transcribed using an
            oligo dT-XhoI primer (Lambda ZAP II cDNA cloning kit,
            Stratagene). Second strand cDNA was made following the
            manufacturer's protocol. EcoRI adaptors were ligated to
            the cDNA, and fragments were ligated into EcoRI/XhoI
            digested vector."
BASE COUNT      255 a      86 c      93 g      218 t
ORIGIN

Query Match      0.8%; Score 20; DB 10; Length 656;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      54 TTCTCTATATAGATGAGAAA 73
      |||||
      267 TTCTCTATATAGATGAGAAA 286
  
```

```

RESULT 39
LOCUS      BH085526/c              656 bp      DNA      linear      GSS 18-JUL-2001
DEFINITION RPCI-24-263118.TVB RPCI-24 Mus musculus genomic clone
ACCESSION  BH085526
VERSION     BH085526.1  GI:14905123
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 656)
AUTHORS   Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akincet, B., Levins, M.,
          Teegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregiorgis, B.,
          Russell, D., de Jong, P. and Fraser, C.M.
          Mouse BAC End Sequences from Library RPCI-24
          Unpublished
          Other GSSs: RPCI-24-263118.TU
          Contact: Shaying Zhao
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 0200
          Fax: 301 838 0208
          Email: szhaoy@tigr.org
          Clones are derived from the mouse BAC library RPCI-24. For BAC
          library availability, please contact Pieter de Jong
          (pjejong@mail.cho.org). Clones may be purchased from BACPAC
          Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end
          page: http://www.tigr.org/cdb/bac\_ends/mouse/bac\_end\_intro.html
          Plate: 263 row: I column: 18
          Seq primer: T7
          Class: BAC ends.
FEATURES
    source
        location/Qualifiers
            1..656
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="RPCI-24-263118"
            /sex="Male"
            /cell_type="Spleen/Brain"
            /clone_lib="RPCI-24"
            /note="Vector: pTRABAC1; Site_1: BamHI; Site_2: BamHI.
            RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
            library was cloned in the pTRABAC1 cloning vector at the
            BamHI sites using MboI partially digested male C57BL/6J
            DNA."
BASE COUNT      159 a      147 c      167 g      183 t
ORIGIN

Query Match      0.8%; Score 20; DB 28; Length 656;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      54 TTCTCTATATAGATGAGAAA 73
      |||||
      289 TTCTCTATATAGATGAGAAA 270
  
```

```

RESULT 40
LOCUS      AZ373971/c              658 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION IM0126P17f Mouse 10kb plasmid UUGCM library Mus musculus genomic
clone UUGCM0126P17 F, genomic survey sequence.
ACCESSION  AZ373971
VERSION     AZ373971.1  GI:10487671
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
  
```

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 658)
 Dunm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright,D., Meiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0126 row: P column: 17
 Seq primer: CGTCTGAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 658.
 Location/Qualifiers
 1..658
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCIM0126P17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCIM library"
 /note="Vector: PMD29v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 225 a 128 c 98 g 207 t
 ORIGIN
 Query Match 0.8%; Score 20; DB 28; Length 658;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1842 TTCATATATGTTGAGCAT 1861
 Db 146 TTCATATATGTTGAGCAT 127

RESULT 41
 BW261677
 LOCUS BW261677 664 bp mRNA linear EST 09-NOV-2002
 DEFINITION BW261677 Nori Satoh unpublished cDNA library, gastrula and neurula
 Ciona intestinalis cDNA clone cign029c12 5', mRNA sequence.
 ACCESSION BW261677
 VERSION BW261677.1 GI:24841595
 KEYWORDS EST.
 SOURCE Ciona intestinalis

ORGANISM Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona. 1 (bases 1 to 664)
 Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
 Expressed genes in Ciona intestinalis (2002c)
 Unpublished
 CONTACT: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satoh@scidian.zool.kyoto-u.ac.jp.
 Location/Qualifiers
 1..664
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="cign029c12"
 /tissue_type="whole body"
 /dev_stage="gastrula and neurula"
 /clone_lib="Nori Satoh unpublished cDNA library, gastrula and neurula"

BASE COUNT 220 a 111 c 150 g 183 t
 ORIGIN
 Query Match 0.8%; Score 20; DB 13; Length 664;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2312 ATCATGCAGAGCAGAAAA 2331
 Db 36 ATCATGCAGAGCAGAAAA 55

RESULT 42
 BG911162 668 bp. mRNA linear EST 05-JUN-2001
 LOCUS BG911162
 DEFINITION 60280663p1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4938831
 5', mRNA sequence.
 ACCESSION BG911162
 VERSION BG911162.1 GI:14291638
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 668)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LAM10874 row: n column: 16
 High quality sequence stop: 195.
 Location/Qualifiers
 1..668
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4938831"
 /tissue_type="anaplastic oligodendroglioma with 1p/19q loss"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Brn67"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NOTI_CGAP Library."

BASE COUNT 297 a 178 c 157 g 36 t

Query Match 0.8%; Score 20; DB 12; Length 669;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 749 AACACAGCAGACACAGCA 768
DB 316 AACACAGCAGACACAGCA 335

RESULT 43
LOCUS AJ453442 689 bp mRNA linear EST 22-APR-2002
DEFINITION AJ453442 riken1 Gallus gallus cDNA clone 34g19r1, mRNA sequence.
ACCESSION AJ453442
VERSION AJ453442.1 GI:20263538
KEYWORDS EST;
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 689)
Buerstedde,J.M.
Gallus gallus bursal lymphocyte EST
UNPUBLISHED
Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinstr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
1..689
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="34g19r1"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/clone_lib="riken1"
/note="CB induced strain"

BASE COUNT 207 a 158 c 142 g 182 t
ORIGIN

Query Match 0.8%; Score 20; DB 9; Length 689;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 751 CACAAGCAACACAGCAACA 770
DB 197 CACAAGCAACACAGCAACA 216

RESULT 44
LOCUS BW262397 689 bp mRNA linear EST 09-NOV-2002
DEFINITION BW262397 Nori Satoh unpublished cDNA library, gastrula and neurula
Ciona intestinalis cDNA clone cign030m24 5', mRNA sequence.
ACCESSION BW262397
VERSION BW262397.1 GI:24842315
KEYWORDS EST;
SOURCE Ciona intestinalis
ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
1 (bases 1 to 689)
Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.

TITLE Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished
CONTACT Nori Satoh
COMMENT Department of Zoology
Kyoto University
Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@acidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1..689
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cign030m24"
/issue_type="whole body"
/dev_stage="gastrula and neurula"
/clone_lib="Nori Satoh unpublished cDNA library, gastrula and neurula"

BASE COUNT 230 a 110 c 157 g 192 t
ORIGIN

Query Match 0.8%; Score 20; DB 13; Length 689;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2312 ATCATGGCAGAGCAGAAA 2331
DB 33 ATCATGGCAGAGCAGAAA 52

RESULT 45
LOCUS BF294340 698 bp mRNA linear EST 04-MAY-2001
DEFINITION 004PBX08 Pb cDNA #17, Tommaso Pace, Marta Ponzi, and Clara Frontali
Plasmodium berghei cDNA 5', mRNA sequence.
ACCESSION BF294340
VERSION BF294340.1 GI:13943267
KEYWORDS EST;
SOURCE Plasmodium berghei
ORGANISM Plasmodium berghei
Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
1 (bases 1 to 698)
Carlton,J.M.-R. and Dame,J.B.
The Plasmodium vivax and P. berghei gene sequence tag projects
Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
Contact: Dame JB
Department of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611-0880, USA
Tel: 352 392 4700
Fax: 352 392 9704
Email: damej@mail.ufl.edu
Seq primer: T3.
Location/Qualifiers
1..698
/organism="Plasmodium berghei"
/mol_type="mRNA"
/strain="ANKA clone HP (gametocyte producer)"
/db_xref="taxon:5821"
/dev_stage="asynchronous blood stage"
/lab_host="Wistar rats"
/clone_lib="Pb cDNA #17, Tommaso Pace, Marta Ponzi, and Clara Frontali"
/note="Vector: pBluescript II vector DNA, excised from lambda ZAP II.; Site 1: EcoRI; Site 2: XhoI; Total RNA was extracted from asynchronous blood stage forms of the cloned ANKA isolate of P. berghei, grown in Wistar rats to 30% parasitemia and 2-5% gametocytemia. Contaminating host white cells had previously been removed and final host cell contamination estimated to be approximately 5%. PolyA+ RNA was extracted and reverse transcribed using an oligo dt-xhoI primer (lambda ZAP II cDNA cloning kit,

Stratagene). Second strand cDNA was made following the manufacturer's protocol. EcoRI adaptors were ligated to the cDNA, and fragments were ligated into EcoRI/XhoI digested vector."

BASE COUNT 264 a 100 c 102 g 232 t

Query Match 0.8%; Score 20; DB 10; Length 698;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 TTTCCTATATAGATGAAAA 73
|||||
274 TTTCCTATATAGATGAAAA 293

RESULT 46
LOCUS BB527573 706 bp mRNA linear EST 25-OCT-2001
DEFINITION BB527573 RIKEN full-length enriched, 15 days embryo head Mus
ACCESSION BB527573
VERSION BB527573.2 GI:16444500
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Muskaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 706)

REFERENCE
AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished
On Jul 28, 2000 this sequence version replaced gi:9579031.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Konodo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, K. I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES
source
1..706
Location/Qualifiers

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="D93004ID13"
/sex="mixed"
/tissue_type="head"
/dev_stage="15 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 15 days embryo head"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTVN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGAGTTATTAATTAATCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLX I"

BASE COUNT 184 a 184 c 159 g 179 t

Query Match 0.8%; Score 20; DB 10; Length 706;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 TTTCCTATATAGATGAAAA 73
|||||
534 TTTCCTATATAGATGAAAA 553

RESULT 47
LOCUS BM027074/c 708 bp mRNA linear EST 13-OCT-2002
DEFINITION BM027074 Nori Satoh unpublished cDNA library, blood cells Ciona intestinalis cDNA clone rc1bd085j10 3', mRNA sequence.
ACCESSION BM027074
VERSION BM027074.1 GI:23942881
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 708)

REFERENCE
AUTHORS Satoh, Y., Satake, M., Azumi, K., Nonaka, M., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002)

TITLE Unpublished
JOURNAL
COMMENT

Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@scidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1..708
/organism="Ciona intestinalis"
/mol_type="mRNA"

FEATURES
source

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/db_xref="taxon:7719"
/clone="rc1bd085j10"
/tissue_type="blood cells"
/clone_id="Nori Satoh unpublished cDNA library, blood
cells"
BASE COUNT      199 a      159 c      116 g      234 t
ORIGIN

Query Match      0.8%; Score 20; DB 13; Length 708;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2312 ATCATGCGAAGACAGAGAAA 2331
|||||
Db      703 ATCATGCGAAGACAGAGAAA 684

RESULT 48
AV862261      712 bp      mRNA      linear      EST 08-NOV-2001
LOCUS      AV862261
DEFINITION      AV862261 Nori Satoh unpublished cDNA library, egg Ciona
intestinalis cDNA clone rc1eg32k05 3', mRNA sequence.
ACCESSION      AV862261
VERSION      AV862261.1 GI:16849785
KEYWORDS      EST.
SOURCE      Ciona intestinalis
ORGANISM      Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE      1 (bases 1 to 712)
AUTHORS      Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.
TITLE      Expressed genes in Ciona intestinalis
JOURNAL      Unpublished
COMMENT      Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@acidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. 712
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rc1eg32k05"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_id="Nori Satoh unpublished cDNA library, egg"
BASE COUNT      197 a      156 c      119 g      240 t
ORIGIN

Query Match      0.8%; Score 20; DB 9; Length 712;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2312 ATCATGCGAAGACAGAGAAA 2331
|||||
Db      546 ATCATGCGAAGACAGAGAAA 527

RESULT 49
CA763329      713 bp      mRNA      linear      EST 27-NOV-2002
LOCUS      CA763329
DEFINITION      BR060002B10D10.abi IRRI clones Oryza sativa (indica cultivar-group)
[Arabidopsis thaliana], mRNA sequence.
ACCESSION      CA763329
VERSION      CA763329.1 GI:25807368
KEYWORDS      EST.
SOURCE      Oryza sativa (indica cultivar-group)
ORGANISM      Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 713)
AUTHORS      Bennett,J., Arumugam,K., Latitte,R., Wen,J. and Bruskewich,R.
TITLE      Rice Microarray
JOURNAL      Unpublished
COMMENT      Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172653473
Email: bohnertlab@life.uiuc.edu
International Rice Information System (IRIS);
http://www.iris.irri.org).
Location/Qualifiers
1. 713
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR64"
/db_xref="taxon:39946"
/clone="BR060002B10D10.abi"
/tissue_type="panicles"
/dev_stage="flowering"
/clone_id="IRRI clones"
/notes="Vector: pBluescript II SK+; Water stress was
applied by not watering for 4 consecutive days. Panicles
were collected from control (well watered) and stressed
plants at 2 days before heading, heading, 50% flowering
and 4 days after 50% flowering."
BASE COUNT      200 a      143 c      125 g      243 t
ORIGIN

Query Match      0.8%; Score 20; DB 14; Length 713;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      384 CAAAAGAGAAATCATCGA 403
|||||
Db      279 CAAAAGAGAAATCATCGA 298

RESULT 50
CNS01FB4      736 bp      DNA      linear      GSS 01-JUN-2001
LOCUS      CNS01FB4
DEFINITION      Anopheles gambiae GSS T7 end of clone 04C02 of NotreDame1 library
from strain PEST of Anopheles gambiae (African malaria mosquito),
genomic survey sequence.
ACCESSION      AL141617
VERSION      AL141617.1 GI:6999735
KEYWORDS      GSS.
SOURCE      Anopheles gambiae (African malaria mosquito)
ORGANISM      Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
1 (bases 1 to 736)
REFERENCE      Genoscope.
TITLE      Direct Submission
AUTHORS      Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
2 (bases 1 to 736)
REFERENCE      Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
TITLE      Direct Submission
AUTHORS      Submitted (16-FEB-2000) BMH, Institut Pasteur, 25, rue du Dr.
JOURNAL      Roux, Paris 75015, France
COMMENT      This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.
Location/Qualifiers
1. 736
/organism="Anopheles gambiae"

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/mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone="04C02"
/clone_lib="Notredame1"
/notes="end: 17"
BASE COUNT      175 a      205 c      175 g      177 t      4 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2141 CCTGCTGACGACGAACTCCC 2160
Db      358 CCTGCTGACGACGAACTCCC 339

RESULT 51
LOCUS      BM132597      748 bp      mRNA      linear      EST 02-NOV-2002
DEFINITION      BM132597 Nori Satoh unpublished cDNA library, gastrula and neurula
ACCESSION      BM132597
VERSION      BM132597.1 GI:24488996
KEYWORDS      EST.
SOURCE      Ciona intestinalis
ORGANISM      Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE      1 (bases 1 to 748)
AUTHORS      Satou,Y., Shin-I., T., Kohara,Y. and Satoh,N.
TITLE      Expressed genes in Ciona intestinalis (2002c)
JOURNAL      Unpublished
COMMENT      Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-Ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES
source
1..748
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcign030m24"
/tissue_type="whole body"
/dev_stage="gastrula and neurula"
/clone_lib="Nori Satoh unpublished cDNA library, gastrula
and neurula"
BASE COUNT      215 a      168 c      121 g      244 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 20; DB 13; Length 748;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2312 ATCATGGCAGAGCAGAAA 2331
Db      713 ATCATGGCAGAGCAGAAA 694

RESULT 52
LOCUS      BZ995097      761 bp      DNA      linear      GSS 25-MAR-2003
DEFINITION      PUDFB72TD ZM 0.6.1.0 KB Zea mays genomic clone ZMBETA172L24,
ACCESSION      BZ995097
VERSION      BZ995097.1 GI:29238514
KEYWORDS      GSS.
SOURCE      Zea mays
ORGANISM      Zea mays

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 761)
Whitefaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Resnick
,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
Maize Genomics Consortium
Unpublished
Contact: Cathy Whitefaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitefaw@tigr.org
Seq primer: TP
Class: sheared ends.
FEATURES
source
1..761
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBETA172L24"
/clone_lib="ZM 0.6.1.0 KB"
/notes="Vector: pCR4-TOP0; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
BASE COUNT      227 a      114 c      144 g      276 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 20; DB 29; Length 761;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      749 AACACAGCACACACGCA 768
Db      56 AACACAGCACACACGCA 37

RESULT 53
LOCUS      BM131850      765 bp      mRNA      linear      EST 02-NOV-2002
DEFINITION      BM131850 Nori Satoh unpublished cDNA library, gastrula and neurula
ACCESSION      BM131850
VERSION      BM131850.1 GI:24488249
KEYWORDS      EST.
SOURCE      Ciona intestinalis
ORGANISM      Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE      1 (bases 1 to 765)
AUTHORS      Satou,Y., Shin-I., T., Kohara,Y. and Satoh,N.
TITLE      Expressed genes in Ciona intestinalis (2002c)
JOURNAL      Unpublished
COMMENT      Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-Ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES
source
1..765
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcign029c12"
/tissue_type="whole body"
/dev_stage="gastrula and neurula"
/clone_lib="Nori Satoh unpublished cDNA library, gastrula
and neurula"
BASE COUNT      220 a      171 c      122 g      252 t
ORIGIN

```

Query Match 0.8%; Score 20; DB 13; Length 765;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2312 ATCATGCGAAGAGCAGAAA 2331
 |||||
 Db 719 ATCATGCGAAGAGCAGAAA 700

RESULT 54
 CDS01MG/c 770 bp DNA linear GSS 14-UN-2001
 LOCUS Anopheles gambiae GSS SP6 end of clone 21250 of Notredame1 library
 DEFINITION from strain PEST of Anopheles gambiae (African malaria mosquito),
 genomic survey sequence.

ACCESSION AL150861
 VERSION AL150861.1 GI:7011340
 KEYWORDS GSS.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.
 1 (bases 1 to 770)

REFERENCE
 AUTHORS Direct Submission
 TITLE Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 EVRI cedex - FRANCE (E-mail : segre@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 2 (bases 1 to 770)
 REFERENCE
 AUTHORS Roch, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J.
 TITLE Direct Submission
 JOURNAL Submitted (16-FEB-2000) BIMI, Institut Pasteur, 25, rue du Dr.
 Roux, Paris 75015, France
 This clone is from an A. gambiae BAC library provided by F.H.
 Collins and sequenced by Genoscope in collaboration with the
 Laboratory of Biochem. and Biol. Molec. of Insects, Institut
 Pasteur.

FEATURES
 location/Qualifiers
 1..770
 /organism="Anopheles gambiae"
 /mol_type="genomic DNA"
 /strain="PEST"
 /db_xref="taxon:7165"
 /clone="21250"
 /clone_lib="Notredame1"
 /note="end : SP6"
 /note="end : SP6"
 BASE COUNT 237 a 152 c 114 g 262 t 5 others
 ORIGIN

Query Match 0.8%; Score 20; DB 29; Length 770;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1594 TTGTGATGAACATGATATA 1613
 |||||
 Db 440 TTGTGATGAACATGATATA 421

RESULT 55
 CDS98673 776 bp mRNA linear EST 03-APR-2003
 LOCUS AGNCNCOURT_12972342 NIH_MGC_178 Mus musculus cDNA clone
 IMAGE:3029054 5', mRNA sequence.
 ACCESSION CDS98673
 VERSION CDS98673.1 GI:29516529
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 776)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein
 CDNA Library Preparation: Michael Brownstein Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: NDCM62 row: 1 column: 15
 High quality sequence stop: 419.

FEATURES
 location/Qualifiers
 1..776
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:3029054"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH_MGC_178"
 /note="Organ: lung and heart; Vector: pDNR-LIB; Site_1:
 SfiI (ggccattggcc); Site_2: SfiI (ggccgctcgcc); CDNA
 made by oligo-dT priming and directionally cloned. 5' and
 3' adaptors were used in cloning as follows:
 5'-AAGCAGTGTATCAACGACAGTGGCATTACGCGCG-3' and
 5'-ATTCTAGAGCGGAGCGGCGCGACATG-dt(30)NN-3'. Full-length
 enriched library was constructed using the Clontech
 Creator SMART kit and size-selected to contain the 0.5 kb
 size fraction. Library created in the laboratory of M.
 Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."

BASE COUNT 208 a 195 c 143 g 230 t
 ORIGIN

Query Match 0.8%; Score 20; DB 14; Length 776;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 942 TCATCCTTACTCTCAATG 961
 |||||
 Db 680 TCATCCTTACTCTCAATG 699

RESULT 56
 BE130716 792 bp mRNA linear EST 20-FEB-2001
 LOCUS L48-922T3 Ice plant Lambda Uni-Zap XR expression library, 48 hours
 DEFINITION NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-922 5',
 mRNA sequence.

ACCESSION BE130716
 VERSION BE130716.1 GI:8578079
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Aizoaceae; Mesembryanthemum.
 1 (bases 1 to 792)

REFERENCE
 Cushman, J.C.
 TITLE An expressed sequence tag database for the common ice plant,
 Mesembryanthemum crystallinum
 JOURNAL Unpublished
 COMMENT Contact: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu
 PCR Primers
 FORWARD: T7
 BACKWARD: T3

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 812)
AUTHORS Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Kazezburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zuvaren, T., McCombie, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)

TITLE Unpublished
COMMENT Contact: W. Richard McCombie
Lila Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: 1903 row: c column: 07
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence stop: 812.

FEATURES
source Location/Qualifiers
1..812
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="1903C07"
/lab_host="DH5a"
/clone_lib="WGS-ZmaysF (DH5a methyl filtered)"
/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I; The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (X/Y reads in M13mp19, b/g reads in pUC19). The same ligation was transformed into DH5a."

BASE COUNT 240 a 152 c 135 g 285 t

ORIGIN

Query Match 0.8%; Score 20; DB 29; Length 812;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1594 TTTGATGACATGATATTA 1613
|||||
Db 646 TTTGATGACATGATATTA 627

RESULT 60
BH045505 831 bp DNA linear GSS 17-JUL-2001
LOCUS RPCI-24-346H17.TV RPCI-24 Mus musculus genomic clone RPCI-24-346H17
DEFINITION , genomic survey sequence.
ACCESSION BH045505
VERSION BH045505.1 GI:14829902
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 831)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Aktunc, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E., Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished
Other GSS: RPCI-24-346H17.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@igir.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.html>). BAC end page: http://www.tigr.org/tbcbac_ends/mouse/bac_end_intro.html
Plate: 346 row: H column: 17
Seq primer: SP6
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..831
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-346H17"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTRABAC1; Site 1: BamHI; Site 2: BamHI; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTRABAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."

BASE COUNT 260 a 128 c 180 g 263 t

ORIGIN

Query Match 0.8%; Score 20; DB 28; Length 831;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2370 TAACTAGGAAAAAATAAAC 2389
|||||
Db 780 TAACTAGGAAAAAATAAAC 799

RESULT 61
CNS07DNK 876 bp DNA linear GSS 08-JUL-2001
LOCUS T3 end of clone BD0A014B06 of library BD0A from strain CBS 94 of
DEFINITION Candida tropicalis, genomic survey sequence.
ACCESSION AL440694
VERSION AL440694.1 GI:12224105
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
1 (bases 1 to 876)
Souci, J.L., Agile, M., Artiguenave, F., Blandin, G., Boletín-Fukuhara, M., Bon, E., Broctier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Florente, B., Malpertuy, A., Neveuglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida tropicalis
JOURNAL MEDLINE
PUBMED 20584711
FBS Lett. 487 (1), 3-12 (2000)
1152876
2 (bases 1 to 876)
Blandin, G., Ozier-Kalogeropoulos, O., Wincker, P., Artiguenave, F. and Dujon, B.
Genomic exploration of the hemiascomycetous yeasts: 16. Candida tropicalis
FBS Lett. 487 (1), 91-94 (2000)
20584726
MEDLINE 20584726
PUBMED 11152891
REFERENCE 3 (bases 1 to 876)
AUTHORS Genoscope.
TITLE Direct Submission

JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seque@genoscope.cns.fr - Web : This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces exiguus*, *Saccharomyces servazii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbolicphila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
source 1..876
/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0A014B06"
/clone_lib="BD0A"
/note="end : 73"
Location/Qualifiers

BASE COUNT 309 a 136 c 152 g 275 t 4 others
ORIGIN

Query Match 0.8%; Score 20; DB 29; Length 876;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1521 AATTGACTACTGAGAC 1540
|||||
108 AATTGACTACTGAGAC 127

RESULT 62 923 bp mRNA linear EST 24-JAN-2001
LOCUS B033498 60301896F1 NIH_MGC_87 Homo sapiens CDNA clone IMAGE:4403567 5',
DEFINITION mRNA sequence.
ACCESSION B033498
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 923)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10113 row: 0 column: 24
High quality sequence stop: 649.
Location/Qualifiers

FEATURES
source 1..923
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4403567"
/tissue="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for

full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 247 a 235 c 199 g 242 t
ORIGIN

Query Match 0.8%; Score 20; DB 10; Length 923;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 926 GGAGTCATTACCTTCAT 945
|||||
Db 738 GGAGTCATTACCTTCAT 757

RESULT 63 957 bp mRNA linear EST 16-JUL-2002
LOCUS B0712408 AGENCOURT_8354094 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6278639 5', mRNA sequence.
DEFINITION B0712408
ACCESSION B0712408
VERSION B0712408.1 GI:21851307
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 957)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM246 row: 0 column: 24
High quality sequence stop: 605.
Location/Qualifiers

FEATURES
source 1..957
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6278639"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOT87; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
Location/Qualifiers

BASE COUNT 262 a 224 c 205 g 266 t
ORIGIN

Query Match 0.8%; Score 20; DB 13; Length 957;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 758 AACACACGCACTTACAG 777
|||||
Db 181 AACACACGCACTTACAG 200

RESULT 64 2185 bp mRNA linear HTC 05-DEC-2002
LOCUS AK037932 AK037932
DEFINITION Mus musculus 16 days neonate thymus cDNA, RIKEN full-length

enriched library, clone: A130064P06 product: interferon regulatory factor 6, full insert sequence.
 AK037932
 AK037932.1 GI:26086171
 HTC: CAP trapper.
 SOURCE
 ORGANISM
 Mus musculus
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 99279253
 10349636
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Mech. Enzymol. 303, 19-44 (1999)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 20499374
 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
 MEDLINE
 PUBMED
 20530913
 11076861
 4
 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanka, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Flischiemann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikolaic, I., Pessle, G., Quackenbush, J., Schriml, L. M., Staudl, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldairelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bona, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hochmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombert, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilmberg, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohlschki, S. and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)

JOURNAL
 MEDLINE
 PUBMED
 21085660
 11217851
 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

JOURNAL
 MEDLINE
 PUBMED
 11217851
 6
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hironaka, I., Hirozawa, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshitake Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/
 Location/Qualifiers
 1..2185
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM:DB:A130064P06"
 /db_xref="taxon:10090"
 /clone="A130064P06"
 /tissue_type="thymus"
 /clone_id="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="16 days neonate"
 1..2185
 /note="interferon regulatory factor 6 (MGI:1859211, GB|NM_016851, evidence: BLASTN, 99%, match=808)"

FEATURES
 source
 misc_feature
 BASE COUNT
 560 a 509 c 539 g 577 t
 ORIGIN
 Query Match 0 8%; Score 20; DB 11; Length 2185;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 20; Conservative 0; Mismatches 0; Gaps 0;
 Db 2188 CCAACTCAAGACAGACAG 2207
 940 CCAACTCAAGACAGACAG 959

RESULT 65
 BH907885
 LOCUS
 DEFINITION
 SALK_044651.46.40.x Arabidopsis thaliana TDNA insertion lines
 survey sequence.
 Arabidopsis thaliana genomic clone SALK_044651.46.40.x, genomic
 survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 GSS.
 BH907885.1 GI:22720818
 GSS.
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; rosids
 1 (bases 1 to 66)
 1 (bases 1 to 66)
 Alonso, J. M., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R., Gadgil, N. B., Jeske, A., Karnes, M., Kim, C. J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J. R.
 A sequence-indexed library of insertion mutations in the Arabidopsis Genome
 unpublished
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

JOURNAL
 MEDLINE
 PUBMED
 11217851
 6
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hironaka, I., Hirozawa, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@sal.k.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated intron of At5g15100.
 Class: TDNA tagged.

FEATURES
 source
 1. .66
 Location/Qualifiers

BASE COUNT
 32 a 9 c 5 g 20 t
 ORIGIN
 Query Match
 Best Local Similarity 100.0%; Score 19; DB 28; Length 66;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 393 AATCATGACAAAACA 411
 12 AATCATGACAAAACA 30
 Db

RESULT 66
 CC021347/c
 LOCUS 3591_1-24_1-A11.2EL_Y_1 110 bp DNA linear GSS 01-APR-2003
 DEFINITION 3591_1-24_1-A11.2EL_Y_1 3591 - Rescued Mu Grid P Zea mays genomic,
 genomic survey sequence.
 ACCESSION CC021347
 VERSION CC021347.1 GI:29435420
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 110)
 Walbot,V.
 Zea genomic sequences found using engineered Rescued Mu transposon
 unpublished
 CONTACT: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 3591_1-24_1 row: 9
 Class: transposon-tagged.
 Location/Qualifiers
 1. 110
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="3591 - Rescued Mu Grid P"
 /note="Organ: leaf; Vector: Rescued Mu (engineered from
 pBluescript backbone); Site 1: BamHI; Site 2: BglII;
 Rescued Mu is a 4.9 Kb, modified maize Mu transposon

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
 source

designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on Rescued Mu, go to the web
 site 'www.zmdb.iastate.edu' and follow the links for
 'Rescued Mu.' Grid P was grown at Mokolai in 2002. DNA was
 extracted from leaf strips, double digested using BamHI
 and BglII, and ligated to form circular plasmids. DH10B
 cells were transformed and then screened on LB plates with
 ampicillin.

BASE COUNT
 36 a 16 c 19 g 39 t
 ORIGIN
 Query Match
 Best Local Similarity 100.0%; Score 19; DB 29; Length 110;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1212 CATCTGAACGTGTAAAA 1230
 80 CATCTGAACGTGTAAAA 62
 Db

RESULT 67
 H74951
 LOCUS 539 Random-primed Brassica napus CDNA clone RRM1328, mRNA sequence.
 DEFINITION H74951
 ACCESSION H74951.1 GI:1048166
 VERSION
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 136)
 Park,Y.S., Kwak,J.M., Kwon,O.Y., Kim,Y.S., Lee,D.S., Cho,M.U., Lee
 H.H. and Nam,H.G.
 Generation of expressed sequence tags of random root CDNA clones of
 Brassica napus by single-run partial sequencing
 Plant Physiol. 103, 359-370 (1993)
 94302145
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 CONTACT: Nam, HG
 Plant Molecular Genetics Laboratory
 Pohang University of Science and Technology
 Dept. of Life Science, Sanji Hyojadong, Pohang Kyungbuk 790-784,
 Korea
 Tel: 825622792111
 Fax: 825622792199
 Email: nam@vision.postech.ac.kr
 Seq primer: M13 reverse
 Location/Qualifiers
 1. 136
 /organism="Brassica napus"
 /mol_type="mRNA"
 /strain="L. cv Naehan"
 /db_xref="taxon:3708"
 /clone="RRM1328"
 /lab_host="E. coli XL-1 Blue"
 /note="Vector: M13mp18; Site 1: EcoRI; Site 2: EcoRI; ESTs
 were generated from the root CDNA library of Brassica
 napus. The cDNAs were primed with random hexamer and were
 cloned into the M13mp18 vector digested with Eco RI."

FEATURES
 source
 1. 136
 /organism="Brassica napus"
 /mol_type="mRNA"
 /strain="L. cv Naehan"
 /db_xref="taxon:3708"
 /clone="RRM1328"
 /lab_host="E. coli XL-1 Blue"
 /note="Vector: M13mp18; Site 1: EcoRI; Site 2: EcoRI; ESTs
 were generated from the root CDNA library of Brassica
 napus. The cDNAs were primed with random hexamer and were
 cloned into the M13mp18 vector digested with Eco RI."
 BASE COUNT
 51 a 19 c 34 g 32 t
 ORIGIN

Query Match
 Best Local Similarity 100.0%; Score 19; DB 14; Length 136;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 ACCAAGGCTATGTCACTTC 183
 96 ACCAAGGCTATGTCACTTC 114
 Db

RESULT 68
BE505229/c
LOCUS BE505229 175 bp mRNA linear EST 06-AUG-2000
DEFINITION dc19g09.x1 NICHD XGC L11 Xenopus laevis cDNA clone IMAGE:3397600
3', mRNA sequence.
ACCESSION BE505229
VERSION BE505229.1 GI:9708760
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 175)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsapb-remail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
DNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/ILNL at: info@image.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 161.
Location/Qualifiers
1..175
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:3397600"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 Kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC
) library."

BASE COUNT 70 a 25 c 29 g 51 t
ORIGIN

Query Match 0.8%; Score 19; DB 10; Length 175;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2285 ACTCTCAATTATGATA 2303
DB 157 ACTCTCAATTATGATA 139

RESULT 69
BH867080
LOCUS BH867080 186 bp DNA linear GSS 05-AUG-2002
DEFINITION hg33b06.y9 WGS-ZmaySF (JMI07 adapted methyl filtered) Zea mays
genomic clone hg33b06 5', genomic survey sequence.
ACCESSION BH867080
VERSION BH867080.1 GI:22102977
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 186)
Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,
Katzenburger, F., King, L., Miller, B., Muller, S., Nascimben, L.,
Zutavern, T., McComb, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)

JOURNAL Unpublished
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: hg93 row: b column: 06
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence stop: 186.
Location/Qualifiers
1..186
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="hg93b06"
/lab_host="JMI07 or DH5a"
/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(x/y reads in M13mp19, b/g reads in pUC19). The same
ligation was transformed in either JMI07 or DH5a."

BASE COUNT 33 a 65 c 56 g 32 t
ORIGIN

Query Match 0.8%; Score 19; DB 28; Length 186;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1777 TGGAGATAGTCACAGCT 1795
DB 41 TGGAGATAGTCACAGCT 59

RESULT 70
AV236691/c
LOCUS AV236691 220 bp mRNA linear EST 15-NOV-2001
DEFINITION AV236691 RIKEN full-length enriched, 10 day neonate skin Mus
musculus cDNA clone 4732415B08 3', mRNA sequence.
ACCESSION AV236691
VERSION AV236691.1 GI:6189204
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 220)
Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai
C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ow, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata
Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H.,
Suzuki, H., Takahashi, F., Tateo, M., Tomioka, N., Tsunoda, Y.,
Watabiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,
Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Kono, H., et al. 1999)
Unpublished
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

JOURNAL Unpublished
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: hg93 row: b column: 06
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence stop: 186.
Location/Qualifiers
1..186
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="hg93b06"
/lab_host="JMI07 or DH5a"
/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(x/y reads in M13mp19, b/g reads in pUC19). The same
ligation was transformed in either JMI07 or DH5a."

Email: genome-res@gscc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
Matsunari, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. *Proc. Natl. Acad. Sci. U.S.A.* 95 (7), 3455-3460 (1998)
Itoh, M., Kikunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation system. *Genome Res.* 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303, 19-44 (1999)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

Source

```

1. .220
/organism="Mus musculus"
/mol_type="mrna"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4732415B08"
/sex="mixed"
/tissue_type="skin"
/dev_stage="10 days neonate"
/lab_host="DH10B"
/clone_lib="RTKEN full-length enriched, 10 day neonate"
/skin="skin"

```

BASE COUNT	67 a	37 c	40 g	76 e
ORIGIN				

Query Match	0.8%;	Score 19;	DB 9;	Length 220;
Best Local Similarity	100.0%;	Pred. No. 7.3e+02;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

2277 ATATTGACTCTTCAAT 2295

Db 41 ATAATTGACTCTCAAT 23

RESULT 71	LOCUS	DEFINITION
AQ948125/c	AQ948125	257 bp DNA linear GSS 27-JAN-2000
		Sheared DNA-47C22, TR Sheared DNA Trypanosoma Brucei genomic clone
		Sheared DNA-47C22, genomic survey sequence.

Gerzard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C., and Adams, M.
Determination of clone end sequences from *Trypanosoma brucei* GUTat 10.1 sheared DNA library

COMMENT

Unpublished

Other_GSSs: Sheared DNA-47C22.TF

Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: nelsayed@tigr.org

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared

DNA library constructed

distribution th

FEATURES

Source

Location/Qualifiers

1.25

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

```
/strain="TREU927/4 GUTat 10.1"
```

```
/db_xref="taxon:5691"
```

```
/clone="Sheared DNA-47C22"
```

```
/clone_lib="She
```

BASE COUNT

40 a	54 c	58 g	105 b
------	------	------	-------

Query Match	0.8%;	Score 19;	DB 28;	Length 257;
Best Local Similarity	100.0%;	Pred. No. 7.5e+02;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 759 ACAACAGCACTAACAG 777

Db 194 ACAACAGCACTAACAG 176

RESULT 72	LOCUS	DEFINITION	EST 15-JUL-2000
BB402033	271 bp	mRNA	
BB402033		RIKEN full-length enriched, ES cells Mus musculus cDNA clone C330025N03.3' similar to AK001942 Homo sapiens CDNA FLJ11080 f1s, clone PLACE1005181, mRNA sequence.	

ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 257)
El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujita, C.,
REFERENCE
AUTHORS

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=ec2-QV0-OT0030-100400-188-d04kt3-2000-04-10&ct=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 230.

FEATURES

source

```

1.303
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="OT0030"
/note="Organ: ovary; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTS PCR (U.S. Letters Patent application No. 196 /16 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT      62 a      65 c      67 g      109 t
ORIGIN

```

Query Match 0.8%; Score 19; DB 10; Length 303;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1224 TTTAAATCTTGAAGCAA 1242
 |||||
 Db 164 TTTAAATCTTGAAGCAA 146

RESULT 75
 LOCUS BM248898 303 bp mRNA linear EST 07-JUN-2003
 DEFINITION K0824E07-3 NIA Mouse 8.5-dpc Whole Embryo cDNA Library (long) Mus
 ACCESSION BM248898
 VERSION BM248898
 KEYWORDS Mus musculus
 SOURCE EST. GI:31503499
 ORGANISM Mus musculus (house mouse)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE 1 (bases 1 to 303)
 PIAO, Y., KO, N.-T., LIM, M.-K. and KO, M.-S. H.
 Construction of long-transcript enriched cDNA libraries from
 submicrogram amounts of total RNAs by a universal PCR amplification
 method

JOURNAL Genome Res. 11 (9), 1553-1558 (2001)
 MEDLINE 21439098
 PUBMED 11544199

COMMENT On Dec 17, 2001 this sequence version replaced gi:17884168.

CONTACT: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.gic.nia.nih.gov
 Plate: K0824 row: E column: 07
 Seq primer: -21M13 Forward
 High quality sequence stop: 303
 POLYA=Yes.

FEATURES

source

```

1.303
/organism="Mus musculus"
/mol_type="mrna"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="NIA:K0824E07 IMAGE:30080694"
/tissue_type="whole embryo including extraembryonic  

tissues at 8.5-days postcoitum"

```

```

/dev_stage="8.5-days postcoitum"
/lab_host="DH10B"
/clone_lib="NIA Mouse 8.5-dpc Whole Embryo cDNA Library  

(long)"
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:  

NotI; Mouse cDNA project by the Laboratory of Genetics,  

National Institute on Aging (NIA), Intramural Research  

Program, NIH (http://igsun.gic.nia.nih.gov/cDNA/). This is  

a long-transcript enriched cDNA library (Ref. Genome Res.  

11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were  

extracted from a pool of 13 embryos at 8.5-days  

postcoitum. Double-stranded cDNAs were synthesized with an  

Oligo (dT) primer (Invitrogen):  

5'-pGACTAGTTCGATCGCGAGCGCCCTTTTCTTTT-3' } from  

9.1 ug of total RNA, treated with T4 DNA polymerase, and  

purified by ethanol-precipitation. The cDNAs were ligated  

to lone-linker L1-SalI, purified by phenol/chloroform, and  

separated from free linkers by Centricon 100. Then, the  

cDNAs were amplified by long-range high fidelity PCR using  

Ex Tag polymerase (Takara) with a primer SalI-S. The  

products were purified by phenol/chloroform and Centricon  

100. The cDNAs were digested with SalI and NotI enzymes  

and cloned into SalI/NotI site of pSPORT1 plasmid vector.  

The DH10B E. coli host was transformed with the ligation  

mixture by the standard chemical method. The average  

insert size is about 2.5 kb. The library was constructed  

by Yulan Piao (NIA)."
```

BASE COUNT 65 a 87 c 67 g 84 t
 ORIGIN

Query Match 0.8%; Score 19; DB 12; Length 303;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1420 CTTGAATGATGATGACT 1438
 |||||
 Db 89 CTTGAATGATGATGACT 71

RESULT 76
 LOCUS BB290438 304 bp mRNA linear EST 09-JUL-2000
 DEFINITION BB290438 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA
 clone B020045P23 3' similar to J04492 Mouse T-cell receptor 4-1BB
 protein mRNA, mRNA sequence.

ACCESSION BB290438
 VERSION BB290438.1 GI:8990887
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE 1 (bases 1 to 304)

CONTACT: Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carinici
 Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
 Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
 Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
 Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata
 Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suganara, Y.,
 Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomioka, N., Toyota
 T., Tanoda, Y., Wachihi, K., Watanabe, S., Yamamura, T., Yamane, I.,
 Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
 M., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Kono, H., et al.)

UNPUBLISHED
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 Tel: 81-45-503-9222

Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
 URL: http://genome-gsc.riken.go.jp/
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Thermostabilization and thermocatalysis of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers
 1..304
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="B020045F23"
 /tissue_type="egg"
 /dev_stage="2 cells"
 /lab_host="DH10B"
 /clone_id="RIKEN full-length enriched, 2 cells egg"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGATTCGAGTAAATTAATTAATCCCCCCCCCC 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGAGTAAATTAATTAATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FLX I."

BASE COUNT 77 a 98 c 54 g 74 t 1 others
 ORIGIN

Query Match 0.8%; Score 19; DB 10; Length 304;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1742 CCATCTCCAGCGCAGATG 1760
 Db 33 CCATCTCCAGCGCAGATG 51

RESULT 77
 BB367558/c 304 bp mRNA linear EST 12-JUL-2000
 LOCUS BB367558 RIKEN full-length enriched, 16 days embryo head Mus
 DEFINITION Musculus cDNA clone C130038G20 3' similar to L38477 Mus musculus (clone Clabp-1) high mobility group 1 protein (HMG-1) mRNA, mRNA sequence
 BB367558
 ACCESSION BB367558.1 GI:9079387
 VERSION BB367558.1 GI:9079387
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 304)
 Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,

TITLE

JOURNAL

COMMENT

Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shihagawa, A., Shitaki, T., Sogabe, T., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, T., Tomimaga, N., Toya, T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamakawa, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.
 RIKEN Mouse ESTs (Kono, H., et al.)
 Unpublished
 Contact: Yoshihide Hayashizaki
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 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
 URL: http://genome-gsc.riken.go.jp/
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Thermostabilization and thermocatalysis of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers
 1..304
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="C130038G20"
 /sex="mixed"
 /tissue_type="head"
 /dev_stage="16 days embryo"
 /lab_host="DH10B"
 /clone_id="RIKEN full-length enriched, 16 days embryo head"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGATTCGAGTAAATTAATTAATCCCCCCCCCC 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGAGTAAATTAATTAATCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FLX I."

BASE COUNT

67 a 51 c 45 g 141 t

ORIGIN

Query Match 0.8%; Score 19; DB 10; Length 304;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1435 GACTAATTAAGAAAATG 1453
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Query Match 0.8%; Score 19; DB 10; Length 317;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 904 TAGAGTGTTCGAGTCCA 922
 |||||
 DB 148 TAGAGTGTTCGAGTCCA 166

RESULT 80
 BB463922/c 319 bp mRNA linear EST 22-JUL-2000
 LOCUS BB463922 RIKEN full-length enriched, 12 days embryo spinal ganglion
 DEFINITION Mus musculus cDNA D130084G04 3', mRNA sequence.
 ACCESSION BB463922
 VERSION BB463922.1 GI:9381111
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 319)
 Konomo, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
 P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
 Hirozane, T., Horii, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
 Izawa, M., Kadoya, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
 Kiyosawa, H., Kojima, Y., Kondo, S., Koyama, S., Kurihara, C., Kusakabe, M.,
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
 Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata
 Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
 Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya
 T., Tsunoda, Y., Watanabe, S., Watanabe, S., Yamamura, T., Yamane, A., I.
 Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
 M., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Konomo, H., et al.)
 Unpublished
 TITLE RIKEN Mouse ESTs (Konomo, H., et al.)
 JOURNAL
 COMMENT
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 The Institute of Physical and Chemical Research (RIKEN)
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 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@rsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
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 N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermostabilization and thermocatalysis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Oza, Y., Muramatsu, M., Okazaki
 Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.etc.riken.go.jp) for
 further details.
 Location/Qualifiers
 1..319
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="D130084G04"
 /tissue_type="spinal ganglion"
 /dev_stage="12 days embryo"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 12 days embryo
 spinal ganglion"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia"

Query Match 0.8%; Score 19; DB 10; Length 319;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1242 AGTTATCAAAACAGAGAG 1260
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 DB 163 AGTTATCAAAACAGAGAG 145

RESULT 81
 AV046714/c 324 bp mRNA linear EST 23-NOV-1999
 LOCUS AV046714 Mus musculus adult C57BL/6J testis Mus musculus cDNA clone
 DEFINITION AV046714.2 GI:4866379
 ACCESSION AV046714
 VERSION AV046714.2 GI:4866379
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 324)
 Carninci, P., Shibata, K., Oza, Y., Konomo, H., Itoh, M., Aizawa, K.,
 Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara
 A., Hayatsu, N., Horii, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
 Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C.,
 Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara
 Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya
 T., Tsunoda, Y., Watanabe, S., Watanabe, S., Yamamura, T., Yamane, A., I.
 Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
 M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 RIKEN Mouse ESTs
 Unpublished
 TITLE RIKEN Mouse ESTs
 JOURNAL
 COMMENT
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 Genome Science Laboratory
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 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098
 Email: genome-res@etc.riken.go.jp
 Thermostabilization and thermocatalysis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Oza, Y., Muramatsu, M., Okazaki
 Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.etc.riken.go.jp) for
 further details.
 Location/Qualifiers
 1..324
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="1700063E04"
 /sex="male"
 /tissue_type="testis"
 /dev_stage="adult"
 /clone_lib="Mus musculus adult C57BL/6J testis"

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BASE COUNT      63 a      92 c      47 g      122 t
ORIGIN
Query Match      0.8%; Score 19; DB 9; Length 324;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2314 CATGCAGACGAGAAAA 2332
      |||||
      174 CATGCAGACGAGAAAA 156

RESULT 82
A1547552/c      333 bp      mRNA      linear      EST 22-MAR-1999
LOCUS
DEFINITION      UI-R-C3-str-e-04-0-UI-s1 UI-R-C3 Rattus norvegicus cDNA clone
ACCESSION      A1547552
VERSION      A1547552
KEYWORDS      EST.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE      1 (bases 1 to 333)
AUTHORS      Ronaldo, M.F., Lennon, G. and Soares, M.B.
TITLE      Normalization and subtraction: two approaches to facilitate gene
JOURNAL      Genome Res. 6 (9), 791-806 (1996)
MEDLINE      97044477
PUBMED      8889548
COMMENT      Contact: Soares, MB
      Coordinated Laboratory for Computational Genomics
      University of Iowa
      375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
      Tel: 319 335 8250
      Fax: 319 335 9565
      Email: bento-soares@iowa.edu
      The sequence contained an oligo-dT track that was present in the
      oligonucleotide that was used to prime the synthesis of first
      strand cDNA and therefore this may represent a bonafide poly A
      tail. The sequence tag present in the cDNA between the NotI site
      and the oligo-dT track served to identify it as a clone from the
      normalized kidney library cDNA library. Preparation: M.B. Soares Lab
      Clone distribution: clones will be available through Research
      Genetics (www.resgen.com)
      Seg primer: M13 Forward.

FEATURES
source
      Location/Qualifiers
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      /organism="Rattus norvegicus"
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      /db_xref="taxon:10116"
      /clone="UI-R-C3-str-e-04-0-UI"
      /dev_stage="adult"
      /lab_host="DH10B (Life Technologies)"
      /clone_1fb="UI-R-C3"
      /note="Vector: pTR73D-Pac (Pharmacia) with a modified
      polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-C3
      library is a subtracted library of a series, ultimately
      derived from a mixture of individually tagged normalized
      libraries from rat placenta, adult lung, brain, liver,
      kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
      embryos, after a series of subtractions to reduce the
      representation of cDNAs from which ESTs had already been
      generated. The following serially subtracted libraries
      were generated in this process: UI-R-C3, UI-R-C2p, UI-R-C1
      , UI-R-C0, UI-R-A1, UI-R-B1. The tag is a string of 3-5
      nucleotides present between the Not I site and the
      oligo-dT track which allows identification of the library
      of origin of a clone within the mixture. The subtracted
      library (UI-R-C3) was constructed as follows: PCR amplified

```

cDNA inserts from UI-R-C2p clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C2p library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C3 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996).

```

BASE COUNT      86 a      83 c      59 g      105 t
ORIGIN
Query Match      0.8%; Score 19; DB 9; Length 333;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1420 CTTGATGATGATGACT 1438
      |||||
      155 CTTGATGATGATGACT 137

RESULT 83
BH294683      335 bp      DNA      linear      GSS 30-NOV-2001
LOCUS
DEFINITION      CH230-122P21 TVB CHORI-230 Segment 1 Rattus norvegicus genomic
ACCESSION      BH294683
VERSION      BH294683.1 GI:17207091
KEYWORDS      GSS.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE      1 (bases 1 to 335)
AUTHORS      Zhao, S., Shetty, J., Shatsman, S., Tseng, G., Geer, K., Shvartsbeyn,
      A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
      Jong, P. and Fraser, C.M.
      Rat BAC End Sequences from Library CHORI-230 EcORI segment
      Unpublished
      Other GSSs: CH230-122P21.TVB
      Contact: Shaying Zhao
      Department of Eukaryotic Genomics
      The Institute for Genomic Research
      9712 Medical Center Dr., Rockville, MD 20850, USA
      Tel: 301 838 0200
      Fax: 301 838 0208
      Email: szhao@tigr.org
      Clones are derived from the rat BAC library CHORI-230
      (http://www.chori.org/bacpac/rat230.htm). For BAC library
      availability, please contact Pieter de Jong (pdejong@mail.cho.org).
      Clones may be purchased from BACPAC Resources
      (http://www.chori.org/bacpac/orering/information.htm). BAC end
      page: http://www.tigr.org/cdb/bac\_ends/rat/bac\_end\_intro.html
      Plate: 122 Row: P Column: 21
      Seg primer: 17
      Clones: BAC ends.

FEATURES
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      /clone="CH230-122P21"
      /sex="Female"
      /cell_type="Brain"
      /clone_1fb="CHORI-230 Segment 1"
      /note="Vector: pTARBAC2.1; Site 1: EcORI; Site 2: EcORI;
      CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
      Pieter de Jong"

BASE COUNT      67 a      46 c      81 g      141 t
ORIGIN

```

Query Match 0.8%; Score 19; DB 28; Length 335;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 452 GATGCTGCTGTGCTTGG 470
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 Db 71 GATGCTGCTGTGCTTGG 89

RESULT 84

AA558478 345 bp mRNA linear EST 08-SEP-1997
 LOCUS nk39d05.s1 NCI_CGAP_GC2 Homo sapiens CDNA clone IMAGE:1015881 3',
 DEFINITION mRNA sequence.

ACCESSION AA558478
 VERSION AA558478.1 GI:2328955
 KEYWORDS EST.

ORGANISM Homo sapiens (human)
 SOURCE

REFERENCE 1 (bases 1 to 345)
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Stratagene, Inc., David B. Krizman,
 Ph.D.

CDNA Library Arraying: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
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 High quality sequence stop: 260.
 Location/Qualifiers

FEATURES

source

1. 345
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="IMAGE:1015881"
 /tissue_type="germ cell tumor"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="NCI CGAP GC2"
 /note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI
 ; Cloned unidirectionally. Primer: Oligo dT. Bulk germ
 cell tumor. 5' adaptor sequence: 5' GAAITGGGACGAG 3' 3'
 adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Average
 insert size: 1.2 kb."
 BASE COUNT 89 a 65 c 48 g 143 t
 ORIGIN

Query Match 0.8%; Score 19; DB 9; Length 345;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2298 TGGATACATAGTATCAT 2216
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 Db 120 TGGATACATAGTATCAT 138

RESULT 85

AA0825612 360 bp DNA linear GSS 27-AUG-1999
 LOCUS HS_5432_B2.A07_S66E RPCI-11 Human Male BAC Library Homo sapiens
 DEFINITION genomic clone Plate=1013 Col=14 Row=B; genomic survey sequence.
 ACCESSION AA0825612

VERSION AA0825612.1 GI:5791674
 GSS.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM

REFERENCE 1 (bases 1 to 360)
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome

JOURNAL MEDLINE
 PUBMED 99380589
 10449764

COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887

Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Resear h Genetics (info@resgen.com). BAC end Web Server:
<http://www.htsc.washington.edu>
 Plate: 1013 row: B column: 14
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 360.
 Location/Qualifiers

FEATURES

source

1. 360
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=1013 Col=14 Row=B"
 /sex="male"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBAC3.6 vector at EcoRI sites"
 BASE COUNT 68 a 67 c 68 g 144 t 13 others
 ORIGIN

Query Match 0.8%; Score 19; DB 28; Length 360;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1458 ATGATTATTTGGCATTCCT 1476
 |||||
 Db 340 ATGATTATTTGGCATTCCT 322

RESULT 86

AA0910031 364 bp DNA linear GSS 09-JAN-2001
 LOCUS GSS06405 Trypanosoma cruzi random genomic library Trypanosoma
 DEFINITION cruzi genomic clone G44B9, genomic survey sequence.
 ACCESSION AA0910031 GI:10137177
 GSS.

ORGANISM Trypanosoma cruzi
 SOURCE Trypanosoma cruzi
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 364)
 Aguiro,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
 A random sequencing approach for the analysis of the trypanosoma
 cruzi genome: general structure, large gene and repetitive DNA

families, and gene discovery
 Genome Res. 10 (12), 1996-2005 (2000)
 MEDLINE 20568489
 PUBMED 1116094
 COMMENT On Sep 14, 2000 this sequence version replaced gi:3377374.
 Contact: Sanchez D.O.
 Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral San Martin)
 Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos Aires, Argentina
 Tel: (54-11) 4580/7255/7
 Fax: (54-11) 4752-9639
 Email: dsanchez@ib. unconam.edu.ar
 Sequences were basecalled with phred and vector was masked with crossmatch (see <http://genome.washington.edu>). Sequences were then trimmed from both ends to remove low quality bases and masked vector.
 Seq primer: T7
 Class: shotgun.
 Location/Qualifiers
 source
 1..364
 /organism="Trypanosoma cruzi"
 /mol_type="genomic DNA"
 /strain="CL-Brener"
 /db_xref="taxon:5693"
 /clone="G4489"
 /cell_type="epimastigote"
 /clone_lib="Trypanosoma cruzi random genomic library"
 /note="Vector: pBS(-) (Stratagene); T. cruzi DNA was randomly sheared using a nebulizer and the 1 to 2 Kb range was gel purified and cloned into the dephosphorylated HincII site of the vector"
 BASE COUNT 100 a 116 c 94 g 54 t
 ORIGIN
 Query Match 0.8%; Score 19; DB 28; Length 364;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 757 CAACAACAGCACTAAC 775
 ||||||||||||||||
 Db 94 CAACAACAGCACTAAC 112
 RESULT 87
 BF376452/c 370 bp mRNA linear EST 24-NOV-2000
 LOCUS BF376452
 DEFINITION M1-TN0045-290800-002-e06 TN0045 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF376452
 VERSION BF376452.1 GI:11338477
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 370)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922

Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR1&c2=MR1-TN0045-290800-002-e06&t3=2000-08-29&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 360.
 Location/Qualifiers
 source
 1..370
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="TN0045"
 /note="Organ: testis normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 67 a 113 c 80 g 110 t
 ORIGIN
 Query Match 0.8%; Score 19; DB 10; Length 370;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 127 AGCAATCAATGCTGAGCAA 145
 ||||||||||||||||
 Db 88 AGCAATCAATGCTGAGCAA 70
 RESULT 88
 BF376477 375 bp mRNA linear EST 24-NOV-2000
 LOCUS BF376477
 DEFINITION M1-TN0045-290800-003-h10 TN0045 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF376477
 VERSION BF376477.1 GI:11338502
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 375)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR1&c2=MR1-TN0045-290800-003-h10&t3=2000-08-29&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 375.
 Location/Qualifiers
 source
 1..375

BASE COUNT	115 a	82 c	102 g	75 t	1 others
ORIGIN					
Query Match	0.8%; Score 19; DB 10; Length 375;				
Best Local Similarity	100.0%; Pred. No. 8e+02;				
Matches	19; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
Db	127 AGGATCAATGCTGAGCA	145			
	302 AGGATCAATGCTGAGCA	320			
RESULT 89					
LOCUS	AI883328	377 bp	mRNA	linear	EST 07-JUN-2001
DEFINITION	fc60e02.y1 zebrafish Mashu MPMPE EST Danio rerio cDNA clone				
ACCESSION	AI883328	IMAGE:3725786 5', mRNA sequence.			
VERSION	AI883328.1	GI:5588492			
KEYWORDS	EST.				
SOURCE	Danio rerio (zebrafish)				
ORGANISM	Danio rerio				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.				
REFERENCE	1 (bases 1 to 377)				
AUTHORS	Clark,M., Johnson,S.L., Lettrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schunk,R., Ritter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.				
TITLE	Washu Zebrafish EST Project 1998				
JOURNAL	Unpublished				
COMMENT	Other ESTs: fc60e02.x1 Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: zbrafish@watson.wustl.edu cDNA Library Preparation: Matthew Clark, cDNA Library Arrayed by: Matthew Clark, DNA Sequencing by: Washington University Genome Sequencing Center, DNA distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and ResourcenzentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de) Seq primer: T3 ET from Amersham High quality sequence stop: 361. Location/Qualifiers 1..377 /organism="Danio rerio" /mol_type="mRNA" /db_xref="taxon:7955" /clone="IMAGE:3725786" /sex="mixed" /tissue type="26 somite embryos, adult livers, shield stage embryos" /lab host="XLA-blue MRF"				
FEATURES					
source					

/clone.lib="zebrafish washu pm1mg EST"
 /note=Vector: pSPORT1; site 1: NotI; site 2: SalI; 1st
 strand cDNA was primed with a Not I... oligo(dT)15 primer
 [5' pGACATGATTCAGTCGCGAGCGGCGCCCTTTTCTTTTCTTTT3']
 double-stranded cDNA was ligated to Sal I adaptors (BRL)
 digested with Not I and cloned into the Not I and Sal I
 sites of the pSPORT1 vector (BRL). Library was constructed
 by Matthew Clark (Lehrbach lab; ICRF, London and Max Planck
 Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
 analysis were selected following oligonucleotide
 hybridization fingerprinting of arrayed clones from
 zebrafish late somitogenesis (26 ss), adult liver or
 embryonic shield stage (5.6 h) libraries. Fingerprint
 data were used to computationally cluster cDNAs, and a
 single cDNA from each cluster was chosen for sequencing.
 In some cases multiple members of the same cluster were
 sequenced to assess clustering parameters or single clones
 were sequenced additional times to assess quality
 control."

MEDLINE
PUBMED
12354683
12466851
COMMENT
Contact: Yoshihide Hayaishizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Science Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane,
T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Komio, H., Miyazaki, A.,
Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K.,
Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami,
M., Waki, K., Watanabe, A., Muramatsu, M. and Hayaishizaki, Y. Direct
Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichipillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Science Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Michela Fagiolini and Takao K. Henrich (
Laboratory for Neuronal Circuit Development Brain Science Institute
RIKEN 2-1 Hirotsawa, Wako-shi, Saitama 351-0198 Japan) whose
assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES
source
Location/Qualifiers
1..386
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="K536040103"
/issue_type="visual cortex"
/clone_lib="RIKEN full-length enriched, visual cortex"
BASE COUNT
109 a 86 c 78 g 113 t
ORIGIN

Query Match 0.8%; Score 19; DB 13; Length 386;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1420 CTTGATGATGATGACT 1438
|||||
Db 36 CTTGATGATGATGACT 54

RESULT 91
LOCUS BF376465 396 bp mRNA linear EST 24-NOV-2000
DEFINITION MRL-TN0045-290800-003-b08 TN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF376465
VERSION BF376465.1 GI:11338490
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 396)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,

MEDLINE
PUBMED
20202663
COMMENT
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL
MEDLINE
10737800
CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL:
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR1&t2=MRI-TN0045-290800-003-b08&t3=2000-08-29&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 375.

FEATURES
source
Location/Qualifiers
1..396
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="TN0045"
/note="Organ: testis normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT
118 a 86 c 114 g 77 t 1 others
ORIGIN

Query Match 0.8%; Score 19; DB 10; Length 396;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 127 AGGAATCAATGCTGAGCAA 145
|||||
Db 323 AGGAATCAATGCTGAGCAA 341

RESULT 92
LOCUS BE002498 401 bp mRNA linear EST 05-JUN-2000
DEFINITION PM3-BN0085-260200-001-e02 BN0085 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE002498
VERSION BE002498.1 GI:8262731
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 401)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare,
M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
Simpson, A. J. G.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL
MEDLINE
20202663

PUBMED
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=et2-PM3-BN0085-260
2000-001-e02&t3=2000-02-26&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 398.
Location/Qualifiers
1. .401
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="BN0085"
/note="Organ: breast, normal; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT
142 a 68 c 68 g 123 t

ORIGIN

Query Match 0.8%; Score 19; DB 10; Length 401;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1550 ATTGCTCAATTAGCTGATA 1568
|||||
224 ATTGCTCAATTAGCTGATA 242

RESULT 93
B2941299/c 401 bp DNA linear GSS 13-JUN-2003
LOCUS B2941299/c 401 bp DNA linear GSS 13-JUN-2003
DEFINITION CH240_91P17.TU CHORI-240 Bos taurus genomic clone CH240_91P17,
Genomic survey sequence.
ACCESSION B2941299
VERSION B2941299.1 GI:31726682
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 401)
Larkin,D.M., Everts-van der Wind,A., Rebeiz,M., Schweitzer,P.,
Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L.,
Womack,J.E., de Jong,P.J., and Lewin,H.A.
A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human
Genome Sequence
Unpublished
Other GSSs: CH240_91P17.TV
Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBMC) by the University of Illinois at Urbana Champaign
, USA with funds provided by grant No. AG202-34480-11828 from
USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock Genome
Sequencing Initiative)
Plate: 91 row: P column: 17
Seq primer: SP6
Class: BAC ends
Location/Qualifiers
1. .401
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Dreud: Hereford"
/db_xref="taxon:9913"
/clone="CH240_91P17"
/sex="Male"
/cell_type="B100d"
/clone_id="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

BASE COUNT
88 a 92 c 73 g 146 t

ORIGIN

Query Match 0.8%; Score 19; DB 29; Length 401;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2163 AAGTAGAGACTGAAAAAGT 2181
|||||
275 AAGTAGAGACTGAAAAAGT 257

RESULT 94
BF885054 402 bp mRNA linear EST 17-JAN-2001
LOCUS BF885054
DEFINITION MRI-TN0045-031000-013-b07 TN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF885054
VERSION BF885054.1 GI:12275663
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 402)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202563
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR1kt2-MRI-TN0045-
031000-013-b07&t3=2000-10-03&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 6
High quality sequence stop: 402.

FEATURES
source

Location/Qualifiers
1. 402
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="TN0045"
/note="Organ: testis normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
118 a 86 c 123 g 75 t

Query Match
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 127 AGGATCATGCTGAGCAA 145
329 AGGATCATGCTGAGCAA 347

RESULT 95
BF554284

LOCUS
UI-R-C1-Kg-a-09-0-UI.r1 UI-R-C1 Rattus norvegicus CDNA clone

ACCESSION
BF554284

VERSION
BF554284.1 GI:11664014

KEYWORDS
EST

SOURCE
Rattus norvegicus (Norway rat)

ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE
1 (bases 1 to 409)
Donald, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene discovery
Genome Res. 6 (9), 791-806 (1996)

JOURNAL
MEDLINE
PUBMED
97044477

COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1763903
Seq primer: MJ3 forward.

FEATURES
source

Location/Qualifiers
1. 409
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C1-Kg-a-09-0-UI"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1lb="UI-R-C1"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-C1 library is a subtracted library derived from the UI-R-Co library, which is a subtracted library derived from the UI-R-A1 and UI-R-F1 libraries. The UI-R-A1 library

consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-F1 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C1) was constructed as follows: PCR amplified cDNA inserts from UI-R-Co clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-Co library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C1 library. This procedure has been previously described (Bonaldi, Lennon and Soares, Genome Research 6: 791-806, 1996)"

BASE COUNT
120 a 94 c 107 g 88 t

Query Match
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1420 CTTGATGATGATGACT 1438
368 CTTGATGATGATGACT 386

RESULT 96
BY605266

LOCUS
BY605266 RIKEN full-length enriched, visual cortex Mus musculus

ACCESSION
BY605266

VERSION
BY605266.1 GI:26940448

KEYWORDS
EST

SOURCE
Mus musculus (house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 412)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Otsu, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gotohori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbett, L.E., Cousins, S., Dalla, E., Dragani, T.A., Flecher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lennard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrowsky, N., Pillai, R., Pontus, J.U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sanderlin, A., Schneider, C., Sempie, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carinici, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Maki, K., Komai, J., Arakawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imutani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation

TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

22354683
12466851

Contact: Yoshihide Hayashiaki

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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/

Aiawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane
, T., Imotani, K., Ishii, Y., Itoh, M., Kawaji, J., Kono, H., Miyazaki, A.,
Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K.,
Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami
, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct
Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Tissues were provided by Michela Fagioli and Takao K. Hensch (
Laboratory for Neuronal Circuit Development Brain Science Institute
RIKEN 2-1 Hirosawa, Wako-shi, Saitama 351-0198 Japan) whose
assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES
source

Location/Qualifiers
1. .412
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="K230038L17"
/tissue_type="visual cortex"
/clone_lib="RIKEN full-length enriched, visual cortex"
BASE COUNT 118 a 90 c 88 g 115 t 1 others
ORIGIN

Query Match 0.8%; Score 19; DB 13; Length 412;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1420 CTTGATGATGATGACT 1438
|||||
Db 61 CTTGATGATGATGACT 79

RESULT 97
AL961018 414 bp mRNA linear EST 27-NOV-2002
LOCUS AL961018 XGC-gastrula silurana tropicalis cDNA clone Tga8103b20 5',
DEFINITION mRNA sequence.
ACCESSION AL961018.1 GI:25784613
VERSION EST.
KEYWORDS silurana tropicalis (western clawed frog)
SOURCE silurana tropicalis
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS Taylor, R., Ashurst, J.L., Croning, M.D.R., Zorn, A.M. and Rogers, J.
TITLE Sanger Xenopus tropicalis EST project 2002
JOURNAL Unpublished
COMMENT Contact: Taylor R
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: Tga8103b20.plcsp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.

FEATURES
source

Location/Qualifiers
1. .414
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="Tga8103b20"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-gastrula"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dt primed from 5' end of poly A+ RNA from stages
10-13 gastrulae. EcoRI/NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."
BASE COUNT 128 a 76 c 111 g 97 t 2 others
ORIGIN

Query Match 0.8%; Score 19; DB 9; Length 414;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1577 ACGTCAGTCGTTACATTT 1595
|||||
Db 273 ACGTCAGTCGTTACATTT 291

RESULT 98
BM248963 415 bp mRNA linear EST 07-JUN-2003
LOCUS BM248963
DEFINITION K0825G07-3 NIA Mouse 8.5-dpc Whole Embryo cDNA Library (Long) Mus
musculus cDNA clone NIA:K0825G07 IMAGE:30080814 3', mRNA sequence.
ACCESSION BM248963
VERSION BM248963.2 GI:31503553
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
TITLE Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method

Genome Res. 11 (9), 1553-1558 (2001)
MEDLINE 21429098
PUBMED 11544199
On Dec 17, 2001 this sequence version replaced gi:17884233.
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun-grc.nia.nih.gov
Plate: K0825 row: G column: 07
Seq primer: -21M13 Forward
High quality sequence stop: 415
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1. .415

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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="nlaesr:X0825G07-3"
/db_xref="taxon:10090"
/clone="NIA:K0825G07 IMAGE:30080814"
/tissue_type="whole embryo including extraembryonic
tissues at 8.5-days postcoitum"
/dev_stage="8.5-days postcoitum"
/lab_host="DH10B"
/clone_1ib="NIA Mouse 8.5-dpc Whole Embryo cDNA Library
(long)"
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://jgsun.gsc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of 13 embryos at 8.5-days
postcoitum. Double-stranded cDNAs were synthesized with an
oligo(dT) primer [Invitrogen:
5'-pGACTGTTCTTACATCGCAGCGCCCTTTTCTTTT-3'] from
9.1 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Tag polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.5 kb. The library was constructed
by Julian Piao (NIA)."
BASE COUNT      116 a      97 c      87 g      115 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1420 CTTGAATGATGATCGACT 1438
      |||||
Db      237 CTTGAATGATGATCGACT 219

RESULT 99
BE505361/c      417 bp      mRNA      linear      EST 06-AUG-2000
LOCUS      dc23a08.x1 NICHDL_XGC_L11 Xenopus laevis cDNA clone IMAGE:3397910
DEFINITION      3', mRNA sequence.
ACCESSION      BE505361
VERSION      BE505361.1 GI:9708892
KEYWORDS      EST.
SOURCE      Xenopus laevis (African clawed frog)
ORGANISM      Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 417)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ccgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaabes@mail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LINT at: info@image.llnl.gov

```

```

Seq primer: -40UP from Gibco
High quality sequence scop: 414.
FEATURES
source
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:3397910"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NICHDL_XGC_L11"
/note="Organ: liver; Vector: pCMV-SPORT6, Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC
) library."
BASE COUNT      132 a      75 c      75 g      134 t      1 others
ORIGIN
Query Match
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2285 ACTCTCAATTATGATGATA 2303
      |||||
Db      142 ACTCTCAATTATGATGATA 124

RESULT 100
BY457007/c      418 bp      mRNA      linear      EST 13-DEC-2002
LOCUS      BY457007 RIKEN full-length enriched, adult male testis Mus musculus
DEFINITION      cDNA clone K630095C12 3', mRNA sequence.
ACCESSION      BY457007
VERSION      BY457007.1 GI:26755150
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 418)
Oikazaki, Y., Oseato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,
Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,
Gojibori, T., Baldarelli, R., Hill, D.P., Bull, C., Hume, D.A.,
Quackendush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S.,
Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chotila, C., Corbani,
L.E., Cousins, S., Dalla, E., Dragani, T.A., Flecher, C.F., Forrest,
A., Frazer, K.S., Gaasterland, T.G., Gariboldi, M., Giesi, C., Godzik, A.,
Gough, J., Grimond, S., Gustincich, S., Hirokawa, N., Jackson, I.J.,
Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M.,
King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons,
P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki,
H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G.,
Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D.,
Ramchandran, S., Ravasi, T., Reed, J.C., Reed, J.U., Reid, J., Ring,
B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempel, C.A., Setou,
M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale,
R.D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y.,
Watanabe, Y., Wells, C., Wilting, L.G., Wynshaw-Boris, A., Yanagisawa,
M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,
Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura,
M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Atakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imachi, K., Ishii,
Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Saeki, D., Shibata,
K., Shingawa, A., Yasuniishi, A., Yoshino, M., Waterston, R., Lander,
E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
JOURNAL
MEDLINE
PUBMED
1246851
1246851
TITLE
COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic

```

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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M., and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

FEATURES

source

Location/Qualifiers

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1. 418
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="K630095C12"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="SOLR"
/clone_lib="RIKEN full-length enriched, adult male testis"
/notice="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAGCGCGCGCATTAATTCGAGTTAATAATTAATCCCGCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites."
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BASE COUNT

120 a 87 c 88 g 123 t

ORIGIN

Query Match 0.8%; Score 19; DB 13; Length 418;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1816 GGAAGAAACGAATTCACATC 1834

Db 74 GGAAGAAACGAATTCACATC 56

Search completed: November 14, 2003, 07:49:18
Job time : 5033 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2003, 03:35:31 ; Search time 147 Seconds
(without alignments)
7173.227 Million cell updates/sec

Title: US-09-765-271-55

Perfect score: 2389

Sequence: 1 TTCTTACGAGTTGGACTGT.....TAAGTAGGAAAAATAAAC 2389

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Database: Issued Patents NA:*

1: /cgn2_6/prodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2389	100.0	2389	3	US-08-961-083-55
2	2389	100.0	2389	4	US-09-536-784-55
3	2389	100.0	2451	4	US-09-468-656A-9
4	2338	97.9	8195	4	US-08-961-527-94
5	53	2.2	2290	3	US-08-961-083-65
6	53	2.2	2290	4	US-09-536-784-65
7	53	2.2	2290	4	US-08-961-527-243
8	53	2.2	2531	4	US-09-468-656A-5
9	53	2.2	2531	4	US-09-468-656A-11
10	44	1.8	973	4	US-08-961-527-355
11	30	1.3	40	3	US-08-961-083-282
12	30	1.3	40	4	US-09-536-784-282
13	30	1.3	40	4	US-09-468-656A-3
14	27	1.1	36	4	US-09-468-656A-1
15	27	1.1	37	3	US-08-961-083-281
16	27	1.1	37	4	US-09-536-784-281
17	26	1.1	35	4	US-09-468-656A-2
18	24	1.0	1342	3	US-08-961-083-181
19	24	1.0	1342	4	US-09-536-784-181
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23	19	0.8	7493	1	US-08-212-133A-7
24	19	0.8	7493	1	US-08-474-503-5
25	19	0.8	7493	2	US-08-670-707A-5
26	19	0.8	7493	3	US-09-37-601-5
27	19	0.8	7493	4	US-09-315-179-5

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30	18	0.8	499	4	US-09-641-638-572	Sequence 572, Appl
31	18	0.8	659	4	US-09-221-017B-390	Sequence 390, Appl
32	18	0.8	987	4	US-09-107-532A-2361	Sequence 2361, Appl
33	18	0.8	1161	4	US-09-107-532A-1110	Sequence 1110, Appl
34	18	0.8	1664976	4	US-08-916-421B-1	Sequence 1, Appl
35	17	0.7	20	2	US-08-448-386A-10	Sequence 10, Appl
36	17	0.7	20	3	US-08-816-426-10	Sequence 10, Appl
37	17	0.7	20	5	PCT-US93-12161-10	Sequence 10, Appl
38	17	0.7	24	3	US-08-981-462-56	Sequence 56, Appl
39	17	0.7	238	4	US-09-491-356C-15	Sequence 15, Appl
40	17	0.7	253	4	US-09-491-356C-13	Sequence 13, Appl
41	17	0.7	265	4	US-09-491-356C-14	Sequence 14, Appl
42	17	0.7	265	4	US-09-491-356C-16	Sequence 16, Appl
43	17	0.7	265	4	US-09-491-356C-17	Sequence 17, Appl
44	17	0.7	265	4	US-09-491-356C-18	Sequence 18, Appl
45	17	0.7	321	1	US-08-175-388-2	Sequence 2, Appl
46	17	0.7	321	2	US-08-779-620-2	Sequence 2, Appl
47	17	0.7	321	2	US-08-818-726-2	Sequence 2, Appl
48	17	0.7	322	3	US-08-961-083-149	Sequence 149, Appl
49	17	0.7	322	3	US-09-536-784-149	Sequence 149, Appl
50	17	0.7	470	4	US-09-056-556-216	Sequence 216, Appl
51	17	0.7	470	4	US-09-072-596-211	Sequence 211, Appl
52	17	0.7	633	4	US-09-134-001C-1953	Sequence 1953, Appl
53	17	0.7	658	4	US-09-221-017B-1007	Sequence 1007, Appl
54	17	0.7	687	4	US-09-328-352-1650	Sequence 1650, Appl
55	17	0.7	768	3	US-08-981-462-1	Sequence 1, Appl
56	17	0.7	706	4	US-09-470-191-60	Sequence 60, Appl
57	17	0.7	762	4	US-09-071-035-373	Sequence 373, Appl
58	17	0.7	876	4	US-09-501-558-1	Sequence 1, Appl
59	17	0.7	882	4	US-09-501-558-3	Sequence 3, Appl
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63	17	0.7	1077	3	US-08-839-711-6	Sequence 6, Appl
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67	17	0.7	1543	4	US-09-359-301A-9	Sequence 9, Appl
68	17	0.7	1578	4	US-09-107-532A-2089	Sequence 2089, Appl
69	17	0.7	1623	4	US-09-613-303-3	Sequence 3, Appl
70	17	0.7	1654	4	US-08-487-589-3	Sequence 3, Appl
71	17	0.7	1756	2	US-08-466-598-3	Sequence 3, Appl
72	17	0.7	1756	2	US-08-700-638-3	Sequence 3, Appl
73	17	0.7	1756	3	US-08-467-574-3	Sequence 3, Appl
74	17	0.7	1756	4	US-09-217-345-3	Sequence 3, Appl
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94	17	0.7	3882	4	US-09-484-970B-68	Sequence 68, Appl
95	17	0.7	4380	4	US-08-955-565A-3	Sequence 3, Appl
96	17	0.7	4634	4	US-09-436-874-1	Sequence 1, Appl
97	17	0.7	6394	4	US-09-491-356C-2	Sequence 2, Appl
98	17	0.7	6999	1	US-08-276-594A-1	Sequence 1, Appl
99	17	0.7	7056	1	US-08-121-202-1	Sequence 1, Appl
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Query Match 100.0%; Score 2389; DB 3; Length 2389;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-536-784-55

Sequence 55, Application US/09536784

Patent No. 6573082

GENERAL INFORMATION:

APPLICANT: Choi et. al.

TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines

NUMBER OF SEQUENCES: 452

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/536,784

FILING DATE: 30-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/961,083

FILING DATE: OCT-30-1997

ATTORNEY/AGENT INFORMATION:

NAME: Michelle S. Marks

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB340P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:

LENGTH: 2389 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 55:

US-09-536-784-55

Query Match 100.0%; Score 2389; DB 4; Length 2389;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
 US-09-468-656A-9
 ; Sequence 9, Application US/09468656A
 ; Patent No. 6582706
 ; GENERAL INFORMATION:
 ; APPLICANT: Johnson, Leslie S.
 ; APPLICANT: Adamou, John E.
 ; TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
 ; TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
 ; FILE REFERENCE: 469201-444
 ; CURRENT APPLICATION NUMBER: US/09/468,656A
 ; PRIOR APPLICATION NUMBER: 60/113,048
 ; PRIOR FILING DATE: 1998-12-21
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 2451
 ; TYPE: DNA
 ; ORGANISM: Streptococcus pneumoniae
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)-(2451)
 ; OTHER INFORMATION: n = a, c, t or g
 US-09-468-656A-9

Query Match 100.0%; Score 2389; DB 4; Length 2451;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTACGAGTTGGAGCTGTATCAAGCTAGAAAGGTTAAGAAATTAATCGTGTTCCTTA 60
 DB 60 TTTCTTACGAGTTGGAGCTGTATCAAGCTAGAAAGGTTAAGAAATTAATCGTGTTCCTTA 119
 QY 61 TATAGATGAAAAAAGAGGAGCGCAAAAACCGAAGATTGCTCTGATGAGGTTAGCAA 120
 DB 120 TATAGATGAAAAAAGAGGAGCGCAAAAACCGAAGATTGCTCTGATGAGGTTAGCAA 179
 QY 121 GCGTGAAGAAATCAATGCTGAGCAAAATGCTCATCAAGATTAACAGACCAAGGCTATGTCAC 180
 DB 180 GCGTGAAGAAATCAATGCTGAGCAAAATGCTCATCAAGATTAACAGACCAAGGCTATGTCAC 239
 QY 181 TTCACATGCGCACTATCATTTATTAACATGATGAAGTTCCTTATGACGCTATCATCAG 240
 DB 240 TTCACATGCGCACTATCATTTATTAACATGATGAAGTTCCTTATGACGCTATCATCAG 299
 QY 241 TGAAGAAATTAATCAATGAAAGATCCAAACTATTAAGCTAAAAAGTGAAGATTTGTTAATGA 300
 DB 300 TGAAGAAATTAATCAATGAAAGATCCAAACTATTAAGCTAAAAAGTGAAGATTTGTTAATGA 359
 QY 301 GGTCAAGAGGTGAGATGTTTATCAAGGTGATGGAATAATGTTATGCTTAAGAGATGC 360
 DB 360 GGTCAAGAGGTGAGATGTTTATCAAGGTGATGGAATAATGTTATGCTTAAGAGATGC 419
 QY 361 TGCCACGCGGATTAAGTCCGTTACAAAAGAGAAATCAATGACAAAAACAAGACATAG 420
 DB 420 TGCCACGCGGATTAAGTCCGTTACAAAAGAGAAATCAATGACAAAAACAAGACATAG 479
 QY 421 TCAATATGTAAGGTGAACTCCCAAGAAAGATGCTGTTGCTTGGCAGCTTTCGA 480
 DB 480 TCAATATGTAAGGTGAACTCCCAAGAAAGATGCTGTTGCTTGGCAGCTTTCGA 539
 QY 481 AGGACGTATATCAATGATGATGTTATATCTTTAATGCTTCTGATATCATAGAGATAC 540

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Db      540 AGGAGCTAATCTACAGATGATGTTATATCTTTAATGCTTCTGATATCATAGAGATAC 599
Qy      541 TGGTATGCTTATATCGTTCCTCATGAGATCATATACATTAATCTCTAAGATGAT 600
Db      600 TGGTATGCTTATATCGTTCCTCATGAGATCATATACATTAATCTCTAAGATGAT 659
Qy      601 ATCAGCTAGCAGATGGCTGTGTCAGAAAGCCTTCTATCTGGTTCAGAGAAATCTGTCAA 660
Db      660 ATCAGCTAGCAGATGGCTGTGTCAGAAAGCCTTCTATCTGGTTCAGAGAAATCTGTCAA 719
Qy      661 TTCAAGAACTTATGCGCCGACAAATATGCGATPAACCTTCAAGAACAACTGGGTAACCTTC 720
Db      720 TTCAAGAACTTATGCGCCGACAAATATGCGATPAACCTTCAAGAACAACTGGGTAACCTTC 779
Qy      721 TGTAGCAATCCAGGAATACAAATACTAACACAAAGCAACACCACTAACAGTCA 780
Db      780 TGTAGCAATCCAGGAATACAAATACTAACACAAAGCAACACCACTAACAGTCA 839
Qy      781 AGCAAGTCAAGATATGACATTTGATAGTCTCTTGAAGACGCTCTCAAACTGCCCTTGTAG 840
Db      840 AGCAAGTCAAGATATGACATTTGATAGTCTCTTGAAGACGCTCTCAAACTGCCCTTGTAG 899
Qy      841 TCAAAGACATGTAGAAATCTGATGGCTTGTCTTTGATCCAGCACAAATCAGAACTCGAAC 900
Db      900 TCAAAGACATGTAGAAATCTGATGGCTTGTCTTTGATCCAGCACAAATCAGAACTCGAAC 959
Qy      901 AGCTAGAGTGTGACAGTCCACACAGGAGATCATTAACACTTACCTCTACTCTCAAT 960
Db      960 AGCTAGAGTGTGACAGTCCACACAGGAGATCATTAACACTTACCTCTACTCTCAAT 1019
Qy      961 GTCTGAATTTGGAAGAACAAATCGCTCGATATATTCCTCGTTATCGTTCAAACTATG 1020
Db      1020 GTCTGAATTTGGAAGAACAAATCGCTCGATATATTCCTCGTTATCGTTCAAACTATG 1079
Qy      1021 GGTATCCAGATTCAGAGCCAGAACAAACAAAGTCCACAACTCCGAACTTAACTCAGG 1080
Db      1080 GGTATCCAGATTCAGAGCCAGAACAAACAAAGTCCACAACTCCGAACTTAACTCAGG 1139
Qy      1081 CCCCAGACCTGACCAAAATCTTAAATAGACTCAAAATCTTCTGTTAGTACAGCTGCT 1140
Db      1140 CCCCAGACCTGACCAAAATCTTAAATAGACTCAAAATCTTCTGTTAGTACAGCTGCT 1199
Qy      1141 ACGAAAGTGTGGGAGAGATATGTATTCGAAGAAAGGAGCATCTCTGTTATGCTTTC 1200
Db      1200 ACGAAAGTGTGGGAGAGATATGTATTCGAAGAAAGGAGCATCTCTGTTATGCTTTC 1259
Qy      1201 GAAAGATTTACATCTGAAACTGTTAAATCTTGAAGCAAGTTATCAAAACAGAGAG 1260
Db      1260 GAAAGATTTACATCTGAAACTGTTAAATCTTGAAGCAAGTTATCAAAACAGAGAG 1319
Qy      1261 TGTTCACACACTTAACTGCTAAAGAAAGAAATGTTCTCTCTGTCGACAAAGATTTT 1320
Db      1320 TGTTCACACACTTAACTGCTAAAGAAAGAAATGTTCTCTCTGTCGACAAAGATTTT 1379
Qy      1321 TGTATTAAGCATATATCTGTTAATCTGAGGCTCATTAAGCCTGTTTGAATTAAGGGTGC 1380
Db      1380 TGTATTAAGCATATATCTGTTAATCTGAGGCTCATTAAGCCTGTTTGAATTAAGGGTGC 1439
Qy      1381 TAAATTCGATTTCCAAAGCCTTAGACAAATTTATAGACGCTTGAATGATGACTAA 1440
Db      1440 TAAATTCGATTTCCAAAGCCTTAGACAAATTTATAGACGCTTGAATGATGACTAA 1499
Qy      1441 TAAAGAAAAATTTGGATGATGATTTATTTGGCATTTCTAGACCAATTAACCAAGAGG 1500
Db      1500 TAAAGAAAAATTTGGATGATGATTTATTTGGCATTTCTAGACCAATTAACCAAGAGG 1559
Qy      1501 ACTTGCAAAACCAATTTCTCAAAATGAGTATACTGAAGCAAGTTCGTATGCTCAAT 1560
Db      1560 ACTTGCAAAACCAATTTCTCAAAATGAGTATACTGAAGCAAGTTCGTATGCTCAAT 1619
Qy      1561 AGCTGATAGATATCAACGTCAGATGTTTATGATGAACATGATATATCATGTA 1620

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Db      1620 AGCTGATAGATATCAACGTCAGATGTTTATCTTTTGAATGACATATATATCATGTA 1679
Qy      1621 TGAAGAGATGACATATGTAACGCTCATATGAGGCTATGTCATGATTTGAAAAAGATAG 1680
Db      1680 TGAAGAGATGACATATGTAACGCTCATATGAGGCTATGTCATGATTTGAAAAAGATAG 1739
Qy      1681 CTTTCTGATTAAGAAAAAGTTGAGCTCAAGCCTATATTAAGAAAAAGGATCTCAAC 1740
Db      1740 CTTTCTGATTAAGAAAAAGTTGAGCTCAAGCCTATATTAAGAAAAAGGATCTCAAC 1799
Qy      1741 TCCATCTTCAGACCCAGATGTTAAAGCAATCCAACTGAGATGTCAGACGCTATTTA 1800
Db      1800 TCCATCTTCAGACCCAGATGTTAAAGCAATCCAACTGAGATGTCAGACGCTATTTA 1859
Qy      1801 CAATCGTGTGAAGGGAAAAAGAAATTCACCTGCTGACCTTCCATATATGTTGAGCA 1860
Db      1860 CAATCGTGTGAAGGGAAAAAGAAATTCACCTGCTGACCTTCCATATATGTTGAGCA 1919
Qy      1861 TACAGTTAGGTTAAAAACGTTAATTTGATTTCTCATTAAGGATCATTAACATATAT 1920
Db      1920 TACAGTTAGGTTAAAAACGTTAATTTGATTTCTCATTAAGGATCATTAACATATAT 1979
Qy      1921 TAAATTTGCTTGGTTTATGATATCACACATACAAAGCTCCAAATGCTATATCTTGAAGA 1980
Db      1980 TAAATTTGCTTGGTTTATGATATCACACATACAAAGCTCCAAATGCTATATCTTGAAGA 2039
Qy      1981 TTTGTTGCGACGATTAAGTACTAGTAAACACCTGAGAGAGTCCACATCTTAATGA 2040
Db      2040 TTTGTTGCGACGATTAAGTACTAGTAAACACCTGAGAGAGTCCACATCTTAATGA 2099
Qy      2041 TGGATGGGGCAATGCGAGTGCATGTTGTTAGGCAAGAAAGCCACAGTAAAGATCCAAA 2100
Db      2100 TGGATGGGGCAATGCGAGTGCATGTTGTTAGGCAAGAAAGCCACAGTAAAGATCCAAA 2159
Qy      2101 TAAAGACTTCAAGCCGATGTAAGAGCCAGTBAAGAAAAACCTGCTGAGCCAGAACTCC 2160
Db      2160 TAAAGACTTCAAGCCGATGTAAGAGCCAGTBAAGAAAAACCTGCTGAGCCAGAACTCC 2219
Qy      2161 TCAAGTAGAGCTGAAAAAGTAGAAGCCCAACTCAAAAGACAGAGTTTGTCTTGCGAA 2220
Db      2220 TCAAGTAGAGCTGAAAAAGTAGAAGCCCAACTCAAAAGACAGAGTTTGTCTTGCGAA 2279
Qy      2221 AGTAACGATTTTACTGTGAAGCCAAATGCAACAGAACTCTAGCTGTTACGAAATTA 2280
Db      2280 AGTAACGATTTTACTGTGAAGCCAAATGCAACAGAACTCTAGCTGTTACGAAATTA 2339
Qy      2281 TTTGACTCTTCAATTTATGATTAACAATAGTATATGCGAGACAGAAAAATTAATTGCT 2340
Db      2340 TTTGACTCTTCAATTTATGATTAACAATAGTATATGCGAGACAGAAAAATTAATTGCT 2399
Qy      2341 GTTGTAAAGGAAGTAACTCTGATCTGTAGTAAAGAAAAATTAAC 2389
Db      2400 GTTGTAAAGGAAGTAACTCTGATCTGTAGTAAAGAAAAATTAAC 2448

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RESULT 4
US-08-961-527-94
; Sequence 94, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33

```

OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/961,527
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Brookes, A. Anders
 REGISTRATION NUMBER: 36,373
 REFERENCE/DOCKET NUMBER: PB340P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ. ID NO.: 94:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8195 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-961-527-94

Query Match 97.9%; Score 2338; DB 4; Length 8195;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTTACGAGTTGGAGCTGTATTAACCTGGAAGGTTAAGAAATTAATCGTGTCTTA 60
 DB 3053 TTCTTACGAGTTGGAGCTGTATTAACCTGGAAGGTTAAGAAATTAATCGTGTCTTA 3112
 QY 61 TATAGTGAAGAAACAGCGACGCAAAAAAGGAAATTTGACCTCGATGAGGTTAGCA 120
 DB 3113 TATAGTGAAGAAACAGCGACGCAAAAAAGGAAATTTGACCTCGATGAGGTTAGCA 3172
 QY 121 GCGTGAAGAAATCAATGCTGAGCAAAATGCTCATCAAGATPACAGCAAGGCTATGTCAC 180
 DB 3173 GCGTGAAGAAATCAATGCTGAGCAAAATGCTCATCAAGATPACAGCAAGGCTATGTCAC 3232
 QY 181 TTCACATGCGGACCACTATCATTTATTAACAATGTTAAGTTCTTATGAGGCTATCATCAG 240
 DB 3233 TTCACATGCGGACCACTATCATTTATTAACAATGTTAAGTTCTTATGAGGCTATCATCAG 3292
 QY 241 TGAAGAAATTAACATGAAGAAATCAAACTATTAAGTAAAGATGAGGATATTGTTAATA 300
 DB 3293 TGAAGAAATTAACATGAAGAAATCAAACTATTAAGTAAAGATGAGGATATTGTTAATA 3352
 QY 301 GGTCAAGGTTGATATGTTATCAAGGTAGATGGAATACTATGTTTACCTTAAGGATGC 360
 DB 3353 GGTCAAGGTTGATATGTTATCAAGGTAGATGGAATACTATGTTTACCTTAAGGATGC 3412
 QY 361 TGGCCACGCGGATACGTCCTGTCACAAAAGGAATCAATCGCAAAAAACAGAGCATAG 420
 DB 3413 TGGCCACGCGGATACGTCCTGTCACAAAAGGAATCAATCGCAAAAAACAGAGCATAG 3472
 QY 421 TCAACATGCTGAAGTGAAGTCAAGTCAAGAAACGATGCTGCTGCTGGACGCTTCGCA 480
 DB 3473 TCAACATGCTGAAGTGAAGTCAAGTCAAGAAACGATGCTGCTGCTGGACGCTTCGCA 3532
 QY 481 AGGACGCTATACTACAGATGATGTTATATCTTAAATGCTTGCATATCAGAGATAC 540
 DB 3533 AGGACGCTATACTACAGATGATGTTATATCTTAAATGCTTGCATATCAGAGATAC 3592
 QY 541 TGGTGAATGCTTATATGTTCTCTCATGAGATCAATTAACATTAATTCCTPAAGATAGTT 600
 DB 3593 TGGTGAATGCTTATATGTTCTCTCATGAGATCAATTAACATTAATTCCTPAAGATAGTT 3652
 QY 601 ATCAGTACGAGTTGGCTGCTGCGAAGGCTTCCATCTGGTCGAGAAATTCGTCAAA 660
 DB 3653 ATCAGTACGAGTTGGCTGCTGCGAAGGCTTCCATCTGGTCGAGAAATTCGTCAAA 3712
 QY 661 TTCAGAACTTATCGCCGACAAATATAGCATTAACATTCAGAAACAACTGGGTACTTTC 720

DB 3713 TTCAGAACTTATCGCCGACAAATATAGGATTAACACTTCAGAAACAACTGGGTACTTTC 3772
 QY 721 TGTAAAGCAATCCAGGACATCAACAATATCAACAAGCAACAAACAGCAACATCAAGTCA 780
 DB 3773 TGTAAAGCAATCCAGGACATCAACAATATCAACAAGCAACAAACAGCAACATCAAGTCA 3832
 QY 781 AGCAAGTCAAGTATGACATTTGATAGTCTCTTGAAGACGCTCTCAAACTGCTTTGAG 840
 DB 3833 AGCAAGTCAAGTATGACATTTGATAGTCTCTTGAAGACGCTCTCAAACTGCTTTGAG 3892
 QY 841 TCAAGCAATGTAGATCTGATGCTTGTCTTGTATCCAGCAAAATCAACAATGCAAC 900
 DB 3893 TCAAGCAATGTAGATCTGATGCTTGTCTTGTATCCAGCAAAATCAACAATGCAAC 3952
 QY 901 AGCTAGAGTGTGAGAGGCCACAGGAGATCATTAACACTTCAATCCCTTACTCTCAAT 960
 DB 3953 AGCTAGAGTGTGAGAGGCCACAGGAGATCATTAACACTTCAATCCCTTACTCTCAAT 4012
 QY 961 GTCTGAATTTGAAGAAGCAATGCTCTGATTTATTCCTCTGTTATCGTTCAAAACATTTG 1020
 DB 4013 GTCTGAATTTGAAGAAGCAATGCTCTGATTTATTCCTCTGTTATCGTTCAAAACATTTG 4072
 QY 1021 GGTACCAATTTCAAGGCCAGAAACAACCAATCCAGACCGACTCCGGAACCTAGTCCAG 1080
 DB 4073 GGTACCAATTTCAAGGCCAGAAACAACCAATCCAGACCGACTCCGGAACCTAGTCCAG 4132
 QY 1081 CCGGCACTGACCAAAATCTTAAATATAGACTCAAAATCTTCTTGTGTTAGCAGCTGGT 1140
 DB 4133 CCGGCACTGACCAAAATCTTAAATATAGACTCAAAATCTTCTTGTGTTAGCAGCTGGT 4192
 QY 1141 AGCAAAAGTTGGGGAAGGATATGTAATTCGAAGAAAGGCACTCTCGTTATGTCCTTTC 1200
 DB 4193 AGCAAAAGTTGGGGAAGGATATGTAATTCGAAGAAAGGCACTCTCGTTATGTCCTTTC 4252
 QY 1201 GAAAGATTTACCATGTGAAACTGTTTAAATCTTGAAGCAAGTTATCAAAACAAGAG 1260
 DB 4253 GAAAGATTTACCATGTGAAACTGTTTAAATCTTGAAGCAAGTTATCAAAACAAGAG 4312
 QY 1261 TGTTCACACACTTTAATCTGCTTAAAGAAAGAAATGTTGCTCTGCTGACCAAGATTTTA 1320
 DB 4313 TGTTCACACACTTTAATCTGCTTAAAGAAAGAAATGTTGCTCTGCTGACCAAGATTTTA 4372
 QY 1321 TGATTAAGCATTAATCTGTTTAACTGAGGCTCATTAAGGCTGTTGNAATTAAGGATG 1380
 DB 4373 TGATTAAGCATTAATCTGTTTAACTGAGGCTCATTAAGGCTGTTGNAATTAAGGATG 4432
 QY 1381 TAATCTGATTTCAAGCCTTAGACAAATTAATTAAGACGCTTGAATGATGAATCGACTAA 1440
 DB 4433 TAATCTGATTTCAAGCCTTAGACAAATTAATTAAGACGCTTGAATGATGAATCGACTAA 4492
 QY 1441 TAAAGAAAAATGTTGATGATTTATTTGGCATTTCTTAGACCAATTAATCCATCCAGAGG 1500
 DB 4493 TAAAGAAAAATGTTGATGATTTATTTGGCATTTCTTAGACCAATTAATCCATCCAGAGG 4552
 QY 1501 ACTTGCAAAACCAATTTCTCAATTAAGATGATCTGAAGCAAGTTCGATTTGCTCAATT 1560
 DB 4553 ACTTGCAAAACCAATTTCTCAATTAAGATGATCTGAAGCAAGTTCGATTTGCTCAATT 4612
 QY 1561 AGCTGTAAGTATTAACAAGCTCAGATGTTTACATTTTGTATGAACAATGATATAATCAGTGA 1620
 DB 4613 AGCTGTAAGTATTAACAAGCTCAGATGTTTACATTTTGTATGAACAATGATATAATCAGTGA 4672
 QY 1621 TGAAGGAGATGATATGTAAGCTCTCATATGAGGCAATGATCACTGATTTGGAAGATAG 1680
 DB 4673 TGAAGGAGATGATATGTAAGCTCTCATATGAGGCAATGATCACTGATTTGGAAGATAG 4732
 QY 1681 CCTTCTGATTAAGAAAAAGTTGCAAGCTCAACCTATTAAGAAAAAGATCTTAC 1740
 DB 4733 CCTTCTGATTAAGAAAAAGTTGCAAGCTCAACCTATTAAGAAAAAGATCTTAC 4792
 QY 1741 TCCATCTCCAGACGAGATGTTTAAAGCAAACTGAAGATAGTGCAGCAGTATTTTA 1800

Db 4793 TCACATCTCCAGACGAGATGTTAAAGCAATCCAACTGAGATAGTGACAGACTATTTA 4852
Qy 1801 CAATCGTGTGAAGGGGAAAAAGCAATCCACTCGTTCGACTTCATATATGTTAGACA 1860
Db 4853 CAATCGTGTGAAGGGGAAAAAGCAATCCACTCGTTCGACTTCATATATGTTAGACA 4912
Qy 1861 TACAGTTAGGTTAAAAAGGTTATTTGATTTATTCCTGATTAAGATCATTTACATATAT 1920
Db 4913 TACAGTTAGGTTAAAAAGGTTATTTGATTTATTCCTGATTAAGATCATTTACATATAT 4972
Qy 1921 TAAATTTGCTGTTGTTGATGATCAACATACAAAGCTCCAAATGCTTACTTGTGAAGA 1980
Db 4973 TAAATTTGCTGTTGTTGATGATCAACATACAAAGCTCCAAATGCTTACTTGTGAAGA 5032
Qy 1981 TTTGTTTCGACGAGTTAAGTACTAGTGAACACCCCTGACGAACTCCACATTTCAATGA 2040
Db 5033 TTTGTTTCGACGAGTTAAGTACTAGTGAACACCCCTGACGAACTCCACATTTCAATGA 5092
Qy 2041 TGGATGGGCAATGCGACGATGATGTTAGCAAGAAAGCAACAGTGAAGATCCAAA 2100
Db 5093 TGGATGGGCAATGCGACGATGATGTTAGCAAGAAAGCAACAGTGAAGATCCAAA 5152
Qy 2101 TAAAGACTTCAAAGCGAGTGAAGACCGATGAGAGAAACCTGCTGACCCAGAAAGTCCC 2160
Db 5153 TAAAGACTTCAAAGCGAGTGAAGACCGATGAGAGAAACCTGCTGACCCAGAAAGTCCC 5212
Qy 2161 TCAAGTAGAGACTGAAAAAGTGAAGACCCCACTCAAGAGAGAGAAAGTTTGTCTGGCAA 2220
Db 5213 TCAAGTAGAGACTGAAAAAGTGAAGACCCCACTCAAGAGAGAGAAAGTTTGTCTGGCAA 5272
Qy 2221 AGTAAAGGATCTAGCTGAAAAGCCCAATGCACACAGAAACTAGCTGTTTACGAATATA 2280
Db 5273 AGTAAAGGATCTAGCTGAAAAGCCCAATGCACACAGAAACTAGCTGTTTACGAATATA 5332
Qy 2281 TTTGACTCTTCAATATATGATGAATCAATATGATCTGCGACAGAGAGAAATTTCTTGC 2340
Db 5333 TTTGACTCTTCAATATATGATGAATCAATATGATCTGCGACAGAGAGAAATTTCTTGC 5392
Qy 2341 GTTGTAAAGAGTAATCTTCACTGTAAGTGAAGAAAAATATAAC 2389
Db 5393 GTTGTAAAGAGTAATCTTCACTGTAAGTGAAGAAAAATATAAC 5441

RESULT 5

US-08-961-083-65
; Sequence 65, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961.083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373

; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-083-65

Query Match 2.2%; Score 53; DB 3; Length 2290;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 983 GCTGTATTATTCCTTCGTTATCGTTCAACCAATGGGTACGAGATTCAAG 1035
Db 944 GCTGTATTATTCCTTCGTTATCGTTCAACCAATGGGTACGAGATTCAAG 996

RESULT 6

US-09-536-784-65
; Sequence 65, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536.784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961.083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-536-784-65

Query Match 2.2%; Score 53; DB 4; Length 2290;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 983 GCTGTATTATTCCTTCGTTATCGTTCAACCAATGGGTACGAGATTCAAG 1035
Db 944 GCTGTATTATTCCTTCGTTATCGTTCAACCAATGGGTACGAGATTCAAG 996

RESULT 7
US-08-961-527-243
; Sequence 243, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 243:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2359 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-243

Query Match 2.2%; Score 53; DB 4; Length 2359;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 983 GCTGTAATTATTCCTTCGTTATGTTCAACCACTGGGTACCGATTCAAG 1035
|||||
Db 1879 GCTCGTATTATTCCTTCGTTATGTTCAACCACTGGGTACCGATTCAAG 1931
|||||

RESULT 8
US-09-468-656A-5
; Sequence 5, Application US/09468656A
; Patent No. 6582706
; GENERAL INFORMATION:
; APPLICANT: Johnson, Leslie S.
; TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
; TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
; FILE REFERENCE: 469201-444
; CURRENT APPLICATION NUMBER: US/09/468,656A
; CURRENT FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/113,048
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2531
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-468-656A-5

Query Match 2.2%; Score 53; DB 4; Length 2531;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 983 GCTGTAATTATTCCTTCGTTATGTTCAACCACTGGGTACCGATTCAAG 1035
|||||
Db 1003 GCTCGTATTATTCCTTCGTTATGTTCAACCACTGGGTACCGATTCAAG 1055
|||||

RESULT 9
US-09-468-656A-11
; Sequence 11, Application US/09468656A
; Patent No. 6582706
; GENERAL INFORMATION:
; APPLICANT: Johnson, Leslie S.
; TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
; TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
; FILE REFERENCE: 469201-444
; CURRENT APPLICATION NUMBER: US/09/468,656A
; CURRENT FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/113,048
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2531
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-468-656A-11

Query Match 2.2%; Score 53; DB 4; Length 2531;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 983 GCTGTAATTATTCCTTCGTTATGTTCAACCACTGGGTACCGATTCAAG 1035
|||||
Db 1000 GCTCGTATTATTCCTTCGTTATGTTCAACCACTGGGTACCGATTCAAG 1052
|||||

RESULT 10
US-08-961-527-355
; Sequence 355, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 973 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-355

Query Match 1.8%; Score 44; DB 4; Length 973;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 572 CATTACCATTCATTCCAGAGATGATTCAGTACGAGCTT 615
Db 722 CATTACCATTCATTCCAGAGATGATTCAGTACGAGCTT 765

RESULT 11

US-08-961-083-282/c
Sequence 282; Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961.083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 282:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-083-282

Query Match 1.3%; Score 30; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2360 CCTCATCTGTAGTAAAGAAAAATAAAC 2389
Db 40 CCTCATCTGTAGTAAAGAAAAATAAAC 11

RESULT 12
US-09-536-784-282/c

Sequence 282; Application US/09536784
Patent No. 6573082

GENERAL INFORMATION:

APPLICANT: Choi et. al.

TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and Vaccines

NUMBER OF SEQUENCES: 452

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/536.784

FILING DATE: 30-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/961.083

FILING DATE: OCT-30-1997

ATTORNEY/AGENT INFORMATION:

NAME: Michelle S. Marks

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB340P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 282:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 282:

US-09-536-784-282

Query Match 1.3%; Score 30; DB 4; Length 40;

Best Local Similarity 100.0%; Pred. No. 3.8e-05;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2360 CCTCATCTGTAGTAAAGAAAAATAAAC 2389
Db 40 CCTCATCTGTAGTAAAGAAAAATAAAC 11

RESULT 13
US-09-468-656A-3/c
Sequence 3; Application US/09468656A
Patent No. 6582706
GENERAL INFORMATION:
APPLICANT: Johnson, Leslie S.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
CURRENT APPLICATION NUMBER: US/09/468.656A
CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3

LENGTH: 40
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Reverse primer

OTHER INFORMATION: used in amplification of the Sp36 gene sequence.
US-09-468-656A-3

Query Match 1.1%; Score 30; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2360 CCTTCATCTGTAGTAAGGAAAAATTAAC 2389
DB 40 CCTTCATCTGTAGTAAGGAAAAATTAAC 11

RESULT 14
US-09-468-656A-1
Sequence 1, Application US/09468656A
Patent No. 6582706
GENERAL INFORMATION:
APPLICANT: Johnson, Leslie S.
APPLICANT: Adamou, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
FILE REFERENCE: 469201-444
CURRENT APPLICATION NUMBER: US/09/468,656A
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Forward primer
OTHER INFORMATION: used in amplification of the Sp36 gene sequence.
US-09-468-656A-1

Query Match 1.1%; Score 27; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTACGAGTTGGAGCTGTATCAAC 27
DB 10 TTCTTACGAGTTGGAGCTGTATCAAC 36

RESULT 15
US-08-961-083-281
Sequence 281, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 281:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-083-281

Query Match 1.1%; Score 27; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTACGAGTTGGAGCTGTATCAAC 27
DB 11 TTCTTACGAGTTGGAGCTGTATCAAC 37

RESULT 16
US-09-536-784-281
Sequence 281, Application US/09536784
Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 281:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 281:
US-09-536-784-281

Query Match 1.1%; Score 27; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTACGAGTTGGAGCTGTATCAAC 27

Db 11 TTCTTACGAGTTGGACGTGTATCAAGC 37

RESULT 17
US-09-468-656A-2

; Sequence 2, Application US/09468656A
; Patent No. 6582706

; GENERAL INFORMATION:

; APPLICANT: Johnson, Leslie S.

; TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus

; TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural

; FILE REFERENCE: 469201-444

; CURRENT APPLICATION NUMBER: US/09/468,656A

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: 60/113,048

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO: 2

; LENGTH: 35

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Forward primer

; OTHER INFORMATION: used in amplification of the sp36 gene sequence.

US-09-468-656A-2

Query Match 1.1%; Score 26; DB 4; Length 35;

Best Local Similarity 100.0%; Pred.No. 0.0038;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ACTGTATCAAGCTAGACGTTAAGC 41

Db 10 ACTGTATCAAGCTAGACGTTAAGC 35

RESULT 18

US-08-961-083-181

; Sequence 181, Application US/08961083

; Patent No. 6159469

; GENERAL INFORMATION:

; APPLICANT: Choi et. al.

; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines

; NUMBER OF SEQUENCES: 452

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/961,083

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Brookes, A. Anders

; REGISTRATION NUMBER: 36,373

; REFERENCE/DOCKET NUMBER: PB340P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 181:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1342 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-08-961-083-181

Query Match 1.0%; Score 24; DB 3; Length 1342;

Best Local Similarity 100.0%; Pred.No. 0.042;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 546 ATGCTTATATGTTCTTCATGAG 569

Db 525 ATGCTTATATGTTCTTCATGAG 548

RESULT 19

US-09-536-784-181

; Sequence 181, Application US/09536784

; Patent No. 6573082

; GENERAL INFORMATION:

; APPLICANT: Choi et. al.

; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines

; NUMBER OF SEQUENCES: 452

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/536,784

; FILING DATE: 30-Oct-1997

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/961,083

; FILING DATE: OCT-30-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Michelle S. Marks

; REGISTRATION NUMBER: 41,971

; REFERENCE/DOCKET NUMBER: PB340P3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 181:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1342 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 181:

US-09-536-784-181

Query Match 1.0%; Score 24; DB 4; Length 1342;

Best Local Similarity 100.0%; Pred.No. 0.042;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 546 ATGCTTATATGTTCTTCATGAG 569

Db 525 ATGCTTATATGTTCTTCATGAG 548

RESULT 20

US-09-468-656A-7

; Sequence 7, Application US/09468656A

; Patent No. 6582706

GENERAL INFORMATION:
APPLICANT: Johnson, Leslie S.
APPLICANT: Adamou, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 7
LENGTH: 1455
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
US-09-468-656A-7

Query Match
Best Local Similarity 100.0%; Score 24; DB 4; Length 1455;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 546 ATGCTTATATCGTCTCATGAG 569
DB 596 ATGCTTATATCGTCTCATGAG 619

RESULT 21
US-08-961-527-192/c
Sequence 192, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 192:
SEQUENCE CHARACTERISTICS:
LENGTH: 6867 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-192

Query Match
Best Local Similarity 100.0%; Score 24; DB 4; Length 6867;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 546 ATGCTTATATCGTCTCATGAG 569
DB 6190 ATGCTTATATCGTCTCATGAG 6167

RESULT 22
US-08-998-416-895
Sequence 895, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION/DOCKET NUMBER: 38, 241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 895:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1559RP
US-08-998-416-895

Query Match
Best Local Similarity 100.0%; Score 19; DB 3; Length 622;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 698 TCAAGAACAACTGGGTAC 716
DB 383 TCAAGAACAACTGGGTAC 401

RESULT 23
US-08-212-133A-7
Sequence 7, Application US/08212133A
Patent No. 5663060
GENERAL INFORMATION:
APPLICANT: Lollar, John S.

APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 100 Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212.133A
FILING DATE: March 11, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU/76677
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-572-6508
TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7493 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus

FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1..407
OTHER INFORMATION: /rpt_type="terminal"
OTHER INFORMATION: /note="5'UTR"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7471..7476
OTHER INFORMATION: /function="PolyA_signal"
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 7368..7493
OTHER INFORMATION: /rpt_type="terminal"
OTHER INFORMATION: /note="3'UTR"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 408..7367
OTHER INFORMATION: /product="Coagulation Factor VIII"
PUBLICATION INFORMATION:
AUTHORS: Elder, F.
AUTHORS: Laskich, D.
AUTHORS: Gitschier, J.
TITLE: Sequence of the Murine Factor VIII cDNA.
Patent No. 5663060

JOURNAL: Genomics
VOLUME: 16
PAGES: 374-379
DATE: 1993

RELEVANT RESIDUES IN SEQ ID NO: 7: FROM 1 TO 7476
US-08-212-133A-7

Query Match 0.8%; Score 19; DB 1; Length 7493;
Best Local Similarity 100.0%; Pred. No. 14;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2347 AAAGAGTAATCCTCA 2365
Db 206 AAAGAGTAATCCTCA 224

RESULT 24
US-08-474-503-5
Sequence 5, Application US/08474503
Patent No. 574446
GENERAL INFORMATION:
APPLICANT: Emory University
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30309

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,503
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pratt, John S.
REGISTRATION NUMBER: 29,476
REFERENCE/DOCKET NUMBER: EMU106CIP(3)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6500
TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7493 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus

FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1..407
OTHER INFORMATION: /rpt_type="terminal"
OTHER INFORMATION: /note="5'UTR"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7471..7476
OTHER INFORMATION: /function="PolyA_signal"
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 7368..7493
OTHER INFORMATION: /rpt_type="terminal"
OTHER INFORMATION: /note="3'UTR"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 408..7367
OTHER INFORMATION: /product="Coagulation Factor VIII"
PUBLICATION INFORMATION:
AUTHORS: Elder, F.
AUTHORS: Laskich, D.
AUTHORS: Gitschier, J.
TITLE: Sequence of the Murine Factor VIII cDNA.
Patent No. 574446

JOURNAL: Genomics
VOLUME: 16
PAGES: 374-379
DATE: 1993
RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 7476
US-08-474-503-5

Query Match
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 AAAAGAGTAATCCTTCA 2365
DB 206 AAAAGAGTAATCCTTCA 224

RESULT 25
US-08-670-707A-5
Sequence 5, Application US/08670707A
Patent No. 5859204
GENERAL INFORMATION:
APPLICANT: Iolliar, John S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: USA
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,707A
FILING DATE: 26-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/13200
FILING DATE: 15-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,133
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Greenlee, Lorraine L.
REGISTRATION NUMBER: 27,894
REFERENCE/DOCKET NUMBER: 75-95F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/499-8080
TELEFAX: 303/499-8089
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7493 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1..407
OTHER INFORMATION: /rpt_type="terminal"
FEATURE:
OTHER INFORMATION: /note="5' UTR"

NAME/KEY: misc feature
LOCATION: 7471..7476
OTHER INFORMATION: /function="polyA signal"
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 7368..7493
OTHER INFORMATION: /rpt_type="terminal"
OTHER INFORMATION: /note="3' UTR"
FEATURE:
NAME/KEY: misc feature
LOCATION: 408..7367
OTHER INFORMATION: /product="coagulation factor VIII"
PUBLICATION INFORMATION:
AUTHORS: Elder, F.
AUTHORS: Iakich, D.
AUTHORS: Gitschier, J.
TITLE: Sequence of the murine Factor VIII cDNA
Patent No. 5859204
JOURNAL: Genomics
VOLUME: 16
PAGES: 374-379
DATE: 1993
US-08-670-707A-5

Query Match
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 AAAAGAGTAATCCTTCA 2365
DB 206 AAAAGAGTAATCCTTCA 224

RESULT 26
US-09-037-601-5
Sequence 5, Application US/09037601
Patent No. 6180371
GENERAL INFORMATION:
APPLICANT: Iolliar, John S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: USA
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,601
FILING DATE: 26-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/13200
FILING DATE: 15-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,133
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 75-95F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/499-8080
TELEFAX: 303/499-8089

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; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7493 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: repeat_unit
; LOCATION: 1..407
; OTHER INFORMATION: /rpt_type="terminal"
; OTHER INFORMATION: /note="5' UTR"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7471..7476
; OTHER INFORMATION: /function="polyA signal"
; FEATURE:
; NAME/KEY: repeat_unit
; LOCATION: 7368..7493
; OTHER INFORMATION: /rpt_type="terminal"
; OTHER INFORMATION: /note="3' UTR"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 408..7367
; OTHER INFORMATION: /product="coagulation factor VIII"
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS: Elder, F.
; AUTHORS: Lakich, D.
; AUTHORS: Gitschier, J.
; TITLE: Sequence of the murine Factor VIII cDNA
; Patent No. 6180371
; JOURNAL: Genomics
; VOLUME: 16
; PAGES: 374-379
; DATE: 1993
; US-09-037-601-5

Query Match      0.8%; Score 19; DB 3; Length 7493;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2347 AAAAGAGTAATCCTTCA 2365
Db      206 AAAAGAGTAATCCTTCA 224

RESULT 27
US-09-315-179-5
; Sequence 5, Application US/09315179
; Patent No. 6376463
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S
; TITLE OF INVENTION: Modified Factor VIII
; FILE REFERENCE: 75-95H
; CURRENT APPLICATION NUMBER: US/09/315,179
; EARLIER FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: U.S. 09/037,601
; EARLIER FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: U.S. 08/670,707
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: PCT/US97/11155
; EARLIER FILING DATE: 1997-06-26
; EARLIER APPLICATION NUMBER: PCT/US94/13200
; EARLIER FILING DATE: 1994-11-15
; EARLIER APPLICATION NUMBER: U.S. 06/212,133
; EARLIER FILING DATE: 1994-03-11
; EARLIER APPLICATION NUMBER: U.S. 07/864,004
; EARLIER FILING DATE: 1992-04-07
; NUMBER OF SEQ ID NOS: 40
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 5
; LENGTH: 7493
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-315-179-5

Query Match      0.8%; Score 19; DB 4; Length 7493;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2347 AAAAGAGTAATCCTTCA 2365
Db      206 AAAAGAGTAATCCTTCA 224

RESULT 28
PCT-US94-13200-5
; Sequence 5, Application PC/TUS9413200
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13200
; FILING DATE: 15-NOV-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patricia L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: EMU106CIP(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-815-6508
; TELEFAX: 404-815-6555
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7493 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: repeat_unit
; LOCATION: 1..407
; OTHER INFORMATION: /rpt_type="terminal"
; OTHER INFORMATION: /note="5'UTR"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7471..7476
; OTHER INFORMATION: /function="polyA signal"
; FEATURE:
; NAME/KEY: repeat_unit
; LOCATION: 7368..7493
; OTHER INFORMATION: /rpt_type="terminal"
; OTHER INFORMATION: /note="3'UTR"
; FEATURE:
; NAME/KEY: misc_feature
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LOCATION: 408..7367
OTHER INFORMATION: /product= "Coagulation Factor VIII"
PUBLICATION INFORMATION:
AUTHORS: Elder, F.
AUTHORS: Lakich, D.
AUTHORS: Gitschier, J.
TITLE: Sequence of the Murine Factor VIII cDNA.
JOURNAL: Genomics
VOLUME: 16
PAGES: 374-379
DATE: 1993
RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 7476
PCT-US94-13200-5

Query Match 0.8%; Score 19; DB 5; Length 7493;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 AAAGAGTAATCCTTCA 2365
DB 206 AAAGAGTAATCCTTCA 224

RESULT 29
US-09-641-638-52/c
Sequence 52, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BI-ALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 52
LENGTH: 499
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 466
OTHER INFORMATION: 12-215-467 : polymorphic base G or T
NAME/KEY: misc_binding
LOCATION: 446_465
OTHER INFORMATION: 12-215-467.misl, potential
NAME/KEY: misc_binding
LOCATION: 467..486
OTHER INFORMATION: 12-215-467.mis2, potential complement
NAME/KEY: primer_bind
LOCATION: 1..20
OTHER INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LOCATION: 479..499
OTHER INFORMATION: downstream amplification primer, complement
NAME/KEY: misc_binding
LOCATION: 454_478
OTHER INFORMATION: 12-215-467 potential probe
NAME/KEY: misc_feature
LOCATION: 87
OTHER INFORMATION: n=a, g, c or t

US-09-641-638-52

Query Match 0.8%; Score 18; DB 4; Length 499;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 751 CACAGCAACACAGCAA 768
DB 76 CACAGCAACACAGCAA 59

RESULT 30
US-09-641-638-572/c
Sequence 572, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BI-ALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 572
LENGTH: 499
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 271
OTHER INFORMATION: 12-215-272 : deletion T
NAME/KEY: misc_binding
LOCATION: 251_270
OTHER INFORMATION: 12-215-272.misl, potential
NAME/KEY: primer_bind
LOCATION: 1..20
OTHER INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LOCATION: 479..499
OTHER INFORMATION: downstream amplification primer, complement
NAME/KEY: misc_feature
LOCATION: 87
OTHER INFORMATION: n=a, g, c or t
US-09-641-638-572

Query Match 0.8%; Score 18; DB 4; Length 499;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 751 CACAGCAACACAGCAA 768
DB 76 CACAGCAACACAGCAA 59

RESULT 31
US-09-221-017B-390/c
Sequence 390, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: Ross, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF

NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 390:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...659
US-09-221-017B-390

Query Match 0.8%; Score 18; DB 4; Length 659;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Indels 0; Gaps 0;

QY 1341 TAACGAGGCTCATTAAG 1358
|||||
DB 525 TAACGAGGCTCATTAAG 508

RESULT 32
US-09-107-532A-2361
Sequence 2361, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Atinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2361:
SEQUENCE CHARACTERISTICS:
LENGTH: 987 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...987
SEQUENCE DESCRIPTION: SEQ ID NO: 2361:
US-09-107-532A-2361

Query Match 0.8%; Score 18; DB 4; Length 987;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1455 TAGATGATTTTGTGGCAT 1472
|||||
DB 446 TAGATGATTTTGTGGCAT 463

RESULT 33
US-09-107-532A-1110/C
Sequence 1110, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1110:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1..1161
SEQUENCE DESCRIPTION: SEQ ID NO: 1110:
US-09-107-532A-1110

Query Match 0.8%; Score 18; DB 4; Length 1161;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 119 AACGCTGAAGATCAAT 136
|||||
DB 408 AAGCGTGAAGATCAAT 391

RESULT 34
US-08-916-421B-1
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco
Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc feature
LOCATION: (28252)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98170)..(98120)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (10398)..(10398)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (16385)..(16385)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (19195)..(19195)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature

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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (11313224)..(11313224)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (11349473)..(11349473)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (11470091)..(11470091)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (11569020)..(11569020)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1664854)..(1664854)
OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

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Query Match 0.8%; Score 18; DB 4; Length 1664976;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 2035 TAATGATGATGGCGCA 2052
DB 789070 TAATGATGATGGCGCA 789087

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RESULT 35
US-08-448-386A-10
Sequence 10, Application US/08448386A
Patent No. 5940708
GENERAL INFORMATION:
APPLICANT: START Technology, Partnership
TITLE OF INVENTION: Administration of Oligonucleotides
TITLE OF INVENTION: Antisense to Dopamine Receptor mRNA for Diagnosis and
TITLE OF INVENTION: Treatment of Pathological Conditions of the Dopaminergic
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,386A
FILING DATE: 14-DEC-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,582
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-448-386A-10

Query Match 0.7%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1735 CCTACTCCTCATCTCCAG 1751
DB 3 CCTACTCCTCATCTCCAG 19

RESULT 36
US-08-816-426-10
Sequence 10, Application US/08816426
Patent No. 6025193
GENERAL INFORMATION:
APPLICANT: START Technology, Partnership
TITLE OF INVENTION: Administration of Oligonucleotides
TITLE OF INVENTION: Antisense to Dopamine Receptor mRNA for Diagnosis and

```

```

; TITLE OF INVENTION: Treatment of Pathological Conditions of the Dopaminergic
; TITLE OF INVENTION: Nervous System
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,426
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,386
; FILING DATE:
; APPLICATION NUMBER: US 07/991,582
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-816-426-10

Query Match          0.7%; Score 17; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CCTACCTCATCTCCAG 1751
Db      3 CCTACCTCATCTCCAG 19

RESULT 37
PCT-US93-12161-10
; Sequence 10, Application PC/TUS9312161
; GENERAL INFORMATION:
; APPLICANT: START Technology Partnership
; TITLE OF INVENTION: Administration of
; TITLE OF INVENTION: Oligonucleotides Antisense to Dopamine Receptor
; TITLE OF INVENTION: mRNA for Diagnosis and Treatment of Pathological
; TITLE OF INVENTION: Conditions of the Dopaminergic Nervous System
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version
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; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12161
; FILING DATE: 14-DEC-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,582
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; PCT-US93-12161-10

Query Match          0.7%; Score 17; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CCTACCTCATCTCCAG 1751
Db      3 CCTACCTCATCTCCAG 19

RESULT 38
US-08-981-462-56
; Sequence 56, Application US/08981462
; Patent No. 6054275
; GENERAL INFORMATION:
; APPLICANT: Morgan, Una
; APPLICANT: Thompson, Richard C.A.
; TITLE OF INVENTION: NOVEL DETECTION METHODS FOR
; TITLE OF INVENTION: CRYPTOSPORIDIUM
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,462
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU96/00387
; FILING DATE: 25-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cawley, Jr., Thomas A.
; REGISTRATION NUMBER: 40,944
; REFERENCE/DOCKET NUMBER: 28594/34423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-981-462-56

Query Match 0.7%; Score 17; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2090 GAAGTCCAATAGAA 2106
DB 2 GAAGTCCAATAGAA 18

RESULT 39
US-09-491-356C-15
Sequence 15, Application US/09491356C
Patent No. 6566061
GENERAL INFORMATION:
APPLICANT: Philibert, Robert A.
APPLICANT: Delisi, Lynn
TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
FILE REFERENCE: 9465.6US11
CURRENT APPLICATION NUMBER: US/09/491.356C
CURRENT FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: PCT/US99/09365
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 60/083,465
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 238
TYPE: DNA
ORGANISM: Homo sapiens
US-09-491-356C-15

Query Match 0.7%; Score 17; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 755 AGCAACAGCAGCAACAC 771
DB 141 AGCAACAGCAGCAACAC 157

RESULT 40
US-09-491-356C-13
Sequence 13, Application US/09491356C
Patent No. 6566061
GENERAL INFORMATION:
APPLICANT: Philibert, Robert A.
APPLICANT: Delisi, Lynn
TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
FILE REFERENCE: 9465.6US11
CURRENT APPLICATION NUMBER: US/09/491.356C
CURRENT FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: PCT/US99/09365
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 60/083,465
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 253
TYPE: DNA
ORGANISM: Homo sapiens
US-09-491-356C-13

Query Match 0.7%; Score 17; DB 4; Length 253;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 755 AGCAACAGCAGCAACAC 771
DB 156 AGCAACAGCAGCAACAC 172

RESULT 41
US-09-491-356C-14
Sequence 14, Application US/09491356C
Patent No. 6566061
GENERAL INFORMATION:
APPLICANT: Philibert, Robert A.
APPLICANT: Delisi, Lynn
TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
FILE REFERENCE: 9465.6US11
CURRENT APPLICATION NUMBER: US/09/491.356C
CURRENT FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: PCT/US99/09365
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 60/083,465
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 265
TYPE: DNA
ORGANISM: Homo sapiens
US-09-491-356C-14

Query Match 0.7%; Score 17; DB 4; Length 265;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 755 AGCAACAGCAGCAACAC 771
DB 156 AGCAACAGCAGCAACAC 172

RESULT 42
US-09-491-356C-16
Sequence 16, Application US/09491356C
Patent No. 6566061
GENERAL INFORMATION:
APPLICANT: Philibert, Robert A.
APPLICANT: Delisi, Lynn
TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
FILE REFERENCE: 9465.6US11
CURRENT APPLICATION NUMBER: US/09/491.356C
CURRENT FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: PCT/US99/09365
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 60/083,465
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 265
TYPE: DNA
ORGANISM: Homo sapiens
US-09-491-356C-16

Query Match 0.7%; Score 17; DB 4; Length 265;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 755 AGCAACAGCAGCAACAC 771
DB 156 AGCAACAGCAGCAACAC 172

```
RESULT 43
US-09-491-356C-17
; Sequence 17, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Gims, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 17
; LENGTH: 265
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-491-356C-17

Query Match
Best Local Similarity 100.0%; Score 17; DB 4; Length 265;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 755 AGCAACAACAGCAACAC 771
DB 156 AGCAACAACAGCAACAC 172

RESULT 44
US-09-491-356C-18
; Sequence 18, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Gims, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 265
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-491-356C-18

Query Match
Best Local Similarity 100.0%; Score 17; DB 4; Length 265;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 755 AGCAACAACAGCAACAC 771
DB 156 AGCAACAACAGCAACAC 172

RESULT 45
US-08-175-388-2/C
; Sequence 2, Application US/08175388
; Patent No. 5641674
; GENERAL INFORMATION:
; APPLICANT: DEHOUX, PIERRE
```

```
APPLICANT: DAVIES, JULIAN
; TITLE OF INVENTION: Nucleotide Sequences and Proteins
; TITLE OF INVENTION: Confering Cycloheximide Resistance
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

US-08-175-388-2

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 321;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1922 AAATTGCTGGTTGA 1938
DB 172 AAATTGCTGGTTGA 156

RESULT 46
US-08-779-620-2/C
; Sequence 2, Application US/08779620
; Patent No. 5830997
; GENERAL INFORMATION:
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DAVIES, JULIAN
; TITLE OF INVENTION: Nucleotide Sequences and Proteins
; TITLE OF INVENTION: Confering Cycloheximide Resistance
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,620
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,388
FILING DATE: 09-JUN-1994
APPLICATION NUMBER: PCT/FR92/00685
FILING DATE: 15-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9108906
FILING DATE: 15-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 583097/man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-071-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-779-620-2

Query Match 0.7%; Score 17; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1922 AATTGCTGCTTGA 1938
Db 172 AATTGCTGCTTGA 156

RESULT 47
US-08-818-726-2/C
Sequence 2, Application US/08818726
Patent No. 5958687
GENERAL INFORMATION:
APPLICANT: DEHOX, PIERRE
APPLICANT: DAVIES, JULIAN
TITLE OF INVENTION: Nucleotide Sequences and Proteins
TITLE OF INVENTION: Confering Cycloheximide Resistance
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,726
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,388
FILING DATE: 09-JUN-1994
APPLICATION NUMBER: PCT/FR92/00685
FILING DATE: 15-JUL-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9108906
FILING DATE: 15-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5958687/man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-071-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-818-726-2

Query Match 0.7%; Score 17; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1922 AATTGCTGCTTGA 1938
Db 172 AATTGCTGCTTGA 156

RESULT 48
US-08-961-083-149
Sequence 149, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Chol et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 322 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-083-149

Query Match 0.7%; Score 17; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;


```
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 211:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-072-586-211

Query Match      0.7% Score 17; DB 4; Length 470;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2138 ACACCTGCTGAGCCAGA 2154
Db      159 ACACCTGCTGAGCCAGA 143

RESULT 52
US-09-134-001C-1953/C
Sequence 1953, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1953
LENGTH: 633
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1953

Query Match      0.7% Score 17; DB 4; Length 633;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1610 ATATCACTGATGAAG 1626
Db      147 ATATCACTGATGAAG 131

RESULT 53
US-09-221-017B-1007/C
Sequence 1007, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
```

```
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1007:
SEQUENCE CHARACTERISTICS:
LENGTH: 658 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...658
US-09-221-017B-1007

Query Match      0.7% Score 17; DB 4; Length 658;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      703 AACAACTGGGTACCTT 719
Db      361 AACAACTGGGTACCTT 345

RESULT 54
US-09-328-352-1650
Sequence 1650, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT FILING DATE: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1650
LENGTH: 687
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-1650

Query Match      0.7% Score 17; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1862 ACAGTTGAGTTAAAAA 1878
Db      370 ACAGTTGAGTTAAAAA 386
```


RESULT 55
US-08-981-462-1/C
; Sequence 1, Application US/08981462
; Patent No. 6054275
; GENERAL INFORMATION:
; APPLICANT: Morgan, Una
; APPLICANT: Thompson, Richard C.A.
; TITLE OF INVENTION: NOVEL DETECTION METHODS FOR
; TITLE OF INVENTION: CRYPTOSPORIDIUM
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,462
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00387
; FILING DATE: 25-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cawley, Jr., Thomas A.
; REGISTRATION NUMBER: 40,944
; REFERENCE/DOCKET NUMBER: 28594/34423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-981-462-1

Query Match 0.7%; Score 17; DB 3; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2090 GAAGATCCAAATAGAA 2106
DB 498 GAAGATCCAAATAGAA 482

RESULT 56
US-09-470-191-60/C
; Sequence 60, Application US/09470191
; Patent No. 6465633
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods of Their Use in
; TITLE OF INVENTION: the Treatment, Prevention and Diagnosis of Tuberculosis
; FILE REFERENCE: 014058-008910US
; CURRENT APPLICATION NUMBER: US/09/470,191
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113,952
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60

LENGTH: 706
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)...(706)
; OTHER INFORMATION: n = any nucleotide
US-09-470-191-60

Query Match 0.7%; Score 17; DB 4; Length 706;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 422 CAACATCGTAGAGTGG 438
DB 101 CAACATCGTAGAGTGG 85

RESULT 57
US-09-071-035-373
; Sequence 373, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gai H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 373:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 762 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-071-035-373

Query Match 0.7%; Score 17; DB 4; Length 762;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 789 AAAGTAATGACATTGAT 805
DB 16 AAAGTAATGACATTGAT 32

RESULT 58
US-09-501-558-1
; Sequence 1, Application US/09501558
; Patent No. 6403784

```

; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sanders, Arthur T.
; TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
; FILE REFERENCE: LEX-0012-USA
; CURRENT APPLICATION NUMBER: US/09/501,558
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-501-558-1

Query Match
Best Local Similarity 100.0%; Score 17; DB 4; Length 876;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1025 CCAGATTCAGGCCAGA 1041
Db 99 CCAGATTCAGGCCAGA 115

RESULT 59
US-09-501-558-3
; Sequence 3, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sanders, Arthur T.
; TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
; FILE REFERENCE: LEX-0012-USA
; CURRENT APPLICATION NUMBER: US/09/501,558
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-501-558-3

Query Match
Best Local Similarity 100.0%; Score 17; DB 4; Length 882;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1025 CCAGATTCAGGCCAGA 1041
Db 99 CCAGATTCAGGCCAGA 115

RESULT 60
US-09-252-991A-1381
; Sequence 1381, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
```

```

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1381
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1381

Query Match
Best Local Similarity 100.0%; Score 17; DB 4; Length 909;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 905 AGAGGTGTGCGATGCC 921
Db 268 AGAGGTGTGCGATGCC 284

RESULT 61
US-09-328-352-3547
; Sequence 3547, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3547
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3547

Query Match
Best Local Similarity 100.0%; Score 17; DB 4; Length 909;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1216 TGAACGTGTTAAATC 1232
Db 213 TGAACGTGTTAAATC 229

RESULT 62
US-09-107-532A-2698
; Sequence 2698, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
```

NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2698:
SEQUENCE CHARACTERISTICS:
LENGTH: 975 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (b) LOCATION 1...975
SEQUENCE DESCRIPTION: SEQ ID NO: 2698:
US-09-107-532A-2698

Query Match 0.7%; Score 17; DB 4; Length 975;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1442 AAGAAATGCTAG 1458
DB 949 AAGAAATGCTAG 965

RESULT 63
US-08-839-711-6
Sequence 6, Application US/08839711
Patent No. 6033870
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN TRANSMEMBRANE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,711
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0270 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1077 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 476343
US-08-839-711-6

Query Match 0.7%; Score 17; DB 3; Length 1077;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1275 TAACTGCTAAAAAGAA 1291
DB 691 TAACTGCTAAAAAGAA 707

RESULT 64
US-09-328-352-3376
Sequence 3376, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 3376
LENGTH: 1080
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-3376

Query Match 0.7%; Score 17; DB 4; Length 1080;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1546 TCGTATGCTCAATTAG 1562
DB 597 TCGTATGCTCAATTAG 613

RESULT 65
US-09-252-991A-1287
Sequence 1287, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1287
LENGTH: 1092
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1287

Query Match 0.7%; Score 17; DB 4; Length 1092;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 905 AGAGGTGTCAGTCC 921
DB 282 AGAGGTGTCAGTCC 298

RESULT 66

US-09-252-991A-1184/c
; Sequence 1184, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUDINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1184
; LENGTH: 1230
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1184

Query Match 0.7%; Score 17; DB 4; Length 1230;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 905 AGAGGTGTCAGTGC 921
|||||
Db 1126 AGAGGTGTCAGTGC 1110

RESULT 67
US-09-359-301A-9/c
; Sequence 9, Application US/09359301A
; Patent No. 6426185
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Monto H.
; APPLICANT: della-Cioppa, Guy R.
; APPLICANT: Erwin, Robert L.
; APPLICANT: McGee, David R.
; TITLE OF INVENTION: METHOD OF DETERMINING THE PRESENCE OF A
; TITLE OF INVENTION: TRAIT IN A PLANT BY TRANSFECTING A NUCLEIC ACID SEQUENCE OF
; TITLE OF INVENTION: A DONOR PLANT INTO A DIFFERENT HOST PLANT IN AN ANTI-SENSE
; FILE REFERENCE: 008010137US04
; CURRENT APPLICATION NUMBER: US/09/359,301A
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1543
; TYPE: DNA
; ORGANISM: Ribgrass mosaic virus
US-09-359-301A-9

Query Match 0.7%; Score 17; DB 4; Length 1543;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 94 GAATTGACTCCTGATG 110
|||||
Db 1213 GAATTGACTCCTGATG 1197

RESULT 68
US-09-107-532A-2089
; Sequence 2089, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2089:
SEQUENCE CHARACTERISTICS:
LENGTH: 1578 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1578
SEQUENCE DESCRIPTION: SEQ ID NO: 2089:
US-09-107-532A-2089

Query Match 0.7%; Score 17; DB 4; Length 1578;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1442 AAAGAAAATTGTAGA 1458
|||||
Db 134 AAAGAAAATTGTAGA 150

RESULT 69
US-09-613-303-3
; Sequence 3, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: fusion sequence
NAME/KEY: CDS
LOCATION: (1)...(1620)
US-09-613-303-3

Query Match 0.7%; Score 17; DB 4; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 422 CAACATCGTAGAGTGG 438
DB 1311 CAACATCGTAGAGTGG 1327

RESULT 70
US-08-487-596-3/C
Sequence 3, Application US/08487596
Patent No. 6440681
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,596
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9951
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1654 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS

LOCATION: 39..1553
OTHER INFORMATION: /product= "ALPHA-3 SUBUNIT"
US-08-487-596-3

Query Match 0.7%; Score 17; DB 4; Length 1654;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1615 CAGTGATGAGGAGATG 1631
DB 813 CAGTGATGAGGAGATG 797

RESULT 71
US-08-466-589-3/C
Sequence 3, Application US/08466589
Patent No. 5857489
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,589
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9950
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1756 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 39..1553
US-08-466-589-3

Query Match 0.7%; Score 17; DB 2; Length 1756;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1615 CAGTGATGAGGAGATG 1631
DB 813 CAGTGATGAGGAGATG 797

RESULT 72

US-08-700-636-3/C
Sequence 3, Application US/08700636
Patent No. 5910582
GENERAL INFORMATION:
APPLICANT: Eliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700.636
FILING DATE: 16-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028.031
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31.192
REFERENCE/DOCKET NUMBER: P41 9368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1756 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 39..1553
US-08-700-636-3

Query Match 0.7%; Score 17; DB 2; Length 1756;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1615 CAGTGATGAGAGATG 1631
|||
DB 813 CAGTGATGAGAGATG 797

RESULT 73
US-08-467-574-3/C
Sequence 3, Application US/08467574
Patent No. 6022704
GENERAL INFORMATION:
APPLICANT: Eliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClaim
STREET: 1660 Union Street
CITY: San Diego
STATE: CA

COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,574
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028.031
FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9949
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1756 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 39..1553
US-08-467-574-3

Query Match 0.7%; Score 17; DB 3; Length 1756;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1615 CAGTGATGAGAGATG 1631
|||
DB 813 CAGTGATGAGAGATG 797

RESULT 74
US-09-217-345-3/C
Sequence 3, Application US/09217345
Patent No. 6303753
GENERAL INFORMATION:
APPLICANT: Eliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller, Brian White & McAniff
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,345
FILING DATE: 21-DEC-98
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,574
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/466,589,
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1756 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 39..1553
US-09-217-345-3

Query Match 0.7%; Score 17; DB 4; Length 1756;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1615 CAGTGATGAAGGATG 1631
DB 813 CAGTGATGAAGGATG 797
|||||

RESULT 75
US-08-755-587-1
Sequence 1, Application US/08755587
Patent No. 6045997
GENERAL INFORMATION:
APPLICANT: Futreal, Phillip A
APPLICANT: Wooster, Richard F
APPLICANT: Ashworth, Alan
APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials and methods relating to the BRCA2 cancer
TITLE OF INVENTION: identification and sequencing of the BRCA2 cancer
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSER: Bell Seltzer Park & Gibson
STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
CITY: Raleigh
STATE: NC
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665

REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1917 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-755-587-1

Query Match 0.7%; Score 17; DB 3; Length 1917;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 652 TCTGCAATTCAAGA 668
DB 582 TCTGCAATTCAAGA 598
|||||

RESULT 76
US-09-613-303-16
Sequence 16, Application US/09613303
Patent No. 6495347
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1920
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
NAME/KEY: CDS
LOCATION: (1)...(1917)
US-09-613-303-16

Query Match 0.7%; Score 17; DB 4; Length 1920;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 422 CAACATCGTGAAGTGG 438
DB 1311 CAACATCGTGAAGTGG 1327
|||||

RESULT 77
US-09-613-303-28
Sequence 28, Application US/09613303
Patent No. 6495347
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 1947
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
NAME/KEY: CDS
LOCATION: (1)...(1944)
US-09-613-303-28

Query Match 0.7%; Score 17; DB 4; Length 1947;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 422 CAACATCGTGAAGTGG 438
|||||
Db 1635 CAACATCGTGAAGTGG 1651

RESULT 78
US-09-370-807-11
Sequence 11, Application US/09370807
Patent No. 6297034
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Falco, S. Carl
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: N-End Rule Pathway Enzymes
FILE REFERENCE: BB-1199
CURRENT APPLICATION NUMBER: US/09/370,807
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: 60/096,225
EARLIER FILING DATE: August 12, 1998
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97
SEQ ID NO 11
LENGTH: 2018
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (17)
FEATURE:
NAME/KEY: unsure
LOCATION: (19)
FEATURE:
NAME/KEY: unsure
LOCATION: (46)
FEATURE:
NAME/KEY: unsure
LOCATION: (50)
FEATURE:
NAME/KEY: unsure
LOCATION: (80)...(81)
FEATURE:
NAME/KEY: unsure
LOCATION: (113)
FEATURE:
NAME/KEY: unsure
LOCATION: (127)
FEATURE:
NAME/KEY: unsure
LOCATION: (158)
FEATURE:
NAME/KEY: unsure
LOCATION: (190)
FEATURE:
NAME/KEY: unsure
LOCATION: (302)
FEATURE:
NAME/KEY: unsure
LOCATION: (308)
FEATURE:
NAME/KEY: unsure
LOCATION: (324)

FEATURE:
NAME/KEY: unsure
LOCATION: (348)
FEATURE:
NAME/KEY: unsure
LOCATION: (364)
FEATURE:
NAME/KEY: unsure
LOCATION: (425)
FEATURE:
NAME/KEY: unsure
LOCATION: (435)
FEATURE:
NAME/KEY: unsure
LOCATION: (442)
US-09-370-807-11

Query Match 0.7%; Score 17; DB 3; Length 2018;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1284 AAAAGAAATGCT 1300
|||||
Db 754 AAAAGAAATGCT 770

RESULT 79
US-09-921-259-11
Sequence 11, Application US/09921259
Patent No. 6465234
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Falco, S. Carl
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: N-End Rule Pathway Enzymes
FILE REFERENCE: BB-1199
CURRENT APPLICATION NUMBER: US/09/921,259
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/096,225
PRIOR FILING DATE: August 12, 1998
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97
SEQ ID NO 11
LENGTH: 2018
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (17)
NAME/KEY: unsure
LOCATION: (19)
NAME/KEY: unsure
LOCATION: (46)
NAME/KEY: unsure
LOCATION: (50)
NAME/KEY: unsure
LOCATION: (80)...(81)
NAME/KEY: unsure
LOCATION: (113)
NAME/KEY: unsure
LOCATION: (127)
NAME/KEY: unsure
LOCATION: (158)
NAME/KEY: unsure
LOCATION: (190)
NAME/KEY: unsure
LOCATION: (302)
NAME/KEY: unsure
LOCATION: (308)
NAME/KEY: unsure
LOCATION: (324)

LOCATION: (348)
NAME/KEY: unsure.
LOCATION: (364)
NAME/KEY: unsure
LOCATION: (425)
NAME/KEY: unsure
LOCATION: (435)
NAME/KEY: unsure
LOCATION: (442)
US-09-921-259-11

Query Match 0.7%; Score 17; DB 4; Length 2018;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1284 AAAAGAAATGTGCT 1300
DB 754 AAAAGAAATGTGCT 770

RESULT 80
US-08-714-918-105/c
Sequence 105 Application US/08714918
Patent No. 6037123

GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ving
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 2255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-714-918-105

Query Match 0.7%; Score 17; DB 3; Length 2255;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1112 TCAATTCCTCTTGT 1128
DB 583 TCAATTCCTCTTGT 567

RESULT 81
US-09-265-315-105/c

Sequence 105, Application US/09265315
Patent No. 6187541

GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714, 918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 2255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-105

Query Match 0.7%; Score 17; DB 3; Length 2255;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1112 TCAATTCCTCTTGT 1128
DB 583 TCAATTCCTCTTGT 567

RESULT 82
US-09-265-315-105/c
Sequence 105, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 2255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-105

Query Match 0.7%; Score 17; DB 3; Length 2255;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1112 TCAATTCTTCTTGT 1128
|||||
Db 583 TCAATTCTTCTTGT 567

RESULT 83
US-09-266-417-105/c
Sequence 105, Application US/09266417
Patent No. 6228588
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.

APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/248
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 2255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-266-417-105

Query Match 0.7%; Score 17; DB 3; Length 2255;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1112 TCAATTCTTCTTGT 1128
|||||
Db 583 TCAATTCTTCTTGT 567

RESULT 84
US-08-913-159-12/c
Sequence 12, Application US/08913159
Patent No. 6300109
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Plasmid-derived type II
TITLE OF INVENTION: restriction-modification systems from Lactococcus lactis
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,159
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0179/95
FILING DATE: 17-FEB-1995
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2355 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Lactococcus lactis subsp. cremoris
STRAIN: W39
FEATURE:
NAME/KEY: CDS
LOCATION: 744..1283
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /codon_start= 744
OTHER INFORMATION: /product= "L1adII restriction endonuclease"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ORF"
OTHER INFORMATION: /number= 1
OTHER INFORMATION: /standard_name= "Gene coding for R.L1adII"
OTHER INFORMATION: /label= "r-l1adII"
OTHER INFORMATION: /note= "The first ten amino acids in this sequence may be doubtful. However, from base 773 this reading frame gives a h
FEATURE:
OTHER INFORMATION: homology with the Bsp61 endonuclease"
NAME/KEY: CDS
LOCATION: 1392..2342
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /codon_start= 1392
OTHER INFORMATION: /product= "L1adII methylase"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ORF"
OTHER INFORMATION: /number= 2
OTHER INFORMATION: /standard_name= "Gene coding for M.L1adII"
OTHER INFORMATION: /label= "m-l1adII"
OTHER INFORMATION: /note= "The sequence shows 60 % identity and 76 % similarity
US-08-913-159-12
Query Match 0.7%; Score 17; DB 4; Length 2355;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 GAAATATCGTGTTC 57
DB 46 GAAATATCGTGTTC 30
RESULT 85
US-08-318-826A-9
Sequence 9, Application US/08318826A
Patent No. 5891725
GENERAL INFORMATION:
APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Eckstein, Fritz
TITLE OF INVENTION: Synthetic Antisense
TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5891725thwestern Hwy., Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: US

ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,826A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 2391.00001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2381 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: fetal
TISSUE TYPE: Brain, Liver
POSITION IN GENOME:
MAP POSITION: 3q26
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 160..1881
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /EC_number= 3.1.1.8
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "BCHR"
OTHER INFORMATION: /note= "butyrylcholinesterase mature peptide"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 76..159
FEATURE:
NAME/KEY: mRNA
LOCATION: 1..2381
FEATURE:
NAME/KEY: CDS
LOCATION: 76..1884
US-08-318-826A-9
Query Match 0.7%; Score 17; DB 2; Length 2381;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2300 GATACAAATGATCAT 2316
DB 1177 GATACAAATGATCAT 1193
RESULT 86
5215909-13
Patent No. 5215909
APPLICANT: SORBO, HERMONA
TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/572,911
FILING DATE: 15-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 87,724
FILING DATE: 21-AUG-1987
APPLICATION NUMBER: 875,737

FILING DATE: 18-JUN-1986
SEQ ID NO:13
LENGTH: 2400
5215909-13

Query Match 0.7%; Score 17; DB 6; Length 2400;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2300 GATACATAGTATCAT 2316
Db 1177 GATACATAGTATCAT 1193

RESULT 87
US-08-318-826A-8
Sequence 8, Application US/08318826A
Patent No. 5891725
GENERAL INFORMATION:
APPLICANT: Sored, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Eckstein, Fritz
TITLE OF INVENTION: Synthetic Antisense
TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
TITLE OF INVENTION: Containing Them
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5891725thwestern Hwy., Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: US
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318.826A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 2391.00001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5050
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2416 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Basal ganglion
POSITION IN GENOME:
MAP POSITION: 3q26
FEATURE:
NAME/KEY: mat_deptide
LOCATION: 214..1935
OTHER INFORMATION: /EC number= 3.1.1.8
OTHER INFORMATION: /gene= "BCHP"
OTHER INFORMATION: /note= "butyrylcholinesterase mature peptide"
NAME/KEY: sig_deptide
LOCATION: 130..213
FEATURE:

NAME/KEY: mRNA
LOCATION: 1..2416
FEATURE:
NAME/KEY: CDS
LOCATION: 130..1938
US-08-318-826A-8

Query Match 0.7%; Score 17; DB 2; Length 2416;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2300 GATACATAGTATCAT 2316
Db 1231 GATACATAGTATCAT 1247

RESULT 88
US-09-334-489-1
Sequence 1, Application US/09334489
Patent No. 6291175
GENERAL INFORMATION:
APPLICANT: Pierre Sevigny
APPLICANT: Keith Schapert
APPLICANT: Heiko Wiesbusch
TITLE OF INVENTION: METHODS FOR TREATING A NEUROLOGICAL
TITLE OF INVENTION: DISEASE BY DETERMINING BCHP GENOTYPE
FILE REFERENCE: 08523/013002
CURRENT APPLICATION NUMBER: US/09/334,489
CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: 60/089,406
PRIOR FILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1
LENGTH: 2416
TYPE: DNA
ORGANISM: Homo sapiens
US-09-334-489-1

Query Match 0.7%; Score 17; DB 3; Length 2416;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2300 GATACATAGTATCAT 2316
Db 1231 GATACATAGTATCAT 1247

RESULT 89
US-09-334-489-2
Sequence 2, Application US/09334489
Patent No. 6291175
GENERAL INFORMATION:
APPLICANT: Pierre Sevigny
APPLICANT: Keith Schapert
APPLICANT: Heiko Wiesbusch
TITLE OF INVENTION: METHODS FOR TREATING A NEUROLOGICAL
TITLE OF INVENTION: DISEASE BY DETERMINING BCHP GENOTYPE
FILE REFERENCE: 08523/013002
CURRENT APPLICATION NUMBER: US/09/334,489
CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: 60/089,406
PRIOR FILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 2416
TYPE: DNA
ORGANISM: Homo sapiens
US-09-334-489-2

Query Match 0.7%; Score 17; DB 3; Length 2416;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2300 GATACCAATAGTATCAT 2316
|||||
Db 1231 GATACCAATAGTATCAT 1247

RESULT 90
US-08-175-388-3/c
; Sequence 3, Application US/08175388
; Patent No. 5641674
; GENERAL INFORMATION:
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DAVIES, JULIAN
; TITLE OF INVENTION: Nucleotide Sequences and Proteins
; TITLE OF INVENTION: Conferring Cycloheximide Resistance
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/175,388
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00685
; FILING DATE: 15-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9108906
; FILING DATE: 15-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, No. 5641674man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-071-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2842 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-175-388-3

Query Match 0.7%; Score 17; DB 1; Length 2842;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1922 AAATTGCTGGTTGA 1938
|||||
Db 1390 AAATTGCTGGTTGA 1374

RESULT 91
US-08-779-620-3/c
; Sequence 3, Application US/08779620
; Patent No. 5830997
; GENERAL INFORMATION:
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DAVIES, JULIAN

;; TITLE OF INVENTION: Nucleotide Sequences and Proteins
;; TITLE OF INVENTION: Conferring Cycloheximide Resistance
;; NUMBER OF SEQUENCES: 3
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; ADDRESS: P.C.
;; STREET: 1755 S. Jefferson Davis Highway, Suite 400
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/779,620
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/175,388
;; FILING DATE: 09-JUN-1994
;; APPLICATION NUMBER: PCT/FR92/00685
;; FILING DATE: 15-JUL-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 9108906
;; FILING DATE: 15-JUL-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OBLON, No. 5830997man F.
;; REGISTRATION NUMBER: 24,618
;; REFERENCE/DOCKET NUMBER: 660-071-0 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 413-3000
;; TELEFAX: (703) 413-2220
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2842 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA (genomic)
US-08-779-620-3

Query Match 0.7%; Score 17; DB 2; Length 2842;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1922 AAATTGCTGGTTGA 1938
|||||
Db 1390 AAATTGCTGGTTGA 1374

RESULT 92
US-08-818-726-3/c
; Sequence 3, Application US/08818726
; Patent No. 5958687
; GENERAL INFORMATION:
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DAVIES, JULIAN
; TITLE OF INVENTION: Nucleotide Sequences and Proteins
; TITLE OF INVENTION: Conferring Cycloheximide Resistance
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,726
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,388
FILING DATE: 09-JUN-1994
APPLICATION NUMBER: PCT/FR92/00685
FILING DATE: 15-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9108906
FILING DATE: 15-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5958687man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-071-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2842 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-818-726-3

Query Match 0.7%; Score 17; DB 2; Length 2842;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1922 AATTGCTGTGTTGA 1938
|||
Db 1390 AATTGCTGTGTTGA 1374

RESULT 93
US-09-613-303-20
Sequence 20, Application US/09613303
Patent No. 6493347
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 2847
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
NAME/KEY: CDS
LOCATION: (1)...(2844)
US-09-613-303-20

Query Match 0.7%; Score 17; DB 4; Length 2847;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 422 CAACATCGTGAAGTGG 438

Db 1371 CAACATCGTGAAGTGG 1387
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RESULT 94
US-09-484-970B-68/C
Sequence 68, Application US/09484970B
Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 68
LENGTH: 3882
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6426186 331276.3CB1
NAME/KEY: unsure
LOCATION: 141
OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-68

Query Match 0.7%; Score 17; DB 4; Length 3882;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1262 GTTTCACACACTTTAAC 1278
|||
Db 1291 GTTTCACACACTTTAAC 1275

RESULT 95
US-08-955-565A-3
Sequence 3, Application US/08955565A
Patent No. 6331388
GENERAL INFORMATION:
APPLICANT: Malkovsky, Mikoslav
APPLICANT: Wells, Andrew
TITLE OF INVENTION: Immune Response Enhancer Therapy
FILE REFERENCE: WARF-02625
CURRENT APPLICATION NUMBER: US/08/955,565A
CURRENT FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 4380
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
US-08-955-565A-3

Query Match 0.7%; Score 17; DB 4; Length 4380;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 422 CAACATCGTGAAGTGG 438
|||
Db 1562 CAACATCGTGAAGTGG 1578

RESULT 96
US-09-436-874-1
Sequence 1, Application US/09436874
Patent No. 6521816
GENERAL INFORMATION:
APPLICANT: Froberg, Claus

```
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES FROM RICE AND THEIR USE FOR THE
; FILE OF INVENTION: PRODUCTION OF MODIFIED STARCH
; FILE REFERENCE: GFB-10
; CURRENT APPLICATION NUMBER: US/09/436,874
; EARLIER FILING DATE: 1999-11-09
; EARLIER APPLICATION NUMBER: US 60/107,883
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(4375)
; US-09-436-874-1

Query Match
Best Local Similarity 100.0%; Score 17; DB 4; Length 4643;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 534 AGGATCTGCTGATGCT 550
DB 1623 AGGATCTGCTGATGCT 1639

RESULT 97
US-09-491-356C-2
; Sequence 2, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Gims, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCT4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 6794
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-491-356C-2

Query Match
Best Local Similarity 100.0%; Score 17; DB 4; Length 6794;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 755 AGCAACAACAGCAACAC 771
DB 6347 AGCAACAACAGCAACAC 6363

RESULT 98
US-08-276-594A-1/C
; Sequence 1, Application US/08276594A
; Patent No. 5693499
; GENERAL INFORMATION:
; APPLICANT: YONEMURA, Hiroshi
; APPLICANT: TAJIMA, Yoshitaka
; APPLICANT: SUGAWARA, Keishin
; APPLICANT: MASUDA, Kenichi
; TITLE OF INVENTION: PROCESS FOR PREPARING HUMAN COAGULATION
; TITLE OF INVENTION: FACTOR VIII PROTEIN COMPLEX
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,594A
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/950,191
; FILING DATE: 24-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 243262/1991
; FILING DATE: 24-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 74129/195/AOPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..6996
; US-08-276-594A-1

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 6999;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1923 AATTGCTTGCTTGAT 1939
DB 3861 AATTGCTTGCTTGAT 3845

RESULT 99
US-08-121-202-1/C
; Sequence 1, Application US/08121202
; Patent No. 5563045
; GENERAL INFORMATION:
; APPLICANT: Pittman, Debora
; APPLICANT: Rehmentulla, Alnawaz
; APPLICANT: Wozney, John W.
; APPLICANT: Kaufman, Randal J.
; TITLE OF INVENTION: CHIMERIC PROCOAGULANT PROTEINS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/121,202
FILING DATE: 14-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weinert, M. C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5195A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1210 X8574
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7056 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..7053
US-08-121-202-1

Query Match 0.7%; Score 17; DB 1; Length 7056;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1923 AATTGCTTGGTTTGAT 1939
|||||
Db 3918 AATTGCTTGGTTTGAT 3902

RESULT 100
5171844-1/c
; Patent No. 5171844
; APPLICANT: VAN COYEN, ALBERT J.J.; PANNKOEK, HANS; VERBEET,
; MARTINUS P.; VAN LEEN, ROBERT W.
; TITLE OF INVENTION: PROTEINS WITH FACTOR VIII ACTIVITY
; PROCESS FOR THEIR PREPARATION USING GENETICALLY-ENGINEERED CELLS
; AND PHARMACEUTICAL COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/205,226
; FILING DATE: 10-JUN-1988
; SEQ ID NO: 1:
; LENGTH: 8241
5171844-1

Query Match 0.7%; Score 17; DB 6; Length 8241;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1923 AATTGCTTGGTTTGAT 1939
|||||
Db 3924 AATTGCTTGGTTTGAT 3908

Search completed: November 14, 2003, 07:51:56
Job time : 179 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 14, 2003, 06:26:11 ; Search time 1698 Seconds

(without alignments)
4598.198 Million cell updates/sec

Title: US-09-765-271-55

Perfect score: 2389

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Searched: 2169961 seqs, 1634102185 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4339922

Minimum DB seq length: 0

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Post-processing: Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	53	2.2	2290	9	US-09-765-272-65
5	53	2.2	2481	11	US-09-769-787-206
6	53	2.2	2639	11	US-09-884-465A-5
7	30	1.3	40	9	US-09-765-272-282
8	27	1.1	37	9	US-09-765-272-281
9	25	1.0	33	11	US-09-884-465A-45
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11	25	1.0	35	11	US-09-884-465A-174
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15	24	1.0	2528	11	US-09-884-465A-9
16	24	1.0	3120	11	US-09-884-465A-1

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18	21	0.9	29	11	US-09-884-465A-44	Sequence 44, Appl
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20	20	0.8	2469	12	US-09-769-736-17	Sequence 17, Appl
21	20	0.8	5215	11	US-09-252-088-13	Sequence 13, Appl
22	19	0.8	164	10	US-09-983-965-4749	Sequence 4749, Ap
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RESULT 1
 US-09-765-272-55
 Sequence 55, Application US/09765272
 Patent No. US20020061545A1
 GENERAL INFORMATION:
 APPLICANT: Choi et. al.
 TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
 NUMBER OF SEQUENCES: 452
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/765,272
 FILING DATE: 22-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/961,083
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Brookes, A. Anders
 REGISTRATION NUMBER: 36,373

ALIGNMENTS

Sequence 767, App

REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 2389 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-765-272-55

Query Match 100.0%; Score 2389; DB 9; Length 2389;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	901	AGCTAGAGGTGTGAGTGCACACGAGATCATTTACACTTTCATCCTTACTCTCAAT	960
DB	901	AGCTAGAGGTGTGAGTGCACACGAGATCATTTACACTTTCATCCTTACTCTCAAT	960
QY	961	GTCGTAATTTGGAAGAAAGATGCGCTGATTAATTCCTTGGTTATGCTTCAACCATTTG	1020
DB	961	GTCGTAATTTGGAAGAAAGATGCGCTGATTAATTCCTTGGTTATGCTTCAACCATTTG	1020
QY	1021	GGTACCAATTCAGGCGAGAAACCAAGTCCACCAACCGACTCCGGAACCTAGTCCAGG	1080
DB	1021	GGTACCAATTCAGGCGAGAAACCAAGTCCACCAACCGACTCCGGAACCTAGTCCAGG	1080
QY	1081	CCCGCAACCTGACCAATCTTTAAATATGACTCAATTTCTTGTGTTAGTCACTGGT	1140
DB	1081	CCCGCAACCTGACCAATCTTTAAATATGACTCAATTTCTTGTGTTAGTCACTGGT	1140
QY	1141	ACGAAAGTTGGGGAGGATATGTTTGAAGAAAGGCAATCTCTGTTATGCTTTGC	1200
DB	1141	ACGAAAGTTGGGGAGGATATGTTTGAAGAAAGGCAATCTCTGTTATGCTTTGC	1200
QY	1201	GAAAGATTTTACCATCTGAAACTGTTAAATCTTGAAGCAAGTTATCAAAACAGAGAG	1260
DB	1201	GAAAGATTTTACCATCTGAAACTGTTAAATCTTGAAGCAAGTTATCAAAACAGAGAG	1260
QY	1261	TGTTTACACACTTAACTGCTTAAAGAAATGTTGCTCTCTGTCGACCAAGATTTTA	1320
DB	1261	TGTTTACACACTTAACTGCTTAAAGAAATGTTGCTCTCTGTCGACCAAGATTTTA	1320
QY	1321	TGATTAAGCATATATCTGTTAAGTGAAGCTCATTAAGCTTGTGTAATTAAGGCTGC	1380
DB	1321	TGATTAAGCATATATCTGTTAAGTGAAGCTCATTAAGCTTGTGTAATTAAGGCTGC	1380
QY	1381	TAAATCTGATTTCCAAAGCTTGAACAAATTTTGAAGCGCTGAATGATGATGACTTA	1440
DB	1381	TAAATCTGATTTCCAAAGCTTGAACAAATTTTGAAGCGCTGAATGATGATGACTTA	1440
QY	1441	TAAAGAAATTTGTTAGATTTATTTGGCATTTCTTACACCAATTCACATCCAGAGCG	1500
DB	1441	TAAAGAAATTTGTTAGATTTATTTGGCATTTCTTACACCAATTCACATCCAGAGCG	1500
QY	1501	ACTGGCAACCAATTTCTCAATTTGATATGATGATGATGATGATGATGATGATGATG	1560
DB	1501	ACTGGCAACCAATTTCTCAATTTGATATGATGATGATGATGATGATGATGATGATG	1560
QY	1561	AGCTGATTAAGTATCAAGCTGATGTTTACATTTTGTATGATGAACATGATATGATGA	1620
DB	1561	AGCTGATTAAGTATCAAGCTGATGTTTACATTTTGTATGATGAACATGATATGATGA	1620
QY	1621	TGAAGAGATGCATATGTTAAGCGCTCATATGAGGCGATAGTCACTGATTTGGAAGATAG	1680
DB	1621	TGAAGAGATGCATATGTTAAGCGCTCATATGAGGCGATAGTCACTGATTTGGAAGATAG	1680
QY	1681	CCTTTCTGATTAAGAAAGTTGAGCTCAAGCTCATCTAAAGAAAGATGATCTTACC	1740
DB	1681	CCTTTCTGATTAAGAAAGTTGAGCTCAAGCTCATCTAAAGAAAGATGATCTTACC	1740
QY	1741	TTCATCTCCAGACGAGATGTTAAAGCAAAATCCAACTGGAATAGTGCAGGACTATTTA	1800
DB	1741	TTCATCTCCAGACGAGATGTTAAAGCAAAATCCAACTGGAATAGTGCAGGACTATTTA	1800
QY	1801	CAATGCTGTAAGGGGAAAAAGCAATTCATCTGTTGACTTCCATATATGTTGAGCA	1860
DB	1801	CAATGCTGTAAGGGGAAAAAGCAATTCATCTGTTGACTTCCATATATGTTGAGCA	1860
QY	1861	TACAGTTAGGTTAAAAAGGTTAATTTGATTAATTTCTATAGAGTCACTTACATTAATAT	1920
DB	1861	TACAGTTAGGTTAAAAAGGTTAATTTGATTAATTTCTATAGAGTCACTTACATTAATAT	1920
QY	1921	TAAATTTGCTTGGTTGATGATCAACATTAAGGCTCAATGCTTATACCTTGGAGA	1980


```

; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-765-272-65
Query Match
Best Local Similarity 100.0%; Pred. No. 7.1e-17; Length 2290;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 983 GCTCGATTATTCCTTCCTGTTATCGTTCAACCAATTGGGTACCAATTCAAG 1035
Db 944 GCTCGATTATTCCTTCCTGTTATCGTTCAACCAATTGGGTACCAATTCAAG 996

RESULT 5
US-09-769-787-206
; Sequence 206, Application US/09769787
; Publication No. US20030091577A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129MO
; CURRENT APPLICATION NUMBER: US/09/769,787
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 206
; LENGTH: 2481
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-769-787-206
Query Match
Best Local Similarity 100.0%; Pred. No. 7.2e-17; Length 2481;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 983 GCTCGATTATTCCTTCCTGTTATCGTTCAACCAATTGGGTACCAATTCAAG 1035
Db 1003 GCTCGATTATTCCTTCCTGTTATCGTTCAACCAATTGGGTACCAATTCAAG 1055

RESULT 6
US-09-884-465A-5
; Sequence 5, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Quillet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
```

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2639
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-884-465A-5
Query Match
Best Local Similarity 100.0%; Pred. No. 7.2e-17; Length 2639;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 983 GCTCGATTATTCCTTCCTGTTATCGTTCAACCAATTGGGTACCAATTCAAG 1035
Db 1113 GCTCGATTATTCCTTCCTGTTATCGTTCAACCAATTGGGTACCAATTCAAG 1165

RESULT 7
US-09-765-272-282/c
; Sequence 282, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 282:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 282:
US-09-765-272-282
Query Match
Best Local Similarity 100.0%; Pred. No. 7.2e-05; Length 40;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2360 CCTCATCTGTAGTAGGAAAAAATAAAC 2389
Db 40 CCTCATCTGTAGTAGGAAAAAATAAAC 11

RESULT 8
US-09-765-272-281
; Sequence 281, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
```

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; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 281:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 37 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: double
;         TOPOLOGY: linear
;     SEQUENCE DESCRIPTION: SEQ ID NO: 281:
;
; US-09-765-272-281
;
; Query Match          1.1%; Score 27; DB 9; Length 37;
; Best Local Similarity 100.0%; Pred. No. 0.0028;
; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy      1  TTCTTACGAGTTGGAGCTGTATCAACG 27
;         |||||||
; Db      11 TTCTTACGAGTTGGAGCTGTATCAACG 37
;
; RESULT 9
; US-09-884-465A-45
; Sequence 45, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; US-09-884-465A-45

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; Query Match          1.0%; Score 25; DB 11; Length 33;
; Best Local Similarity 100.0%; Pred. No. 0.032;
; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy      998 CTTCGTTATCGTTCAACCAATGGG 1022
;         |||||||
; Db      9  CTTCGTTATCGTTCAACCAATGGG 33
;
; RESULT 10
; US-09-884-465A-47
; Sequence 47, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; US-09-884-465A-47
;
; Query Match          1.0%; Score 25; DB 11; Length 34;
; Best Local Similarity 100.0%; Pred. No. 0.032;
; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy      797 GACATGTAGTCTCTTGAACACG 821
;         |||||||
; Db      10 GACATGTAGTCTCTTGAACACG 34
;
; RESULT 11
; US-09-884-465A-174
; Sequence 174, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 174
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; US-09-884-465A-174

```

Query Match 1.0%; Score 25; DB 11; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 797 GACATGTAGTCTTGAACAGC 821
|||||
Db 11 GACATGTAGTCTTGAACAGC 35

RESULT 12
US-09-765-272-181
Sequence 181, Application US/09765272
Patent No. US2002061545A1
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 181:
SEQUENCE CHARACTERISTICS:
LENGTH: 1342 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 181:
US-09-765-272-181

Query Match 1.0%; Score 24; DB 9; Length 1342;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 546 ATGCTTATATGCTTCATGAG 569
|||||
Db 525 ATGCTTATATGCTTCATGAG 548

RESULT 13
US-09-769-787-246
Sequence 246, Application US/09769787
Publication No. US20030091577A1
GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P2112SWO
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 246
LENGTH: 1455
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
US-09-769-787-246

Query Match 1.0%; Score 24; DB 11; Length 1455;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 546 ATGCTTATATGCTTCATGAG 569
|||||
Db 596 ATGCTTATATGCTTCATGAG 619

RESULT 14
US-09-769-744A-23
Sequence 23, Application US/09769744A
Publication No. US20030134407A1
GENERAL INFORMATION:
APPLICANT: Le Page, Richard WF
APPLICANT: Wells, Jeremy M
APPLICANT: Hanniffy, Sean B
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P2112SWO
CURRENT APPLICATION NUMBER: US/09/769,744A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/GB99/02452
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: GB 9816336.3
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125329
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 23
LENGTH: 1455
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
US-09-769-744A-23

Query Match 1.0%; Score 24; DB 12; Length 1455;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 546 ATGCTTATATGCTTCATGAG 569
|||||
Db 596 ATGCTTATATGCTTCATGAG 619

RESULT 15
US-09-884-465A-9
Sequence 9, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683

PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 2528
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
US-09-884-465A-9

Query Match 1.0%; Score 24; DB 11; Length 2528;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 546 ATGCTTATATCGTTCCTCATGAG 569
DB 536 ATGCTTATATCGTTCCTCATGAG 559

RESULT 16
US-09-884-465A-1
Sequence 1, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 3120
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
US-09-884-465A-1

Query Match 1.0%; Score 24; DB 11; Length 3120;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 546 ATGCTTATATCGTTCCTCATGAG 569
DB 596 ATGCTTATATCGTTCCTCATGAG 619

RESULT 17
US-09-884-465A-2
Sequence 2, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 5048

TYPE: DNA
ORGANISM: Streptococcus pneumoniae
US-09-884-465A-2

Query Match 1.0%; Score 24; DB 11; Length 5048;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 546 ATGCTTATATCGTTCCTCATGAG 569
DB 2372 ATGCTTATATCGTTCCTCATGAG 2395

RESULT 18
US-09-884-465A-44
Sequence 44, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 44
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Unknown Organism
US-09-884-465A-44

Query Match 0.9%; Score 21; DB 11; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 621 CTGAGAGCGCTTCCTATCTG 641
DB 9 CTGAGAGCGCTTCCTATCTG 29

RESULT 19
US-09-769-736-23
Sequence 23, Application US/09769736
Publication No. US20030138775A1
GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Le Page, Richard WF
APPLICANT: Wells, Jeremy M
APPLICANT: Hanniffy, Sean B
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21089wo
CURRENT APPLICATION NUMBER: US/09/769,736
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: GB 9816335.5
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125163
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 1146
TYPE: DNA
ORGANISM: Streptococcus agalactiae
US-09-769-736-23

Query Match 0.8%; Score 20; DB 12; Length 1146;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 479 CAAGGACGCTATCTACTACAGA 498
|||||
DB 571 CAAGGACGCTATCTACTACAGA 590

RESULT 20

US-09-769-736-17
; Sequence 17, Application US/09769736
; Publication No. US2003013875A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Le Page, Richard WF
; APPLICANT: Wells, Jeremy M
; APPLICANT: Hamilfy, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21089wo
; CURRENT APPLICATION NUMBER: US/09/769,736
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: GB 9816335.5
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/125163
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 2469
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
US-09-769-736-17

Query Match 0.8%; Score 20; DB 12; Length 2469;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 479 CAAGGACGCTATCTACTACAGA 498
|||||
DB 571 CAAGGACGCTATCTACTACAGA 590

RESULT 21

US-09-252-088-13
; Sequence 13, Application US/09252088
; Publication No. US20030031682A1
; GENERAL INFORMATION:
; APPLICANT: BRODEUR, Bernard R.
; APPLICANT: RIOUX, Clement
; APPLICANT: BOYER, Martine
; APPLICANT: CHARLEBOIS, Isabelle
; APPLICANT: HAMEL, Jose
; APPLICANT: MARTIN, Denis
; TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
; FILE REFERENCE: 8331-9002
; CURRENT APPLICATION NUMBER: US/09/252,088
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: US/60/075,425
; EARLIER FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 5215
; TYPE: DNA
; ORGANISM: group B streptococcus

FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(122)
FEATURE:
NAME/KEY: CDS
LOCATION: (133)..(2511) *

FEATURE:
NAME/KEY: CDS
LOCATION: (367)..(2511)

NAME/KEY: CDS
LOCATION: Complement((2716)..(2946))
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((12995)..(3252))
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((3299)..(3676))
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((3837)..(4124))
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((4351)..(5214))
US-09-252-088-13

Query Match 0.8%; Score 20; DB 11; Length 5215;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 479 CAAGGACGCTATCTACTACAGA 498
|||||
DB 616 CAAGGACGCTATCTACTACAGA 635

RESULT 22

US-09-983-965-4749/c
; Sequence 4749, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 4749
; LENGTH: 164
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 17-LIB34-068-Q1-E1-E1
US-09-983-965-4749

Query Match 0.8%; Score 19; DB 10; Length 164;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1112 TCAATTCCTTCTTGTTA 1130
|||||
DB 83 TCAATTCCTTCTTGTTA 65

RESULT 23

US-10-027-632-231121
; Sequence 231121, Application US/10027632
; Publication No. US20030204075A8
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome

```
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 231121
LENGTH: 533
TYPE: DNA
ORGANISM: Human
US-10-027-632-231121

Query Match      0.8%; Score 19; DB 12; Length 533;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1212 CATCTGAAACTGTTAAAAA 1230
Db      31 CATCTGAAACTGTTAAAAA 49

RESULT 24
US-10-027-632-231122
Sequence 231122, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 231122
LENGTH: 533
TYPE: DNA
ORGANISM: Human
US-10-027-632-231122

Query Match      0.8%; Score 19; DB 12; Length 533;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1212 CATCTGAAACTGTTAAAAA 1230
Db      31 CATCTGAAACTGTTAAAAA 49
```

```
Db      31 CATCTGAAACTGTTAAAAA 49

RESULT 25
US-10-027-632-231123
Sequence 231123, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 231121
LENGTH: 533

Query Match      0.8%; Score 19; DB 12; Length 533;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1212 CATCTGAAACTGTTAAAAA 1230
Db      31 CATCTGAAACTGTTAAAAA 49

RESULT 26
US-10-027-632-231121
Sequence 231121, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 231121
LENGTH: 533
```

```

; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231121

Query Match
Best Local Similarity 100.0%; Score 19; DB 13; Length 533;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1212 CATCTGAACCTGTTAAAA 1230
Db      31 CATCTGAACCTGTTAAAA 49

RESULT 27
US-10-027-632-231122
; Sequence 231122, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231122
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231122

Query Match
Best Local Similarity 100.0%; Score 19; DB 13; Length 533;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1212 CATCTGAACCTGTTAAAA 1230
Db      31 CATCTGAACCTGTTAAAA 49

RESULT 28
US-10-027-632-231123
; Sequence 231123, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; FILE REFERENCE: 108827.129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231123
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231123
```

```

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231123
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231123

Query Match
Best Local Similarity 100.0%; Score 19; DB 13; Length 533;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1212 CATCTGAACCTGTTAAAA 1230
Db      31 CATCTGAACCTGTTAAAA 49

RESULT 29
US-10-027-632-118539
; Sequence 118539, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118539
; LENGTH: 1112
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-118539

Query Match
Best Local Similarity 100.0%; Score 19; DB 12; Length 1112;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1513 AAATCTCAATTCAGTAT 1531
Db      891 AAATCTCAATTCAGTAT 909

RESULT 30
US-10-027-632-118540
; Sequence 118540, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118540
; LENGTH: 1112
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-118540
```

```

; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118540
; LENGTH: 1112
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-118540

Query Match          0.8%; Score 19; DB 12; Length 1112;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1513 AAATTCGAATTGAGTAT 1531
      |||||||
Db      891 AAATTCGAATTGAGTAT 909
```

```

RESULT 31
US-10-027-632-118539
; Sequence 118539, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118539
; LENGTH: 1112
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-118539
```

```

Query Match          0.8%; Score 19; DB 13; Length 1112;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1513 AAATTCGAATTGAGTAT 1531
      |||||||
Db      891 AAATTCGAATTGAGTAT 909
```

```

RESULT 32
US-10-027-632-118540
; Sequence 118540, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118540
; LENGTH: 1112
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-118540

Query Match          0.8%; Score 19; DB 13; Length 1112;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1513 AAATTCGAATTGAGTAT 1531
      |||||||
Db      891 AAATTCGAATTGAGTAT 909
```

```

RESULT 33
US-10-027-632-117222
; Sequence 117222, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117222
; LENGTH: 1213
; TYPE: DNA
; ORGANISM: Human
```

US-10-027-632-117222

Query Match 0.8%; Score 19; DB 12; Length 1213;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1759 TGTAAAGCAATCCAACT 1777

Db 776 TGTAAAGCAATCCAACT 794

RESULT 34

US-10-027-632-117223

; Sequence 117223, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 117223

; LENGTH: 1213

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-117223

Query Match 0.8%; Score 19; DB 12; Length 1213;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1759 TGTAAAGCAATCCAACT 1777

Db 776 TGTAAAGCAATCCAACT 794

RESULT 35

US-10-027-632-117224

; Sequence 117224, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 117224

; LENGTH: 1213

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-117224

Query Match 0.8%; Score 19; DB 12; Length 1213;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1759 TGTAAAGCAATCCAACT 1777

Db 776 TGTAAAGCAATCCAACT 794

RESULT 36

US-10-027-632-117222

; Sequence 117222, Application US/10027632

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 117222

; LENGTH: 1213

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-117222

Query Match 0.8%; Score 19; DB 13; Length 1213;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1759 TGTAAAGCAATCCAACT 1777

Db 776 TGTAAAGCAATCCAACT 794

RESULT 37

US-10-027-632-117223

; Sequence 117223, Application US/10027632

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

```

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 117223
; LENGTH: 1213
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-117223
```

```
Query Match          0.8%; Score 19; DB 13; Length 1213;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1759 TGTAAAGCAATCCAACT 1777
      |||||
Db      776 TGTAAAGCAATCCAACT 794
```

```
RESULT 38
US-10-027-632-117224
```

```

; Sequence 117224, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 117224
; LENGTH: 1213
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-117224
```

```
Query Match          0.8%; Score 19; DB 13; Length 1213;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1759 TGTAAAGCAATCCAACT 1777
      |||||
Db      776 TGTAAAGCAATCCAACT 794
```

RESULT 39

```

US-09-769-736-71
; Sequence 71, Application US/09769736
; Publication No. US2003013875A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Le Page, Richard WF
; APPLICANT: Wells, Jeremy M
; APPLICANT: Hammitfy, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21089wo
; CURRENT APPLICATION NUMBER: US/09/769,736
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: GB 9816335.5
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/125163
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 71
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
US-09-769-736-71
```

```
Query Match          0.8%; Score 19; DB 12; Length 1455;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1583 GATGTTACATTTTGTATG 1601
      |||||
Db      343 GATGTTACATTTTGTATG 361
```

RESULT 40

```

US-10-131-510A-5
; Sequence 5, Application US/10131510A
; Publication No. US20030166536A1
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S
; TITLE OF INVENTION: Modified Factor VIII
; FILE REFERENCE: 75-957
; CURRENT APPLICATION NUMBER: US/10/131,510A
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: U.S. 09/315,179
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: U.S. 09/037,601
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: U.S. 08/670,707
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: PCT/US97/11155
; PRIOR FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: PCT/US94/13200
; PRIOR FILING DATE: 1994-11-15
; PRIOR APPLICATION NUMBER: U.S. 08/212,133
; PRIOR FILING DATE: 1994-03-11
; PRIOR APPLICATION NUMBER: U.S. 07/864,004
; PRIOR FILING DATE: 1992-04-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 5
; LENGTH: 7493
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-131-510A-5
```

```
Query Match          0.8%; Score 19; DB 12; Length 7493;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      2347 AAAAGAAATATCTTCA 2365
      |||||
Db      206 AAAAGAAATATCTTCA 224
```

RESULT 41
US-10-187-319-5
GENERAL INFORMATION:
APPLICANT: Lollar, John S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: USA
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/187,319
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/523,656
FILING DATE: 2000-03-10
APPLICATION NUMBER: US 09/037,601
FILING DATE: 1998-03-10
APPLICATION NUMBER: WO PCT/US97/11155
FILING DATE: 1997-06-26
APPLICATION NUMBER: US 08/670,707
FILING DATE: 1996-06-26
ATTORNEY/AGENT INFORMATION:
NAME: Greenlee, Lorraine L.
REGISTRATION NUMBER: 27,894
REFERENCE/DOCKET NUMBER: 75-95K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/499-8080
TELEFAX: 303/499-8089
TITLE: Sequence of the murine Factor VIII cDNA
JOURNAL: Genomics
VOLUME: 16
PAGES: 374-379
DATE: 1993
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-187-319-5
Query Match 0.8%; Score 19; DB 14; Length 7493;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2347 AAAAGAGTAATCCTTCA 2355
DB 206 AAAAGAGTAATCCTTCA 224
RESULT 42
US-09-729-920-3/c
Sequence 3, Application US/09799920
Patent No. US20020103115A1
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/729,920
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 143306
TYPE: DNA

ORGANISM: Human
US-09-729-920-3
Query Match 0.8%; Score 19; DB 10; Length 143306;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 321 TCAGGTAGATGGAATA 339
DB 18852 TCAGGTAGATGGAATA 18834
RESULT 43
US-09-983-965-5888/c
Sequence 5888, Application US/09983965
Patent No. US20020137160A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 5888
LENGTH: 324
TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
OTHER INFORMATION: Clone ID: 63-LIB34-039-Q1-E1-H4
US-09-983-965-5888
Query Match 0.8%; Score 18; DB 10; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1101 TTAATAGACTCAATT 1118
DB 108 TTAATAGACTCAATT 91
RESULT 44
US-09-925-302-17
Sequence 17, Application US/09925302
Patent No. US20020044941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 17
LENGTH: 372
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (357)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (367)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-17

Query Match 0.8%; Score 18; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2195 AAGAGCAGAGCTTTG 2212
|||||
DB 99 AAGAGCAGAGCTTTG 116

RESULT 45
US-10-060-036-10
Sequence 10, Application US/10060036
Publication No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yugu

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566

CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10

LENGTH: 372
TYPE: DNA

ORGANISM: Homo sapiens
US-10-060-036-10

Query Match 0.8%; Score 18; DB 14; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 TATCATCGTGAAGATT 249
|||||
DB 228 TATCATCGTGAAGATT 245

RESULT 46
US-10-027-632-192700
Sequence 192700, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 192700
LENGTH: 442
TYPE: DNA
ORGANISM: Human
US-10-027-632-192700

Query Match 0.8%; Score 18; DB 12; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 754 AAGCAACAGCAACAC 771
|||||
DB 237 AAGCAACAGCAACAC 254

RESULT 47
US-10-027-632-192700
Sequence 192700, Application US/10027632
Publication No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 192700
LENGTH: 442
TYPE: DNA

ORGANISM: Human
US-10-027-632-192700

Query Match 0.8%; Score 18; DB 13; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 754 AAGCAACAGCAACAC 771
|||||
DB 237 AAGCAACAGCAACAC 254

RESULT 48
US-09-796-692-4166/C
Sequence 4166, Application US/09796692
Publication No. US20020198362A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200

CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17


```

; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 4166
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-765-692-4166
```

```

Query Match      0.8%; Score 18; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1740 CTCGATCTCCAGCGCAG 1757
Db      122 CTCGATCTCCAGCGCAG 105
```

```

RESULT 49
US-10-040-862-4166/c
; Sequence 4166, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
```

```

; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 4166
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-4166
```

```

Query Match      0.8%; Score 18; DB 14; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1740 CTCGATCTCCAGCGCAG 1757
Db      122 CTCGATCTCCAGCGCAG 105
```

```

RESULT 50
US-10-027-632-35253
; Sequence 35253, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 35253
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-35253

Query Match      0.8%; Score 18; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      702 GAACAACCTGGGTACCTT 719
Db      248 GAACAACCTGGGTACCTT 265

RESULT 51
US-10-027-632-75653
; Sequence 75653, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
```

```

; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75653
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75653

Query Match          0.8%; Score 18; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      702 GAACAACTGGGTACCTT 719
      |||||
Db      248 GAACAACTGGGTACCTT 265

RESULT 52
US-10-027-632-76294
; Sequence 76294, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76294
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-76294

Query Match          0.8%; Score 18; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      702 GAACAACTGGGTACCTT 719
      |||||
Db      248 GAACAACTGGGTACCTT 265
```

```

RESULT 53
US-10-027-632-313657
; Sequence 313657, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313657
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-313657

Query Match          0.8%; Score 18; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      702 GAACAACTGGGTACCTT 719
      |||||
Db      248 GAACAACTGGGTACCTT 265

RESULT 54
US-10-027-632-35253
; Sequence 35253, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35253
; LENGTH: 480
; TYPE: DNA
```

```
; ORGANISM: Human
US-10-027-632-35253

Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 480;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 702 GAACAACCTGGGTACCTT 719
   |||||
Db 248 GAACAACCTGGGTACCTT 265

RESULT 55
US-10-027-632-75653
; Sequence 75653, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75653
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75653

Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 480;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 702 GAACAACCTGGGTACCTT 719
   |||||
Db 248 GAACAACCTGGGTACCTT 265

RESULT 56
US-10-027-632-76294
; Sequence 76294, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
```

```
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76294
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-76294

Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 480;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 702 GAACAACCTGGGTACCTT 719
   |||||
Db 248 GAACAACCTGGGTACCTT 265

RESULT 57
US-10-027-632-313657
; Sequence 313657, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313657
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-313657

Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 480;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 702 GAACAACCTGGGTACCTT 719
   |||||
Db 248 GAACAACCTGGGTACCTT 265

RESULT 58
US-10-027-632-3008
; Sequence 3008, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
```

PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3008
LENGTH: 484
TYPE: DNA
ORGANISM: Human
US-10-027-632-3008

Query Match 0.8%; Score 18; DB 12; Length 484;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 702 GACCAACTGGGTACTT 719
|||||
Db 244 GACCAACTGGGTACTT 261

RESULT 59
US-10-027-632-3008
Sequence 3008, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3008
LENGTH: 484
TYPE: DNA
ORGANISM: Human
US-10-027-632-3008

Query Match 0.8%; Score 18; DB 13; Length 484;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 702 GACCAACTGGGTACTT 719
|||||
Db 244 GACCAACTGGGTACTT 261

RESULT 60

US-10-029-386-11258
Sequence 11258, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AECOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 11258
LENGTH: 536
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO D87009.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.38
OTHER INFORMATION: NT HIT: AF223676.1, EVALUATE 6.00e-10
OTHER INFORMATION: SWISSPROT HIT: Q9HNB4, EVALUATE 2.20e+00
OTHER INFORMATION: EST_HUMAN HIT: BG473533.1, EVALUATE 1.00e-125
US-10-029-386-11258

Query Match 0.8%; Score 18; DB 12; Length 536;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1111 CTCAAATCTCTTTGGT 1128
|||||
Db 218 CTCAAATCTCTTTGGT 235

RESULT 61
US-10-027-632-284258/c
Sequence 284258, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 284258
LENGTH: 563
TYPE: DNA
ORGANISM: Human
US-10-027-632-284258

Query Match 0.8%; Score 18; DB 12; Length 563;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 275 CTAAGATGAGATATT 292

```
Db          482 CTTAAAGATGAGGATATT 465

RESULT 62
US-10-027-632-284259/c
; Sequence 284259, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284259
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-284259

Query Match          0.8%; Score 18; DB 12; Length 563;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          275 CTTAAAGATGAGGATATT 292
Db          482 CTTAAAGATGAGGATATT 465

RESULT 63
US-10-027-632-284258/c
; Sequence 284258, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284258
```

```
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-284258

Query Match          0.8%; Score 18; DB 13; Length 563;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          275 CTTAAAGATGAGGATATT 292
Db          482 CTTAAAGATGAGGATATT 465

RESULT 64
US-10-027-632-284259/c
; Sequence 284259, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284259
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-284259

Query Match          0.8%; Score 18; DB 13; Length 563;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          275 CTTAAAGATGAGGATATT 292
Db          482 CTTAAAGATGAGGATATT 465

RESULT 65
US-10-027-632-81822
; Sequence 81822, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
```

```
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 81822
;; LENGTH: 577
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)_(577)
;; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-81822
```

```
Query Match      0.8%; Score 18; DB 12; Length 577;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1679 AGCCTTCTGATAGGAA 1696
      |||||
Db      385 AGCCTTCTGATAGGAA 402
```

```
RESULT 66
US-10-027-632-81822
; Sequence 81822, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 81822
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(577)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-81822
```

```
Query Match      0.8%; Score 18; DB 13; Length 577;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1679 AGCCTTCTGATAGGAA 1696
      |||||
Db      385 AGCCTTCTGATAGGAA 402
```

```
RESULT 67
US-10-027-632-185059
; Sequence 185059, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 185059
; LENGTH: 608
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-185059
```

```
Query Match      0.8%; Score 18; DB 12; Length 608;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      320 ATCAAGTACATGAGAAA 337
      |||||
Db      183 ATCAAGTACATGAGAAA 200
```

```
RESULT 68
US-10-027-632-185059
; Sequence 185059, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 185059
; LENGTH: 608
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-185059
```

Query Match 0.8%; Score 18; DB 13; Length 608;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 320 ATCAAGTGTGATGAAAA 337
|||||
Db 183 ATCAAGTGTGATGAAAA 200

RESULT 69
US-10-027-632-27877/c
; Sequence 27877, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27877
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-27877

Query Match 0.8%; Score 18; DB 12; Length 674;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1693 GGAAGAGTTCAGCTCA 1710
|||||
Db 594 GGAAGAGTTCAGCTCA 577

RESULT 70
US-10-027-632-27877/c

; Sequence 27877, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27877
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-27877

Query Match 0.8%; Score 18; DB 13; Length 674;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1693 GGAAGAGTTCAGCTCA 1710
|||||
Db 594 GGAAGAGTTCAGCTCA 577

RESULT 71
US-09-815-242-9810/c
; Sequence 9810, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9810
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Salmonella typhi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(924)
; NAME/KEY: misc_feature
; LOCATION: (1)...(924)
; OTHER INFORMATION: n = A,T,C or G
US-09-815-242-9810

Query Match 0.8%; Score 18; DB 9; Length 924;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2106 ACTTCAAGCGGATGAAG 2123
|||||
Db 854 ACTTCAAGCGGATGAAG 837

RESULT 72
US-09-070-927A-278
Sequence 278, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunesh
Patrick J. Dillon
Steven Barash
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 278:
SEQUENCE CHARACTERISTICS:
LENGTH: 1587 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 278:
US-09-070-927A-278
Query Match 0.8%; Score 18; DB 10; Length 1587;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2297 ATGATAACAATAGTATC 2314
Db 410 ATGATAACAATAGTATC 427

RESULT 73
US-10-029-386-24974
Sequence 24974, Application US/10029386
Patent No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 24974
LENGTH: 1619
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO D87009.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.38
OTHER INFORMATION: EST_HUMAN HIT: N39816.1, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: Q60821, EVALUE 7.00e-10
OTHER INFORMATION: NT HIT: G115300639, EVALUE 7.00e-43
US-10-029-386-24974
Query Match 0.8%; Score 18; DB 12; Length 1619;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1111 CTCGAATTCCTTTGGT 1128
Db 1567 CTCGAATTCCTTTGGT 1584

RESULT 74
US-10-029-386-25318
Sequence 25318, Application US/10029386
Patent No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 25318
LENGTH: 1629
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO D87011.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: SWISSPROT HIT: Q60821, EVALUE 6.00e-09
OTHER INFORMATION: NT HIT: G115300639, EVALUE 2.00e-43
OTHER INFORMATION: EST_HUMAN HIT: N39816.1, EVALUE 0.00e+00
US-10-029-386-25318
Query Match 0.8%; Score 18; DB 12; Length 1629;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1111 CTCGAATTCCTTTGGT 1128
Db 1577 CTCGAATTCCTTTGGT 1594

RESULT 75
US-09-833-381-1943/c
Sequence 1943, Application US/09833381
Patent No. US20020132090A1
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSeq for Windows Version 3.0

Query Match	Score 18;	DB 14;	Length 2956;
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Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1905 ATCATTACCATAATATTA 1922

Db 317 ATCATTACCATAATATTA 300

RESULT 80

US-10-044-090-38

; Sequence 38, Application US/10044090
; Publication No. US20020137081A1

; GENERAL INFORMATION:

; APPLICANT: Olga Bandman

; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION

; FILE REFERENCE: PA-0028 US

; CURRENT APPLICATION NUMBER: US/10/044,090

; CURRENT FILING DATE: 2002-01-09

; NUMBER OF SEQ ID NOS: 850

; SOFTWARE: PERL Program

; SEQ ID NO 38

; LENGTH: 3154

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. US20020137081A1 1519105CB1

US-10-044-090-38

Query Match 0.8%; Score 18; DB 13; Length 3154;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2195 AAAGAGCAGAAAGTTTG 2212

Db 83 AAAGAGCAGAAAGTTTG 100

RESULT 81

US-10-340-097-5

; Sequence 5, Application US/10340097

; Publication No. US20030162276A1

; GENERAL INFORMATION:

; APPLICANT: Ratner, Amir

; APPLICANT: Sun, Hui

; APPLICANT: Lupski, James R.

; APPLICANT: Nathans, Jeremy

; APPLICANT: Anderson, Kent L.

; APPLICANT: Leppert, Mark

; APPLICANT: Dean, Michael

; APPLICANT: Singh, Nanda

; APPLICANT: Shroyer, No. US20030162276A1h F.

; APPLICANT: Smallwood, Philip M.

; APPLICANT: Allikmets, Rando

; APPLICANT: Lewis, Richard A.

; APPLICANT: Li, Yixin

; TITLE OF INVENTION: Nucleic Acid And Amino Acid Sequences For ATP-Binding Cassette

; TITLE OF INVENTION: Transporter And Methods Of Screening For Agents That Modify ATP-

; FILE REFERENCE: BYLR0065

; CURRENT APPLICATION NUMBER: US/10/340,097

; CURRENT FILING DATE: 2003-01-10

; PRIOR APPLICATION NUMBER: US/09/032,438A

; PRIOR FILING DATE: 1998-02-27

; PRIOR APPLICATION NUMBER: 60/039,388

; PRIOR FILING DATE: 1997-02-27

; NUMBER OF SEQ ID NOS: 120

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 6705

; TYPE: DNA

; ORGANISM: Homo sapiens

Query Match 0.8%; Score 18; DB 12; Length 6705;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2095 TCCAATATAGAACTTCAA 2112

Db 3699 TCCAATATAGAACTTCAA 3716

RESULT 82

US-10-336-215-5

; Sequence 5, Application US/10336215

; Publication No. US20030170852A1

; GENERAL INFORMATION:

; APPLICANT: Allikmets, Rando

; APPLICANT: Anderson, Kent L.

; APPLICANT: Dean, Michael

; APPLICANT: Leppert, Mark

; APPLICANT: Lewis, Richard A.

; APPLICANT: Li, Yixin

; APPLICANT: Lupski, James R.

; APPLICANT: Nathans, Jeremy

; APPLICANT: Ratner, Amir

; APPLICANT: Shroyer, No. US20030170852A1h F.

; APPLICANT: Singh, Nanda

; APPLICANT: Smallwood, Philip

; APPLICANT: Sun, Hui

; TITLE OF INVENTION: Methods Of Screening And Diagnostics Using ATP-Binding Cassette

; TITLE OF INVENTION: Transporter

; FILE REFERENCE: APPI0089

; CURRENT APPLICATION NUMBER: US/10/336,215

; CURRENT FILING DATE: 2003-04-11

; PRIOR APPLICATION NUMBER: 60/039,388

; PRIOR FILING DATE: 1997-02-27

; PRIOR APPLICATION NUMBER: 09/032,438

; PRIOR FILING DATE: 1998-02-27

; NUMBER OF SEQ ID NOS: 120

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 5

; LENGTH: 6705

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-336-215-5

Query Match 0.8%; Score 18; DB 12; Length 6705;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2095 TCCAATATAGAACTTCAA 2112

Db 3699 TCCAATATAGAACTTCAA 3716

RESULT 83

US-10-336-219-5

; Sequence 5, Application US/10336219

; Publication No. US20030170853A1

; GENERAL INFORMATION:

; APPLICANT: Allikmets, Rando

; APPLICANT: Anderson, Kent L.

; APPLICANT: Dean, Michael

; APPLICANT: Leppert, Mark

; APPLICANT: Lewis, Richard A.

; APPLICANT: Li, Yixin

; APPLICANT: Lupski, James R.

; APPLICANT: Nathans, Jeremy

; APPLICANT: Ratner, Amir

; APPLICANT: Shroyer, No. US20030170853A1h F.

; APPLICANT: Singh, Nanda

; APPLICANT: Smallwood, Philip

; APPLICANT: Sun, Hui

; TITLE OF INVENTION: Methods Of Gene Therapy Using Nucleic Acid Sequences For


```
US-09-736-960-86
; Sequence 86, Application US/09736960
; Patent No. US20020102267A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter
; APPLICANT: Garman, Jonathan David
; APPLICANT: Candia III, Albert Frederick
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: CLASP-5 Transmembrane Protein
; FILE REFERENCE: 020054-000511US
; CURRENT APPLICATION NUMBER: US/09/736,960
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 09/547,276
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/196,267
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/196,460
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/196,527
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/196,528
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 09/687,837
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/240,503
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/240,508
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/240,539
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/240,543
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 66686
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: ordered human genomic DNA at CLASP-5 locus
US-09-736-960-86

Query Match          0.8%; Score 18; DB 10; Length 66686;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2144 GGTGACCCAGAAATCCCT 2161
Db      30662 GGTGACCCAGAAATCCCT 30679
```

```
RESULT 91
US-10-010-942B-18/c
; Sequence 18, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
```

```
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 131
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-010-942B-18

Query Match          0.7%; Score 17; DB 12; Length 131;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      615 TGGCTGCTGCAGAGCC 631
Db      33 TGGCTGCTGCAGAGCC 17
```

```
RESULT 92
US-10-010-942B-19
; Sequence 19, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 146
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-010-942B-19
```

```
Query Match          0.7%; Score 17; DB 12; Length 146;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      615 TGGCTGCTGCAGAGCC 631
Db      9 TGGCTGCTGCAGAGCC 25
```

```
RESULT 93
US-09-878-574-6546/c
; Sequence 6546, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 6546
```

```

; LENGTH: 271
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701098572H1
US-09-878-574-6546

Query Match
Best Local Similarity 100.0%; Score 17; DB 10; Length 271;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 92 GAGATTGACTCCTGA 108
Db 67 GAGATTGACTCCTGA 51

RESULT 94
US-09-923-876-4422
; Sequence 4422, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (lto)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 4422
; LENGTH: 295
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700455016H1
; NAME/KEY: 7, 107, 194, 204, 243, 254, 256, 260, 278, 288, 292-293
; LOCATION: 7, 107, 194, 204, 243, 254, 256, 260, 278, 288, 292-293
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-4422

Query Match
Best Local Similarity 100.0%; Score 17; DB 9; Length 295;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1287 AAGAAATGTGCTCCT 1303
Db 212 AAGAAATGTGCTCCT 228

RESULT 95
US-10-106-698-2167/c
; Sequence 2167, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patentin Ver. 3.0
; SEQ ID NO 2167
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```

; LENGTH: 316
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (212)..(212)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (268)..(268)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (276)..(276)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (283)..(284)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (311)..(311)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-2167

Query Match
Best Local Similarity 100.0%; Score 17; DB 14; Length 316;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2116 GGATGAAGCCACTAG 2132
Db 141 GGATGAAGCCACTAG 125

RESULT 96
US-09-765-272-149
; Sequence 149, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
; APPLICANT: Choi et al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 322 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
```

SEQUENCE DESCRIPTION: SEQ ID NO: 149:
US-09-765-272-149

Query Match 0.7%; Score 17; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1439 AATAAAGAAAATTGCT 1455
DB 38 AATAAAGAAAATTGCT 54

RESULT 97
US-10-060-036-2151/c
; Sequence 2151, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 2151
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-2151

Query Match 0.7%; Score 17; DB 14; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGCAAAAAGTTGCAG 1706
DB 73 TAAGCAAAAAGTTGCAG 57

RESULT 98
US-09-878-574-3595
; Sequence 3595, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3595
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-008-Q1-B1-C2
US-09-878-574-3595

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Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 755 AGCAACAAGCAACAC 771

DB 282 AGCAACAAGCAACAC 298

RESULT 99
US-09-757-781-26/c
; Sequence 26, Application US/09757781
; Patent No. US20020137166A1
; GENERAL INFORMATION:
; APPLICANT: Reddy, Roopa
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Krasnow, Randi E.
; TITLE OF INVENTION: ASIP-RELATED PROTEINS
; FILE REFERENCE: PC-0032 US
; CURRENT APPLICATION NUMBER: US/09/757,781
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PERL Program
; SEQ ID NO 26
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Inocyte ID No. US20020137166A1 5627320R8
US-09-757-781-26

Query Match 0.7%; Score 17; DB 10; Length 375;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 AAGATGAGATATTGTT 295
DB 135 AAGATGAGATATTGTT 119

RESULT 100
US-09-918-995-36324
; Sequence 36324, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 36324
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-36324

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Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1715 TATCTAAAGAAAAGG 1731
DB 386 TATCTAAAGAAAAGG 402

Search completed: November 14, 2003, 10:32:45
Job time : 1716 secs

BEST AVAILABLE COPY

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 10:38:30 ; Search time 462 Seconds
(without alignments)
273.477 Million cell updates/sec

Title: US-09-765-271-56

Perfect score: 796

Sequence: 1 SYELGYQARTVKNRNVSY.....KLALKGNPSVSKERIN 796

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 200 summaries

Database : A.Geneseq_19Jun03:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	795	99.9	796	19	AAW55090
2	795	99.9	796	23	ABP54584
3	695	87.3	802	24	ABU01598
4	695	87.3	819	21	AAU01468
5	80	10.1	334	21	AAU01468
6	80	10.1	334	23	AAU04027
7	80	10.1	690	21	AAU04027
8	80	10.1	690	23	AAU04027
9	80	10.1	821	21	AAU04027

10	80	10.1	821	21	AAU04026	Streptococcus pneu
11	80	10.1	821	23	AAU04026	Streptococcus pneu
12	80	10.1	840	23	AAU04026	Streptococcus pneu
13	80	10.1	840	23	AAU04026	Streptococcus pneu
14	80	7.5	805	21	AAU04026	Streptococcus pneu
15	80	7.5	807	21	AAU04026	Streptococcus pneu
16	80	7.5	811	21	AAU04026	Streptococcus pneu
17	80	7.5	811	21	AAU04026	Streptococcus pneu
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19	80	7.5	811	21	AAU04026	Streptococcus pneu
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24	80	7.5	819	21	AAU04026	Streptococcus pneu
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28	80	7.5	820	21	AAU04026	Streptococcus pneu
29	80	7.5	826	21	AAU04026	Streptococcus pneu
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31	80	7.5	834	21	AAU04026	Streptococcus pneu
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33	80	7.5	838	21	AAU04026	Streptococcus pneu
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37	80	7.5	840	21	AAU04026	Streptococcus pneu
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81	80	7.5	840	21	AAU04026	Streptococcus pneu
82	80	7.5	840	21	AAU04026	Streptococcus pneu

83	24	3.0	555	21	AAB12734	Streptococcus pneu
84	24	3.0	555	23	AAU84047	Truncated variant
85	24	3.0	559	23	AAU84051	S. pneumoniae deri
86	24	3.0	999	23	AAU84052	S. pneumoniae deri
87	24	3.0	1126	23	AAU84058	S. pneumoniae deri
88	24	3.0	1238	23	AAU84056	S. pneumoniae deri
89	24	3.0	1365	23	AAU84057	S. pneumoniae deri
90	23	2.9	94	23	AAU83827	S. pneumoniae anti
91	17	2.1	163	23	AAU05752	Streptococcus pneu
92	17	2.1	381	21	AAU91286	Group B Streptococ
93	17	2.1	793	20	AAU27347	Group B Streptococ
94	17	2.1	822	21	AAU91283	Group B Streptococ
95	17	2.1	822	22	AAU00028	Streptococcus agal
96	17	2.1	822	22	AAU00030	Streptococcus agal
97	17	2.1	822	23	ABP28904	Streptococcus poly
98	17	2.1	822	23	ABP28703	Streptococcus poly
99	17	2.1	823	21	AAU81746	Streptococcus pneu
100	17	2.1	824	21	AAU81747	Streptococcus pneu
101	17	2.1	825	22	AAU00026	Streptococcus pyog
102	17	2.1	825	22	AAU00029	Streptococcus pyog
103	17	2.1	825	23	ABP26207	Streptococcus poly
104	15	1.9	1057	21	AAU81725	Streptococcus pneu
105	15	1.9	1058	23	AAU84097	S. pneumoniae deri
106	14	1.8	487	21	AAU81729	Streptococcus pneu
107	14	1.8	487	23	AAU84028	Truncated variant
108	14	1.8	487	23	AAU84090	Truncated variant
109	13	1.6	132	21	AAU81737	Truncated variant
110	13	1.6	132	23	AAU84050	Truncated variant
111	12	1.5	203	21	AAU81739	Truncated variant
112	12	1.5	203	23	AAU84086	Truncated variant
113	12	1.5	214	23	AAU84095	Truncated variant
114	12	1.5	342	23	AAU84030	Truncated variant
115	12	1.5	715	20	AAU27348	Group B Streptococ
116	12	1.5	807	23	AAU83997	Truncated variant
117	12	1.5	913	23	AAU84059	S. pneumoniae deri
118	12	1.5	1152	23	AAU84054	S. pneumoniae deri
119	11	1.4	485	21	AAU91310	Group B Streptococ
120	10	1.3	189	24	ABU01420	S. pneumoniae type
121	9	1.1	121	21	AAU81273	Streptococcus pneu
122	9	1.1	121	23	AAU84049	Truncated variant
123	9	1.1	272	23	AAU84040	Variant of S. pneu
124	9	1.1	921	15	AAU84087	TATTA-binding prote
125	9	1.1	921	17	AAU06077	Drosophila TATA-bi
126	9	1.1	921	18	AAU06078	TATA-binding prote
127	9	1.1	921	22	ABU61528	Drosophila melanog
128	9	1.1	921	22	ABU61528	Drosophila melanog
129	8	1.0	86	23	AAU83838	S. pneumoniae anti
130	8	1.0	270	23	AAU84042	Variant of S. pneu
131	8	1.0	272	23	AAU76153	Streptococcus pneu
132	8	1.0	272	23	AAU84033	Variant of S. pneu
133	8	1.0	323	23	ABU50997	Helicobacter pylori
134	8	1.0	379	23	ABP26206	Streptococcus poly
135	8	1.0	481	23	ABU51004	Helicobacter pylori
136	8	1.0	482	22	AAU33905	Staphylococcus aur
137	8	1.0	488	22	AAU36971	Staphylococcus epi
138	8	1.0	490	23	ABP40271	Modified Interfero
139	8	1.0	503	22	AAU51503	Human intracellular
140	8	1.0	503	22	AAU50329	S. pneumoniae deri
141	8	1.0	895	23	AAU84069	S. pneumoniae deri
142	8	1.0	896	23	AAU84077	S. pneumoniae deri
143	8	1.0	901	23	AAU84068	S. pneumoniae deri
144	8	1.0	902	23	AAU84076	S. pneumoniae deri
145	8	1.0	907	23	AAU84060	S. pneumoniae deri
146	8	1.0	907	23	AAU84061	S. pneumoniae deri
147	8	1.0	907	23	AAU84062	S. pneumoniae deri
148	8	1.0	907	23	AAU84063	S. pneumoniae deri
149	8	1.0	907	23	AAU84064	S. pneumoniae deri
150	8	1.0	907	23	AAU84065	S. pneumoniae deri
151	8	1.0	1104	24	ABU25604	Aerergillus fumiga
152	8	1.0	1289	22	ABU26204	Mycobacterium tube
153	8	1.0	1353	24	ABP81332	Streptococcus pneu
154	8	1.0	1659	24	ABU00861	S. pneumoniae type
155	8	1.0	1659	24	ABU00861	S. pneumoniae type

156	7	0.9	27	21	AAU84205	Human Lyn A kinase
157	7	0.9	27	23	AAU84631	Human tyrosine kin
158	7	0.9	34	22	ABU89647	N-terminal peptide
159	7	0.9	41	23	AAU83839	Streptococcus pneu
160	7	0.9	45	21	AAU814203	Human Lyn B kinase
161	7	0.9	45	21	AAU814203	Human tyrosine kin
162	7	0.9	46	22	AAU85490	Human immune/haema
163	7	0.9	47	23	ABP26643	Streptococcus poly
164	7	0.9	49	22	ABU822724	Protein #4723 enco
165	7	0.9	49	22	ABU822724	Human peptide enco
166	7	0.9	50	18	AAU45409	N-terminal amino a
167	7	0.9	53	23	ABP04572	Human ORFX protein
168	7	0.9	53	23	ABP34598	Human ORFX351 prot
169	7	0.9	63	22	AAU02094	Human polypeptide
170	7	0.9	66	21	AAU84202	Human Lyn A kinase
171	7	0.9	66	23	AAU84658	Human tyrosine kin
172	7	0.9	66	23	ABP32888	Human ORF1861 prot
173	7	0.9	70	21	AAU82963	Human secreted pro
174	7	0.9	76	21	AAU84881	Human secreted pro
175	7	0.9	76	21	AAU84882	Human colon cancer
176	7	0.9	81	22	AAU74664	Human polypeptide
177	7	0.9	85	22	AAU08815	Eucalyptus grandis
178	7	0.9	86	21	AAU832570	Human testicular a
179	7	0.9	91	22	ABU85891	Human reproductive
180	7	0.9	91	22	AAU85192	Eucalyptus grandis
181	7	0.9	94	21	AAU83325	Novel human neopla
182	7	0.9	97	22	AAU21570	Novel human neopla
183	7	0.9	97	22	AAU21740	Novel human neopla
184	7	0.9	99	11	AAU05700	MPB-57 protein. M
185	7	0.9	99	23	ABU42619	Human ovarian anti
186	7	0.9	100	22	AAU81221	Mycobacterium tube
187	7	0.9	100	23	AAU824631	Mycobacterium tube
188	7	0.9	100	23	AAU50739	Mycobacterium tube
189	7	0.9	103	22	ABU81747	Human nervous syst
190	7	0.9	110	23	ABU85465	Lactococcus lactis
191	7	0.9	115	23	AAU81188	Staphylococcus epi
192	7	0.9	117	23	ABU839740	Novel human diagno
193	7	0.9	129	22	ABU808365	Novel human diagno
194	7	0.9	145	22	ABU805153	Listeria monocytog
195	7	0.9	145	23	ABU848072	Novel human diagno
196	7	0.9	154	23	ABU810403	Catalpa acid triac
197	7	0.9	157	21	AAU32303	S. aureus grea prot
198	7	0.9	158	23	AAU78484	Human prey protein
199	7	0.9	158	23	ABU70181	C glutamicum prote
200	7	0.9	166	22	AAU92915	C glutamicum prote

ALIGNMENTS

RESULT 1						
AAU55090	AAU55090 standard; Protein; 796 AA.					
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XX	02-OCT-1998 (first entry)					
XX	Streptococcus pneumoniae SP0036 protein.					
DE	Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;					
XX	Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;					
KW	detection; pneumonia; otitis media; meningitis.					
XX	Streptococcus pneumoniae.					
OS	Streptococcus pneumoniae.					
XX	Key					
XX	Location/Qualifiers					
FT	Misc-difference 456					
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FT	/note=-"encoded by GNA"					
XX	W09818930-A2.					
XX	07-MAY-1998.					

XX 30-OCT-1997; 97WO-US19422.
XX
XX 31-OCT-1996; 96US-0029960.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Choi GH, Hromockyj A, Johnson LS, Kunsch CA;
XX
XX WPI; 1998-272224/24.
XX N-PSDB; AAV27351.
XX
XX Nucleic acid encoding antigenic peptide(s) from Streptococcus
XX pneumoniae - or their epitope-containing fragments, useful in
XX protective or therapeutic vaccines, and for diagnosis
XX
XX Claim 11; Page 59-60; 118pp; English.
XX
XX The present sequence represents a protein from Streptococcus pneumoniae.
XX The nucleic acid sequence encoding the Streptococcus pneumoniae protein
XX can be useful in vaccines for inducing protective antibodies against
XX Streptococcus pneumoniae, for treatment or prevention of infection e.g.
XX pneumonia, otitis media or meningitis. Probes based on the nucleic acid
XX are used to detect Streptococcus infection (by usual hybridisation or
XX amplification methods), also for isolating Streptococcus genes or their
XX allelic variants. The protein can be used similarly to detect specific
XX antibodies in standard immunoassays, especially for diagnosing or
XX monitoring infections. Antibodies which bind the protein are used to
XX detect corresponding antigens, to purify the protein and for passive
XX immunisation (optionally coupled to a toxin). Vaccines are administered,
XX e.g. by injection, orally or through the skin, typically at 0.01-1000
XX (especially 10-300) mu g/ml per dose.
XX
XX Sequence 796 AA:

Query Match 99.9%; Score 795; DB 19; Length 796;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 SHGDHYHYNGKVPYDAIISEBLMKDPYKLEKEDIIVNEVKGYIYKDGKYYVYLKDA 120
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DB 121 AHAADVRYKEINRQKQESHQREGGTPRNDGAVALARSGRYTTDDGYIFNADIIEDT 180
QY 181 GDAIVYPHGDHYHYTRKNEISASELAAEAFISGRGLNSRTRYRQNSDNTSRTWVPS 240
DB 181 GDAIVYPHGDHYHYTRKNEISASELAAEAFISGRGLNSRTRYRQNSDNTSRTWVPS 240
QY 241 VSNPGTTNTNTSNSTNSQASQNDISLKLQYLPISQORVSDGLVFDPAQITSTPT 300
DB 241 VSNPGTTNTNTSNSTNSQASQNDISLKLQYLPISQORVSDGLVFDPAQITSTPT 300
QY 301 ARGVAVPHGDHYHYFISQWSELEERIRIIPLYRSNHWVPDPRPEQSPQPTPEPSRQ 360
DB 301 ARGVAVPHGDHYHYFISQWSELEERIRIIPLYRSNHWVPDPRPEQSPQPTPEPSRQ 360
QY 361 POPAPMLKIDSNSLSQVLRKYGEGVPEBKISRYVFAKDLPSSTVKNLESKLSKQBS 420
DB 361 POPAPMLKIDSNSLSQVLRKYGEGVPEBKISRYVFAKDLPSSTVKNLESKLSKQBS 420
QY 421 VSHITLAKKENVAPRODFYDKAYNLTLEAHKALFNKKGNSFOALDKLELNESTN 480
DB 421 VSHITLAKKENVAPRODFYDKAYNLTLEAHKALFNKKGNSFOALDKLELNESTN 480
QY 481 KERLVDDLAFIAPITHPERLGRNSQIEYTEDEVAIAQLADKYTTSDDGYIPDEHDIISD 540
DB 481 KERLVDDLAFIAPITHPERLGRNSQIEYTEDEVAIAQLADKYTTSDDGYIPDEHDIISD 540

DB 481 KERLVDDLAFIAPITHPERLGRNSQIEYTEDEVAIAQLADKYTTSDDGYIPDEHDIISD 540
QY 541 EGDAYVTPHMGSHHIGKDSLSDKEKVAQAATYKKGILPPSPDADVKANPTGDSAAAY 600
DB 541 EGDAYVTPHMGSHHIGKDSLSDKEKVAQAATYKKGILPPSPDADVKANPTGDSAAAY 600
QY 601 NRKGEKRIPLVRLPYMEHTVEVKNGLIIPKHQYHNKIKFAPDDHTYKAPNGYTLSD 660
DB 601 NRKGEKRIPLVRLPYMEHTVEVKNGLIIPKHQYHNKIKFAPDDHTYKAPNGYTLSD 660
QY 661 LPAITIKYVHEHDEPHSHDGNASERYLGGKHSSEDPNKNFKADEEVEESTPAPEVP 720
DB 661 LPAITIKYVHEHDEPHSHDGNASERYLGGKHSSEDPNKNFKADEEVEESTPAPEVP 720
QY 721 QVETEKVEAQLKEAEVYLAKVTDSILKANATEETLAGLRNLTLOIWDNNSIIMAEKLLA 780
DB 721 QVETEKVEAQLKEAEVYLAKVTDSILKANATEETLAGLRNLTLOIWDNNSIIMAEKLLA 780
QY 781 LKGSNPSVSKKIN 796
DB 781 LKGSNPSVSKKIN 796

RESULT 2
ABP54584
ID ABP54584 standard; Protein; 796 AA.
XX
AC ABP54584;
XX
DT 04-SEP-2002 (first entry)
XX
DE S. pneumoniae SP036 protein sequence SEQ ID NO:56.
XX
KW Streptococcus pneumoniae; epitope; vaccine; antigenic protein;
KW antibacterial; Streptococcal infection; detection.
XX
XX Streptococcus pneumoniae.
XX
XX US2002061545-A1.
XX
XX 23-MAY-2002.
XX
XX 22-JAN-2001; 2001US-0765272.
XX
XX 30-OCT-1997; 97US-0961083.
XX
XX (CHOI/) CHOI G H.
XX (KUNS/) KUNSCH C A.
XX (BARA/) BARASH S C.
XX (DILL/) DILLON P J.
XX (DOUG/) DOUGHERTY B.
XX (FANN/) FANNON M R.
XX (ROSE/) ROSEN C A.
XX
XX Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR;
XX Rosen CA;
XX WPI; 2002-479261/51.
XX N-PSDB; AB084819.
XX
XX New Streptococcus pneumoniae antigens, useful for detecting
XX Streptococcus and for preventing or attenuating disease caused by
XX Streptococcus infection -
XX
XX Claim 11; Page 27; 70pp; English.
XX
XX AB084792 to AB084904 represents nucleic acids which encode the
XX Streptococcus pneumoniae antigens given in ABP54557 to ABP54669.
XX The S. pneumoniae antigens have antibacterial activity and can be
XX used in vaccines. The S. pneumoniae antigens can also be used to
XX prevent or attenuate a Streptococcal infection in an animal. The
XX polynucleotides encoding the S. pneumoniae antigens can be used to
XX detect Streptococcus nucleic acids. AB084905 to AB085130 represent

CC primers used in the cloning of *S. pneumoniae* ORFs (open reading frames)
 CC which are used in an example from the present invention.

XX Sequence 796 AA.

Query Match 99.9%; Score 795; DB 23; Length 796;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 SYELGLYQARTYKNNRVSVIDGKATOKTENLTPDEVSKREGINAEOIVIKITDQGYVT 60
DB 1 SYELGLYQARTYKNNRVSVIDGKATOKTENLTPDEVSKREGINAEOIVIKITDQGYVT 60
OY 61 SHGDHYHYNGKVPYDAIIESEELMKDPYKDKDINEVGVGVIVIKDGYYYYLKDA 120
DB 61 SHGDHYHYNGKVPYDAIIESEELMKDPYKDKDINEVGVGVIVIKDGYYYYLKDA 120
OY 121 AHADNVRTKEEINRQKSHQREGGTPRNDGAVALARSGRYTTDDGYIFNADIIEDT 180
DB 121 AHADNVRTKEEINRQKSHQREGGTPRNDGAVALARSGRYTTDDGYIFNADIIEDT 180
OY 181 GDAYIVPHGDHYHYIPKNELSASELAABAFISGRGNISNRTYRONSNTSRNWPVS 240
DB 181 GDAYIVPHGDHYHYIPKNELSASELAABAFISGRGNISNRTYRONSNTSRNWPVS 240
OY 241 VSNPGTNTNTNSNTNSQASQSDIDSLKQLYKLPLOSRYVSDGLVPDPAITRT 300
DB 241 VSNPGTNTNTNSNTNSQASQSDIDSLKQLYKLPLOSRYVSDGLVPDPAITRT 300
OY 301 ARGVAVPHGDHYHYIPYSQMSLEERIRIIPLYRSNHWVDSRPEQSPQPTPEPSPG 360
DB 301 ARGVAVPHGDHYHYIPYSQMSLEERIRIIPLYRSNHWVDSRPEQSPQPTPEPSPG 360
OY 361 POPAPNLKIDNSSLSVQVVRVGVGVYFEEKIGIRYFADLPBETVYNLESKSKSES 420
DB 361 POPAPNLKIDNSSLSVQVVRVGVGVYFEEKIGIRYFADLPBETVYNLESKSKSES 420
OY 421 VSHITLAKENAVPDDOEFYDKAYMLTEAHKALFXNKGNSDFQALDKLERLDESTN 480
DB 421 VSHITLAKENAVPDDOEFYDKAYMLTEAHKALFXNKGNSDFQALDKLERLDESTN 480
OY 481 KEKLVDDLAPLAPITHEBERLGPNSQIEYTEDEVRIAQDLADKYTTSQGYIFDEHDIISD 540
DB 481 KEKLVDDLAPLAPITHEBERLGPNSQIEYTEDEVRIAQDLADKYTTSQGYIFDEHDIISD 540
OY 541 EGDAYVTPHMGSHWIGDLSDEKKAQAQAYTEKKGILPPSPDADVQANPTGDSAAIY 600
DB 541 EGDAYVTPHMGSHWIGDLSDEKKAQAQAYTEKKGILPPSPDADVQANPTGDSAAIY 600
OY 601 NRVGGEKRIPLVRLPYWVEHTVEVKNGLIIPKHCHYNIKFAWPDHITYKAPNGYTLSD 660
DB 601 NRVGGEKRIPLVRLPYWVEHTVEVKNGLIIPKHCHYNIKFAWPDHITYKAPNGYTLSD 660
OY 661 LFAITIKYVEHPDERPHSNDGMASEHVILGKSHSDPNKNFKADEEVEETPAEPEVP 720
DB 661 LFAITIKYVEHPDERPHSNDGMASEHVILGKSHSDPNKNFKADEEVEETPAEPEVP 720
OY 721 QVETEKVEAQKAEAVLLAKYTDSSLKANATETLAGLRNNLTLOIMNNSIMAEEKLLA 780
DB 721 QVETEKVEAQKAEAVLLAKYTDSSLKANATETLAGLRNNLTLOIMNNSIMAEEKLLA 780
OY 781 LKGSNPSVSKEKIN 796
DB 781 LKGSNPSVSKEKIN 796

```

RESULT 3
 ABU01598
 ID ABU01598 standard; Protein; 802 AA.

XX ABU01598;
 XX 11-FEB-2003 (first entry)
 DT

```

XX DE S. pneumoniae type 4 strain protein from coding region #174.
XX XX Bacterial meningitis; pneumonia; sepsis; otitis media;
XX KM ear infection; antiinflammatory; antibacterial; immunostimulant;
XX KW auditory; respiratory; gene therapy; vaccine.
XX OS Streptococcus pneumoniae type 4 strain.
XX XX WO200277021-A2.
XX XX 03-OCT-2002.
XX PD 27-MAR-2002; 2002WO-1B02163.
XX XX 27-MAR-2001; 2001GB-0007658.
XX ER (CHIR-) CHIRON SPA.
XX PA (GENO-) INST GENOMIC RES.
XX XX Maignant V, Tettelin H, Fraser C;
PI WPI; 2003-040579/03.
XX DR N-PSDB; ABX06886.
XX DR
XX PT New proteins and nucleic acid molecules from Streptococcus pneumoniae,
PT useful as medicaments for treating a disease or infection
PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
PT or ear infection
PT
XX Claim 1; SEQ ID No 2348; 56bp; English.
XX PS
XX CC The invention relates to a protein comprising or having at least 50%
XX CC identity to any of the 2469 amino acid sequences, identified in the
XX CC specification (available on a computer readable format), or its fragment,
XX CC expressed from 2469 of 2489 identified DNA coding regions from the
XX CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
XX CC AB556654. Also included are an antibody which binds one of the
XX CC proteins, treating a patient by administering the protein, DNA or
XX CC antibody (in a composition), a kit comprising first and second primers,
XX CC which are the nucleic acid cited above or fragments between nucleotides
XX CC 8-100 of a sequence not defined in the specification, for amplifying a
XX CC target sequence contained within a Streptococcus nucleic acid sequence,
XX CC where the first primer is substantially complementary to the target
XX CC sequence and the second primer is substantially complementary to the
XX CC complement of the target sequence, and where the pairs of the primers
XX CC having substantial complementarity define the termin of the target
XX CC sequence to be amplified, assay comprising contacting a test compound
XX CC with the protein, and determining whether the test compound binds to the
XX CC protein and a Streptococcus pneumoniae bacterium, where one or more
XX CC genes encoding the proteins has been rendered inactive. The proteins,
XX CC nucleic acid molecules, antibody and compositions are useful as
XX CC medicaments for treating or preventing a disease or infection due to
XX CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia,
XX CC sepsis, otitis media or ear infection. They are also useful in developing
XX CC vaccines, diagnostics and antibiotics. The methods are useful for
XX CC identifying immunodominant proteins. The present sequence is one of
XX CC the 2469 proteins expressed by the identified coding regions from the
XX CC genomic sequence.
XX CC Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic
XX CC format directly from WPIO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX XX
XX SQ Sequence 802 AA;

```

Query Match 87.3%; Score 695; DB 24; Length 802;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 SYELGLYQARTYKNNRVSVIDGKATOKTENLTPDEVSKREGINAEOIVIKITDQGYVT 60
DB 7 SYELGLYQARTYKNNRVSVIDGKATOKTENLTPDEVSKREGINAEOIVIKITDQGYVT 66

```

QY		61	SHGDHYHYNGVVPDAIISEELLMKDPVYKLDEDIINVEVKGYYIKYDGYKYVYLKXA	120
Dp		67	SHGDHYHYNGVVPDAIISELLMKDPYKLKDEDIVNEVKGGYIKVDGKYVYLKXA	126
QY		121	AHADVRTEKEINRQKHQSQRREGTPPNDGVALAFSQGRITTDGVIFFNADIIEDT	180
Dp		127	AHADVRTEKEINRQKHQSQRREGTPPNDGAVALARQGRYTIDDGVIFFNADIIEDT	186
QY		181	GDAYIVPHGDHYHYPKHELASASELAABAFSGRGNTLSNRTYRRONS DNTSRTMVPS	240
Dp		187	GDAYIVPHGDHYHYPKHELSASELAAABAFSGRGNTLSNRTYRRQNSDNTRSMTWVS	246
QY		241	VSNPCTTTNTSNSNTNSQAASQSDIDBLKQLYKLPLSORHVESDGLVFPAQTTSRT	300
Dp		247	VSNPCTTTNTSNSNTNSQAASQSDIDBLKQLYKLPLSORHVESDGLVFPAQTTSRT	306
QY		301	ARGVAVPHGDHYHFPYSOMSELEERIAIIPLRYSNMWPSPREOPSPOPTPEPSPG	360
Dp		307	ARGVAVPHGDHYHFPYSOMSELEERIAIIPLRYSNMWPSPREOPSPOPTPEPSPG	366
QY		361	PQAPNLKIDSNSLVSQLVRKVGBGVBEKGISRYEAKDLPSERTVNLESKLSQKS	420
Dp		367	PQAPNLKIDSNSLVSQLVRKVGBGVBEKGISRYEAKDLPSERTVNLESKLSQKS	426
QY		421	VSHTLTAKKENAVPRDOEFYDKAYNLLTEAHKALFYNKGRNSDFQALDKLERLNDESTN	480
Dp		427	VSHTLTAKKENAVPRDOEFYDKAYNLLTEAHKALFENKGRNSDFQALDKLERLNDESTN	486
QY		481	KEKLVDDLLAFLAPlTHPERLKQPNSQIEYTEDEVYIAQLADXYTISDGIIPEHDIIISD	540
Dp		487	KEKLVDDLLAFLAPlTHPERLKQPNSQIEYTEDEVYIAQLADXYTISDGIIPEHDIIISD	546
QY		541	EGDADVTPMHMGSHMIGKDSLDEKEVAQAATYKEKGI.LPPSPDADVKANPTGDSAAAIY	600
Dp		547	EGDADVTPMHMGSHMIGKDSLDEKEVAQAATYKEKGI.LPPSPDADVKANPTGDSAAAIY	606
QY		601	NRVKGEKRIPLVRLPYMVEHIVEVXNGNLIIPHKHGHANI.KFAMPDDHTYKAENGTYLED	660
Dp		607	NRVKGEKRIPLVRLPYMVEHIVEVXNGNLIIPHKHGHANI.KFAMPDDHTYKAENGTYLED	666
QY		661	LFATIKYYVEHDERPHSNDGWNASEHVLGKKDHSEDNKNFKADEEPVEETPAPEVP	720
Dp		667	LFATIKYYVEHDERPHSNDGWNASEHVLGKKDHSEDNKNFKADEEPVEETPAPEVP	726
QY		721	OVERTEKVEAOLEAEVELLAKTVDSLSKANATEITAGLRNNLTLOIMDNNS IMAEAEXLA	780
Dp		727	OVERTEKVEAOLEAEVELLAKTVDSLSKANATEITAGLRNNLTLOIMDNNS IMAEAEXLA	786
QY		781	LLKGSNPSSVSXEKXIN 796	
Dp		787	LLKGSNPSSVSXEKXIN 802	
RESULT 4				
AAB01468				
ID	AAB01468 standard; Protein; 819 AA.			
XX				
AC	AAB01468;			
XX				
DT	20-OCT-2000 (first entry)			
XX				
DE	Recombinant variant of Sp36 (Sp36A) of S. pneumoniae.			
XX				
KW	Streptococcus pneumoniae; infection; vaccine; coiled coil region; histidine triad residue; sp36; antibody; otitis media; nasopharyngeal infection; bronchial infection; bronchitis; sepsis; meningitis; lobar pneumonia.			
KW				
OS	Streptococcus pneumoniae.			
XX				
Key	Location/Qualifiers			
FT	Region 63..68			

Query	Match	Best local similarity	795; Conservative	87.3%; Pred. No. 0; Mismatches	Score 695; DB 21; Length 819;	Indels	Gaps
FT	Region	/label= Histidine triad residue	118..145				
FT	Region	/label= Coiled coil region	189..194				
FT	Region	/label= Histidine triad residue	309..314				
FT	Region	/label= Histidine triad residue	406..434				
FT	Region	/label= Coiled coil region	462..493				
FT	Region	/label= Coiled coil region	550..555				
FT	Region	/label= Histidine triad residue	634..639				
FT	Region	/label= Histidine triad residue	724..751				
XX	Region	/label= Coiled coil region					
PM	WO20037105-A2.						
PD	29-JUN-2000.						
PF	21-DEC-1999; 99WO-US30390.						
PR	21-DEC-1998; 98US-0113048.						
XX	(MEDI-) MEDIMUNE INC.						
PI	Johnson LS, Koenig S, Adamou JE;						
XX	WPI: 2000-452129/39.						
DR	N-PSDB; AAA47604.						
XX	Vaccine useful for prophylaxis and treatment of pneumococcal infections						
PT	such as otitis media, nasopharyngeal and bronchial infections,						
PT	comprises Streptococcus pneumoniae proteins						
XX	Claim 1; Page 61-64; 70pp; English.						
XX	Although a number of proteins have been suggested as being involved						
CC	in the pathogenicity of Streptococcus pneumoniae, there still remains						
CC	a need to identify polypeptides having epitopes in common from						
CC	various strains of S. pneumoniae in order to utilise such						
CC	polypeptides in vaccines to protect against a wide variety of						
CC	S. pneumoniae. New vaccine compositions are described which comprise a						
CC	Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino						
CC	acids in length that comprise at least one histidine triad residue						
CC	(HXXHX) or a coiled-coil region, or an antibody directed against						
CC	these features. The vaccine is useful in protecting against infection						
CC	by Streptococcus pneumoniae. The vaccine composition comprising						
CC	antibodies to its useful for passive immunization for treating						
CC	pneumococcal infections which includes otitis media, nasopharyngeal						
CC	and bronchial infections.						
XX	Sequence 819 AA;						
XX	Query Match	87.3%; Score 695; DB 21; Length 819;					
XX	Best local similarity	99.9%; Pred. No. 0; Mismatches	1; Indels	0; Gaps	0		
XX	Matches 795; Conservative	0; Mismatches	1; Indels	0; Gaps	0		
QY	1 SYELGLYQARFVKKENRNVSYIDGKATOKTENTLPDEVSKREGINAEQIVIKITDGGYVT	60					
DB	21 SYELGLYQARFVKKENRNVSYIDGKATOKTENTLPDEVSKREGINAEQIVIKITDGGYVT	80					
QY	61 SHGDHYHYHYNGKVPYDAIISEELMKDPNYKDKEDIINEVKGQYIVIKDGYKYYVYLKDA	120					
DB	81 SHGDHYHYHYNGKVPYDAIISEELMKDPNYKDKEDIINEVKGQYIVIKDGYKYYVYLKDA	140					
QY	121 AAADNVPRKEINIQKQEHSHQREGGTFRNGAVAVLARSQGGYTTDDGTFNAAADIEPT	180					
DB	141 AAADNVPRKEINIQKQEHSHQREGGTFRNGAVAVLARSQGGYTTDDGTFNAAADIEPT	200					
QY	181 GDAIVTPGTDGHHYIIPKNELASBELAAEAFLSGGRGNLSNRTYRRONSDNTRTNWVPS	240					

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Db 201 GDAYVPHGDHYHYIPKNELSASELAAAEAFISGNGNSNSTRYRQNSDNTSRTNWPS 260
Qy 241 VSNNGTTNTNSNTNSOASQSDNDISLKQYKPLSQRHVSDPLVDPQITSTRT 300
Db 261 VSNNGTTNTNSNTNSOASQSDNDISLKQYKPLSQRHVSDPLVDPQITSTRT 320
Qy 301 ARGVAVPHGDHYHYIPYSQMSLEERIRIIRPLRYSNHWVPDSRPEQSPQPTPEPSG 360
Db 321 ARGVAVPHGDHYHYIPYSQMSLEERIRIIRPLRYSNHWVPDSRPEQSPQPTPEPSG 380
Qy 361 POPAPNKLIDNSNLVSQLVKRVGEGYVPEEKGISRYVPAKDLPSSETVKNLESKLSKQES 420
Db 381 POPAPNKLIDNSNLVSQLVKRVGEGYVPEEKGISRYVPAKDLPSSETVKNLESKLSKQES 440
Qy 421 VSHLTAKENAVAPDQEFYDQKAYNLLTEAHKALFXNKGKNSDFQALDKLERLNDSTN 480
Db 441 VSHLTAKENAVAPDQEFYDQKAYNLLTEAHKALFXNKGKNSDFQALDKLERLNDSTN 500
Qy 481 KEKLVDDLALFAPITTPHERLQKPNQSEIYTEDEVRIAQADKYTSDGYIFDEHDIISD 540
Db 501 KEKLVDDLALFAPITTPHERLQKPNQSEIYTEDEVRIAQADKYTSDGYIFDEHDIISD 560
Qy 541 EGDAYVTPHMGSHWIGKDSLSDKEKVAQAAYTEKGIILPPSPDADVKANPTGDSAAIY 600
Db 561 EGDAYVTPHMGSHWIGKDSLSDKEKVAQAAYTEKGIILPPSPDADVKANPTGDSAAIY 620
Qy 601 NRVAGEKRIPLVRLPYMVEHTEVEVNGNLII PKKHYNINIKFAMWDDHTYKAPNGYTLSD 660
Db 621 NRVAGEKRIPLVRLPYMVEHTEVEVNGNLII PKKHYNINIKFAMWDDHTYKAPNGYTLSD 680
Qy 661 LFATIKYVVEHDEPHSDNGMGNASEHVLGKKDSEDPNNKFKADEEVEETPAPEVP 720
Db 681 LFATIKYVVEHDEPHSDNGMGNASEHVLGKKDSEDPNNKFKADEEVEETPAPEVP 740
Qy 721 QVETEKVEAQKEAEVLLAKYTDSSLKANATETTLAQLNNLTLOIMDNNSIMAEKELLA 780
Db 741 QVETEKVEAQKEAEVLLAKYTDSSLKANATETTLAQLNNLTLOIMDNNSIMAEKELLA 800
Qy 781 LKGSNPSVSKEKIN 796
Db 801 LKGSNPSVSKEKIN 816

RESULT 5
AAB12728
ID AAB12728 standard; Protecin, 334 AA.
XX
AC AAB12728;
XX
DT 21-NOV-2000 (first entry)
XX
DE Streptococcus pneumoniae BVH-11A protein antigen SEQ ID NO:61.
XX
KW Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KW otitis media; pneumonia; immunisation; bactericidal.
XX
OS Streptococcus pneumoniae.
XX
PN WO200039299-A2.
XX
PD 06-JUL-2000.
XX
PF 20-DEC-1999; 99WO-CA01218.
XX
PR 23-DEC-1998; 98US-0113800.
XX
PA (BIOC-) BIOCHEM PHARMA INC.
XX
PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
XX
DR WPI; 2000-452397/39.

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```

XX
PT Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT otitis media, bacteraemia and/or pneumonia -
XX
PS Claim 18; Fig 26; 106pp; English.
XX
CC The present invention describes nucleic acids (I) encoding protein
CC antigens (II) from Streptococcus pneumoniae. The protein antigens
CC have bactericidal activity. The nucleic acids, encoding the proteins
CC antigens, may be used for the recombinant production of the proteins
CC they encode. The protein antigens may then be used as vaccines for the
CC prevention and treatment of Streptococcal infections in mammals
CC (especially humans) which result in, e.g. meningitis, otitis media,
CC bacteraemia and/or pneumonia. The present sequence represents the
CC S. pneumoniae BVH-11A protein antigen.
XX
SQ Sequence 334 AA;
Query Match 10.1%; Score 80; DB 21; Length 334;
Best Local Similarity 100.0%; Pred. No. 2,6e-68;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 TVKENNRVSYIDGKQATQKTEMLTPDEVSKREGINAEQIVYKITDQGVYSHGHHYNN 70
Db 12 TVKENNRVSYIDGKQATQKTEMLTPDEVSKREGINAEQIVYKITDQGVYSHGHHYNN 71
Qy 71 GKVPYDAIISBELMKDPNY 90
Db 72 GKVPYDAIISBELMKDPNY 91

RESULT 6
AAU84027
ID AAU84027 standard; Peptide, 334 AA.
XX
AC AAU84027;
XX
DT 08-MAY-2002 (first entry)
XX
DE Truncated variant of S. pneumoniae BVH-11, BVH-11A.
XX
KW BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
KW pneumonia; streptococcal bacterial infection; mutant; mutein.
XX
OS Streptococcus pneumoniae.
XX
PN WO200198334-A2.
XX
PD 27-DEC-2001.
XX
PF 19-JUN-2001; 2001WO-CA00908.
XX
PR 20-JUN-2000; 2000US-212683P.
XX
PA (SHIR-) SHIRE BIOCHEM INC.
XX
PI Hamel J, Quillet C, Charland N, Martin D, Brodeur B;
XX
DR WPI; 2002-122272/16.
XX
PT New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
PT epitope-bearing polypeptides, useful as vaccine components for treating
PT or preventing Streptococcal infections such as otitis media,
PT meningitis, and bacteraemia -
XX
PS Example 1; Page -; 113pp; English.
XX
CC The invention describes an isolated polypeptide (I) with 70-90*
CC identity to Streptococcus pneumoniae protein BVH-3, BVH-11, variants of
CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC comprising (I) is useful for therapeutic or prophylactic treatment of
CC meningitis, otitis media, bacteraemia or pneumonia infection in an

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individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus pyogenes, group B Streptococcus such as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. norcardia or Streptococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a truncate of a Streptococcus pneumoniae gene used to obtain antigenic peptides, described in the method of the invention.

Note: This sequence does not appear in the specification but has been created according to information given in the invention.

Sequence 334 AA;

Query Match 10.1%; Score 80; DB 23; Length 334;
Best Local Similarity 100.0%; Pred. No. 2.6e-68;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 TVKENNRVSYIDGKATQKTEMLTPDEVSKREGINAEOIVIKITDQGYVTSFGDHYHYN 70
DB 12 TVKENNRVSYIDGKATQKTEMLTPDEVSKREGINAEOIVIKITDQGYVTSFGDHYHYN 71
OY 71 GKVPYDAIISBELMKDPNY 90
DB 72 GKVPYDAIISBELMKDPNY 91

RESULT 7

AAB12745
ID AAB12745 standard; Protein; 690 AA.

AC AAB12745;

DT 23-NOV-2000 (first entry)

XX Streptococcus pneumoniae NEM16 protein antigen SEQ ID NO:79.

XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KM prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KW otitis media; pneumonia; immunisation; bactericidal.

XX Streptococcus pneumoniae.

OS Streptococcus pneumoniae.

PN WO20039299-A2.

XX 06-JUL-2000.

XX 20-DEC-1999; 99WO-CA01218.

XX 23-DEC-1998; 98US-0113800.

XX (BIOC-) BIOCHEM PHARMA INC.

XX Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;

XX WPI, 2000-452397/39.

XX Streptococcal antigens useful for vaccinating against e.g. meningitis,

XX otitis media, bacteraemia and/or pneumonia -

XX Claim 18; Fig 44; 106pp; English.

XX The present invention describes nucleic acids (I) encoding protein
CC antigens (II) from Streptococcus pneumoniae. The protein antigens
CC have bactericidal activity. The nucleic acids, encoding the protein
CC antigens, may be used for the recombinant production of the proteins
CC they encode. The protein antigens may then be used as vaccines for the

CC prevention and treatment of Streptococcal infections in mammals
CC (especially humans) which result in, e.g. meningitis, otitis media,
CC bacteraemia and/or pneumonia. The present sequence represents the
CC S. pneumoniae NEM16 protein antigen.

Sequence 690 AA;

Query Match 10.1%; Score 80; DB 21; Length 690;
Best Local Similarity 100.0%; Pred. No. 5e-68;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 TVKENNRVSYIDGKATQKTEMLTPDEVSKREGINAEOIVIKITDQGYVTSFGDHYHYN 70
DB 12 TVKENNRVSYIDGKATQKTEMLTPDEVSKREGINAEOIVIKITDQGYVTSFGDHYHYN 71
OY 71 GKVPYDAIISBELMKDPNY 90
DB 72 GKVPYDAIISBELMKDPNY 91

RESULT 8

AAU84093
ID AAU84093 standard; Peptide; 690 AA.

AC AAU84093;

DT 08-MAY-2002 (first entry)

XX Truncated variant of S. pneumoniae BVH-11, NEM16.

XX BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;

KW pneumonia; streptococcal bacterial infection; mutant; munein.

XX Streptococcus pneumoniae.

XX WO200198334-A2.

XX 27-DEC-2001.

XX 19-JUN-2001; 2001WO-CA00908.

XX 20-JUN-2000; 2000US-212683P.

XX (SHIR-) SHIRE BIOCHEM INC.

XX Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;

XX WPI, 2002-122272/16.

XX New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
PT epitope-bearing polypeptides, useful as vaccine components for treating
PT or preventing streptococcal infections such as otitis media,
XX meningitis, and bacteraemia -

XX Example 1; Page -; 113pp; English.

XX The invention describes an isolated polypeptide (I) with 70-90%
CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC comprising (I) is useful for therapeutic or prophylactic treatment of
CC meningitis, otitis media, bacteraemia or pneumonia infection in an
CC individual susceptible to these disorders. (II) is also useful for
CC therapeutic or prophylactic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. norcardia or
CC Streptococcus aureus) in an individual susceptible to the infection.
CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for S. pneumoniae infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating S. pneumonia nucleic acid in a sample for

CC diagnosing streptococcal infections. This sequence represents a truncate
CC of a Streptococcus pneumoniae gene used to obtain antigenic peptides,
CC described in the method of the invention.
CC Note: This sequence does not appear in the specification but has
CC been created according to information given in the invention.

XX Sequence 690 AA;

Query Match 10.1%; Score 80; DB 23; Length 690;
Best Local Similarity 100.0%; Pred. No. 5e-68;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TVKENNRVSYIDGKATQKTENLTPDEVSKREGINAQIVIKITDQGYVTSHGHHYNN 70
Db 12 TVKENNRVSYIDGKATQKTENLTPDEVSKREGINAQIVIKITDQGYVTSHGHHYNN 71

Qy 71 GKVPYDAIISEELMKDPNY 90
Db 72 GKVPYDAIISEELMKDPNY 91

RESULT 9

AAB12727
ID AAB12727 standard; Protein; 821 AA.

XX AAB12727;

DT 21-NOV-2000 (first entry)

XX Streptococcus pneumoniae BVH-11M protein antigen SEQ ID NO:60.

XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KW otitis media; pneumonia; immunisation; bactericidal.

XX Streptococcus pneumoniae.

PN WO200039299-A2.

PD 06-JUL-2000.

PF 20-DEC-1999; 99WO-CA01218.

PR 23-DEC-1998; 98US-0113800.

PA (BIOC-) BIOCHEM PHARMA INC.

P1 Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;

DR WPI; 2000-452397/39.

XX Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT otitis media, bacteraemia and/or pneumonia -

PS Claim 18; Fig 25; 106pp; English.

XX The present invention describes nucleic acids (I) encoding protein
CC antigens (II) from Streptococcus pneumoniae. The protein antigens
CC have bactericidal activity. The nucleic acids, encoding the protein
CC antigens, may be used for the recombinant production of the proteins
CC they encode. The protein antigens may then be used as vaccines for the
CC prevention and treatment of Streptococcal infections in mammals
CC (especially humans) which result in, e.g. meningitis, otitis media,
CC bacteraemia and/or pneumonia. The present sequence represents the
CC S. pneumoniae BVH-11M protein antigen.

XX Sequence 821 AA;

Query Match 10.1%; Score 80; DB 21; Length 821;

Best Local Similarity 100.0%; Pred. No. 5.8e-68;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TVKENNRVSYIDGKATQKTENLTPDEVSKREGINAQIVIKITDQGYVTSHGHHYNN 70

Db 12 TVKENNRVSYIDGKATQKTENLTPDEVSKREGINAQIVIKITDQGYVTSHGHHYNN 71
Qy 71 GKVPYDAIISEELMKDPNY 90
Db 72 GKVPYDAIISEELMKDPNY 91

RESULT 10

AAB12766
ID AAB12766 standard; Protein; 821 AA.

XX AAB12766;

DT 21-NOV-2000 (first entry)

XX Streptococcus pneumoniae strain SP64 BVH-11 protein antigen.

XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KW otitis media; pneumonia; immunisation; bactericidal.

XX Streptococcus pneumoniae.

PN WO200039299-A2.

PD 06-JUL-2000.

PF 20-DEC-1999; 99WO-CA01218.

PR 23-DEC-1998; 98US-0113800.

PA (BIOC-) BIOCHEM PHARMA INC.

P1 Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;

DR WPI; 2000-452397/39.

XX Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT otitis media, bacteraemia and/or pneumonia -

PS Disclosure; Fig 12; 106pp; English.

XX The present invention describes nucleic acids (I) encoding protein
CC antigens (II) from Streptococcus pneumoniae. The protein antigens
CC have bactericidal activity. The nucleic acids, encoding the protein
CC antigens, may be used for the recombinant production of the proteins
CC they encode. The protein antigens may then be used as vaccines for the
CC prevention and treatment of Streptococcal infections in mammals
CC (especially humans) which result in, e.g. meningitis, otitis media,
CC bacteraemia and/or pneumonia. The present sequence represents a
CC S. pneumoniae BVH-11 protein antigen, from the present invention.

XX Sequence 821 AA;

Query Match 10.1%; Score 80; DB 21; Length 821;

Best Local Similarity 100.0%; Pred. No. 5.8e-68;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TVKENNRVSYIDGKATQKTENLTPDEVSKREGINAQIVIKITDQGYVTSHGHHYNN 70
Db 12 TVKENNRVSYIDGKATQKTENLTPDEVSKREGINAQIVIKITDQGYVTSHGHHYNN 71

Qy 71 GKVPYDAIISEELMKDPNY 90
Db 72 GKVPYDAIISEELMKDPNY 91

RESULT 11

AAU84026
ID AAU84026 standard; Peptide; 821 AA.

XX AAU84026;

PN WO200198334-A2.
 XX
 XX 27-DEC-2001.
 PD
 XX
 XX 19-JUN-2001; 2001WO-CA00908.
 PF
 XX 20-JUN-2000; 2000US-212683P.
 PR
 XX (SHIR-) SHIRE BIOCHEM INC.
 PA
 XX Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
 PI WPI; 2002-122272/16.
 DR N-PSDBJ; ABK15103.
 XX
 XX New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
 PT epitope-bearing polypeptides, useful as vaccine components for treating
 PT or preventing streptococcal infections such as otitis media,
 PT meningitis, and bacteraemia -
 XX
 XX Example 1; Fig 7; 113pp; English.
 PS
 XX The invention describes an isolated polypeptide (I) with 70-90%
 CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
 CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
 CC comprising (I) is useful for therapeutic or prophylactic treatment of
 CC meningitis, otitis media, bacteraemia or pneumonia infection in an
 CC individual susceptible to these disorders. (II) is also useful for
 CC therapeutic or prophylactic treatment of any streptococcal bacterial
 CC infection (e.g., caused by Streptococcus pneumoniae, group A
 CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
 CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardiae or
 CC Staphylococcus aureus) in an individual susceptible to the infection.
 CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
 CC techniques. The Streptococcus polypeptides are useful in a diagnostic
 CC test for S. pneumoniae infection. (III) is useful for designing DNA
 CC probes for use in detecting the presence of Streptococcus in a biological
 CC sample suspected of containing the bacteria. The DNA probes may also be
 CC used for detecting circulating S. pneumonia nucleic acid in a sample for
 CC diagnosing streptococcal infections. This is the amino acid sequence of
 CC Streptococcus pneumoniae protein BVH-11, used to create the antigenic
 CC peptides described in the method of the invention.
 CC
 CC Sequence 840 AA;
 XX
 XX
 XX Query Match 10.1%; Score 80; DB 23; Length 840;
 Best Local Similarity 100.0%; Pred. No. 6e-68;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 TVKENNRVSYIDGKATOKTENLTPEDEVSKREGINAQIVIKITDQGYVTSHGHHYNN 70
 Db 31 TVKENNRVSYIDGKATOKTENLTPEDEVSKREGINAQIVIKITDQGYVTSHGHHYNN 90
 QY 71 GKVPYDAIISSELLMKDPNY 90
 Db 91 GKVPYDAIISSELLMKDPNY 110
 RESULT 14
 AAB12764
 ID AAB12764 standard; Protein; 805 AA.
 AC AAB12764;
 XX
 XX 21-NOV-2000 (first entry)
 DT
 XX Streptococcus pneumoniae strain JNR7/87 BVH-11 protein antigen.
 DE
 XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
 KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
 KM otitis media; pneumonia; immunisation; bactericidal.
 XX
 XX Streptococcus pneumoniae.
 OS

XX
 PN WO200039299-A2.
 XX
 XX 06-JUL-2000.
 PD
 XX
 XX 20-DEC-1999; 99WO-CA01218.
 PF
 XX 23-DEC-1998; 98US-0113800.
 PR
 XX (BIOC-) BIOCHEM PHARMA INC.
 PA
 XX Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
 PI WPI; 2000-452397/39.
 DR
 XX
 XX Streptococcal antigens useful for vaccinating against e.g. meningitis,
 PT otitis media, bacteraemia and/or pneumonia -
 PT Disclosure; Fig 12; 106pp; English.
 PS
 XX The present invention describes nucleic acids (I) encoding protein
 CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein
 CC antigens, may be used for the recombinant production of the proteins
 CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals
 CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence represents a
 CC S. pneumoniae BVH-11 protein antigen, from the present invention.
 CC
 CC Sequence 805 AA;
 XX
 XX
 XX Query Match 7.5%; Score 60; DB 21; Length 805;
 Best Local Similarity 100.0%; Pred. No. 1.2e-48;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 31 ENLTPDEVSKREGINAQIVIKITDQGYVTSHGHHYNNKVPYDAIISSELLMKDPNY 90
 Db 33 ENLTPDEVSKREGINAQIVIKITDQGYVTSHGHHYNNKVPYDAIISSELLMKDPNY 92
 RESULT 15
 AAB12765
 ID AAB12765 standard; Protein; 807 AA.
 AC AAB12765;
 XX
 XX 21-NOV-2000 (first entry)
 DT
 XX Streptococcus pneumoniae strain SP63 BVH-11 protein antigen.
 DE
 XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
 KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
 KM otitis media; pneumonia; immunisation; bactericidal.
 XX
 XX Streptococcus pneumoniae.
 OS
 PN WO200039299-A2.
 XX
 XX 06-JUL-2000.
 PD
 XX
 XX 20-DEC-1999; 99WO-CA01218.
 PF
 XX 23-DEC-1998; 98US-0113800.
 PR
 XX (BIOC-) BIOCHEM PHARMA INC.
 PA
 XX Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
 PI WPI; 2000-452397/39.
 DR
 XX
 XX Streptococcal antigens useful for vaccinating against e.g. meningitis,
 PT otitis media, bacteraemia and/or pneumonia -
 PT

```

XX  Disclosure; Fig 12; 106pp; English.
PS
XX  The present invention describes nucleic acids (I) encoding protein
CC  antigens (II) from Streptococcus pneumoniae. The protein antigens
CC  have bactericidal activity. The nucleic acids, encoding the protein
CC  antigens, may be used for the recombinant production of the proteins
CC  they encode. The protein antigens may then be used as vaccines for the
CC  prevention and treatment of Streptococcal infections in mammals
CC  (especially humans) which result in, e.g. meningitis, otitis media,
CC  bacteraemia and/or pneumonia. The present sequence represents a
CC  S. pneumoniae BVH-11 protein antigen, from the present invention.
XX
SQ  Sequence 807 AA;

Query Match 7.5%; Score 60; DB 21; Length 807;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  31 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYNGKVPYDAIISEBLMKDPNY 90
DB  33 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYNGKVPYDAIISEBLMKDPNY 92

RESULT 16
AAB12760
XX  AAB12760 standard; Protein; 811 AA.
XX
XX  AAB12760;
XX
DT  21-NOV-2000 (first entry)
XX
DE  Streptococcus pneumoniae strain P4241 BVH-11 protein antigen.
XX
KM  Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KM  prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KM  otitis media; pneumonia; immunisation; bactericidal.
XX
OS  Streptococcus pneumoniae.
XX
PN  WO200039299-A2.
XX
XX  06-JUL-2000.
XX
PF  20-DEC-1999; 99WO-CA01218.
XX
PR  23-DEC-1998; 98US-0113800.
XX
PA  (BIOC-) BIOCHEM PHARMA INC.
XX
PI  Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
XX  WPI; 2000-452397/39.
XX
PT  Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT  otitis media, bacteraemia and/or pneumonia -
XX
PS  Disclosure; Fig 12; 106pp; English.
XX
XX  The present invention describes nucleic acids (I) encoding protein
CC  antigens (II) from Streptococcus pneumoniae. The protein antigens
CC  have bactericidal activity. The nucleic acids, encoding the protein
CC  antigens, may be used for the recombinant production of the proteins
CC  they encode. The protein antigens may then be used as vaccines for the
CC  prevention and treatment of Streptococcal infections in mammals
CC  (especially humans) which result in, e.g. meningitis, otitis media,
CC  bacteraemia and/or pneumonia. The present sequence represents a
CC  S. pneumoniae BVH-11 protein antigen, from the present invention.
XX
SQ  Sequence 811 AA;

Query Match 7.5%; Score 60; DB 21; Length 811;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  31 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYNGKVPYDAIISEBLMKDPNY 90
DB  33 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYNGKVPYDAIISEBLMKDPNY 92

RESULT 17
AAB12761
XX  AAB12761 standard; Protein; 811 AA.
XX
XX  AAB12761;
XX
DT  21-NOV-2000 (first entry)
XX
DE  Streptococcus pneumoniae strain WU2 BVH-11 protein antigen.
XX
KM  Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KM  prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KM  otitis media; pneumonia; immunisation; bactericidal.
XX
OS  Streptococcus pneumoniae.
XX
PN  WO200039299-A2.
XX
XX  06-JUL-2000.
XX
PF  20-DEC-1999; 99WO-CA01218.
XX
PR  23-DEC-1998; 98US-0113800.
XX
PA  (BIOC-) BIOCHEM PHARMA INC.
XX
PI  Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
XX  WPI; 2000-452397/39.
XX
PT  Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT  otitis media, bacteraemia and/or pneumonia -
XX
PS  Disclosure; Fig 12; 106pp; English.
XX
XX  The present invention describes nucleic acids (I) encoding protein
CC  antigens (II) from Streptococcus pneumoniae. The protein antigens
CC  have bactericidal activity. The nucleic acids, encoding the protein
CC  antigens, may be used for the recombinant production of the proteins
CC  they encode. The protein antigens may then be used as vaccines for the
CC  prevention and treatment of Streptococcal infections in mammals
CC  (especially humans) which result in, e.g. meningitis, otitis media,
CC  bacteraemia and/or pneumonia. The present sequence represents a
CC  S. pneumoniae BVH-11 protein antigen, from the present invention.
XX
SQ  Sequence 811 AA;

Query Match 7.5%; Score 60; DB 21; Length 811;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  31 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYNGKVPYDAIISEBLMKDPNY 90
DB  33 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYNGKVPYDAIISEBLMKDPNY 92

RESULT 18
AAB12762
XX  AAB12762 standard; Protein; 811 AA.
XX
XX  AAB12762;
XX
DT  21-NOV-2000 (first entry)
XX
DE  Streptococcus pneumoniae strain A66 BVH-11 protein antigen.
XX

```

XX	DR		WPI; 2000-452397/39.
XX	PT	Streptococcal antigens useful for vaccinating against e.g. meningitis,	
XX	PT	otitis media, bacteremia and/or pneumonia -	
XX	PS	Disclosure; Fig 12; 106pp; English.	
XX	XX		
CC	CC	The present invention describes nucleic acids (I) encoding protein	
CC	CC	antigens (II) from Streptococcus pneumoniae. The protein antigens	
CC	CC	have bactericidal activity. The nucleic acids, encoding the protein	
CC	CC	antigens, may be used for the recombinant production of the proteins	
CC	CC	they encode. The protein antigens may then be used as vaccines for the	
CC	CC	prevention and treatment of Streptococcal infections in mammals	
CC	CC	(especially humans) which result in, e.g. meningitis, otitis media,	
CC	CC	bacteremia and/or pneumonia. The present sequence represents a	
CC	CC	S. pneumoniae BVH-11 protein antigen, from the present invention.	
XX	XX		
SO	Sequence	811 AA;	
Oy	Query Match	7.5%; Score 60; DB 21; Length 811;	
	Best Local Similarity	100.0%; Pred. No. 1.2e-48;	
	Matches 60; Conservative	0; Mismatches 0; Indels 0; Gaps	
Dn	31 ENLTPDVSRRGINAEQIVIKITDGGYTSHEGDHYHYNGKVPDAIISSEILMDPNY	900	
	33 ENLTPDVSRRGINAEQIVIKITDGGYTSHEGDHYHYNGKVPDAIISSEILMDPNY	920	
RESULT 20			
AAB12756	ID AAB12756 standard; Protein; 816 AA.		
AC	AAB12756;		
XX			
DT	21-NOV-2000 (first entry)		
XX			
DB	Streptococcus pneumoniae strain P4241 BVH-11-2 protein antigen.		
XX			
KM	Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;		
KW	prophylaxis; therapy; infection; diagnosis; meningitis; bacteremia;		
KX	otitis media; pneumonia; immunisation; bactericidal.		
OS	Streptococcus pneumoniae.		
XX			
PN	WO200039299-A2.		
PD	06-JUL-2000.		
XX			
Pf	20-DEC-1999; 99MO-CA01218.		
XX			
PR	23-DEC-1998; 98US-0113800.		
XX			
PA	(BIOC-) BIOCHEM PHARMA INC.		
XX			
P1	Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;		
XX			
DR	WPI; 2000-452397/39.		
XX			
PT	Streptococcal antigens useful for vaccinating against e.g. meningitis,		
XX	otitis media, bacteremia and/or pneumonia -		
XX			
PS	Disclosure; Fig 12; 106pp; English.		
XX			
CC	The present invention describes nucleic acids (I) encoding protein		
CC	antigens (II) from Streptococcus pneumoniae. The protein antigens		
CC	have bactericidal activity. The nucleic acids, encoding the proteins		
CC	antigens, may be used for the recombinant production of the proteins		
CC	they encode. The protein antigens may then be used as vaccines for the		
CC	prevention and treatment of Streptococcal infections in mammals		
CC	(especially humans) which result in, e.g. meningitis, otitis media,		
CC	bacteremia and/or pneumonia. The present sequence represents a		
CC	S. pneumoniae BVH-11-2 protein antigen, from the present invention.		

[illegible]

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XX      21-NOV-2000 (first entry)
DT
XX      Streptococcus pneumoniae strain WU2 BVH-11-2 protein antigen.
DE
XX      Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW      prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KM      otitis media; pneumonia; immunisation; bactericidal.
XX
XX      Streptococcus pneumoniae.
OS
PN      WO200039299-A2.
XX
PD      06-JUL-2000.
XX
PF      20-DEC-1999; 99WO-CA01218.
XX
PR      23-DEC-1998; 98US-0113800.
XX
PA      (BIOC-) BIOCHEM PHARMA INC.
XX
PI      Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
DR      WPI; 2000-452397/39.
XX
XX      Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT      otitis media, bacteraemia and/or pneumonia -
XX
PS      Disclosure; Fig 12; 106pp; English.
XX
CC      The present invention describes nucleic acids (I) encoding protein
CC      antigens (II) from Streptococcus pneumoniae. The protein antigens
CC      have bactericidal activity. The nucleic acids, encoding the proteins
CC      antigens, may be used for the recombinant production of the proteins
CC      they encode. The protein antigens may then be used as vaccines for the
CC      prevention and treatment of Streptococcal infections in mammals
CC      (especially humans) which result in, e.g. meningitis, otitis media,
CC      bacteraemia and/or pneumonia. The present sequence represents a
CC      S. pneumoniae BVH-11-2 protein antigen, from the present invention.
SQ
Sequence      816 AA;

Query Match          7.5%; Score 60; DB 21; Length 816;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches    60; Conservative   0; Mismatches    0; Indels    .0; Gaps    0;

Cy      31 ENLTPDEVSRREGINAEQIVYIKITDGGVYMSHGHHYYNGKVPYDAIISPELLMKDPNY 90
Db      33 ENLTPDEVSRREGINAEQIVYIKITDGGVYSHGHHYYNGKVPYDAIISELLMKDPNY 92

RESULT 23
AAB12740
ID      AAB12740 standard; Protein; 819 AA.
XX
AC      AAB12740;
XX
DT      21-NOV-2000 (first entry)
XX
DE      Streptococcus pneumoniae BVH-11-2M protein antigen SEQ ID NO:73.
XX
KW      Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW      prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KW      otitis media; pneumonia; immunisation; bactericidal.
XX
OS      Streptococcus pneumoniae.
XX
PN      WO200039299-A2.
XX
PD      06-JUL-2000.
XX
PF      20-DEC-1999; 99WO-CA01218.
XX

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PR 23-DEC-1998; 98US-0113800.
 PA (BIOC-) BIOCHEM PHARMA INC.
 XX
 XX Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
 XX WPI; 2000-452397/39.
 DR
 XX Streptococcal antigens useful for vaccinating against e.g. meningitis,
 PT otitis media, bacteraemia and/or pneumonia -
 XX
 PS Claim 18; Fig 38; 106pp; English.
 XX
 CC The present invention describes nucleic acids (I) encoding protein
 CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein
 CC antigens, may be used for the recombinant production of the proteins
 CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals
 CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence represents the
 CC S. pneumoniae BVH-11-2M protein antigen.
 CC
 XX
 SQ Sequence 819 AA;
 SQ
 Query Match 7.5%; Score 60; DB 21; Length 819;
 Best Local Similarity 100.0%; Pred. No. 1.2e-48;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 31 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGHDHYHYNGKVPYDAIISSELLMKDPNY 90
 Db 33 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGHDHYHYNGKVPYDAIISSELLMKDPNY 92
 RESULT 24
 AAB12754
 ID AAB12754 standard; Protein; 819 AA.
 XX
 AC AAB12754;
 XX
 DT 21-NOV-2000 (first entry)
 XX
 DE Streptococcus pneumoniae strain SP64 BVH-11-2 protein antigen.
 XX
 KM Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen, vaccine;
 KM prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
 KM otitis media; pneumonia; immunisation; bactericidal.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN WO200039299-A2.
 XX
 PD 06-JUL-2000.
 XX
 PF 20-DEC-1999; 99WO-CA01218.
 XX
 PR 23-DEC-1998; 98US-0113800.
 XX
 PA (BIOC-) BIOCHEM PHARMA INC.
 XX
 PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
 XX WPI; 2000-452397/39.
 DR
 XX Streptococcal antigens useful for vaccinating against e.g. meningitis,
 PT otitis media, bacteraemia and/or pneumonia -
 XX
 PS Disclosure; Fig 12; 106pp; English.
 XX
 CC The present invention describes nucleic acids (I) encoding protein
 CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein
 CC antigens, may be used for the recombinant production of the proteins

CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals
 CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence represents a
 CC S. pneumoniae BVH-11-2 protein antigen, from the present invention.
 CC
 XX
 SQ Sequence 819 AA;
 SQ
 Query Match 7.5%; Score 60; DB 21; Length 819;
 Best Local Similarity 100.0%; Pred. No. 1.2e-48;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 31 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGHDHYHYNGKVPYDAIISSELLMKDPNY 90
 Db 33 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGHDHYHYNGKVPYDAIISSELLMKDPNY 92
 RESULT 25
 AAB01469
 ID AAB01469 standard; Protein; 819 AA.
 XX
 AC AAB01469;
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE Recombinant variant of Sp36 (Sp36B) of S. pneumoniae.
 XX
 KM Streptococcus pneumoniae; infection, vaccine; coiled coil region;
 KM histidine triad residue; Sp36; antibody; otitis media;
 KM nasopharyngeal infection; bronchial infection; bronchitis; sepsis;
 KM meningitis; lobar pneumonia.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN WO200037105-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 21-DEC-1999; 99WO-US30390.
 XX
 PR 21-DEC-1998; 98US-0113048.
 XX
 PA (MEDI-) MEDIMUNE INC.
 XX
 PI Johnson LS, Koenig S, Adamou JB;
 XX WPI; 2000-452129/39.
 DR N-PSDB; AAA47605.
 XX
 PT Vaccine useful for prophylaxis and treatment of pneumococcal infections
 PT such as otitis media, nasopharyngeal and bronchial infections,
 PT comprises Streptococcus pneumoniae proteins
 XX
 PS Claim 1; Page 65-69; 70pp; English.
 XX
 CC Although a number of proteins have been suggested as being involved
 CC in the pathogenicity of Streptococcus pneumoniae, there still remains
 CC a need to identify polypeptides having epitopes in common from
 CC various strains of S. pneumoniae in order to utilise such
 CC polypeptides in vaccines to protect against a wide variety of
 CC S. pneumoniae. New vaccine compositions are described which comprise a
 CC Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino
 CC acids in length that comprise at least one histidine triad residue
 CC (HxxHxx) or a coiled-coil region, or an antibody directed against
 CC these features. The vaccine is useful in protecting against infection
 CC by Streptococcus pneumoniae. The vaccine composition comprising
 CC antibodies to its useful for passive immunization for treating
 CC pneumococcal infections which includes otitis media, nasopharyngeal
 CC and bronchial infections.
 CC
 XX
 SQ Sequence 819 AA;
 SQ
 Query Match 7.5%; Score 60; DB 21; Length 819;

Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 ENLTPDEVSKREGINAEQIVIKITDQGYVTSFGDHYHYNGVPPYDAITSEELMKDPNY 90
Db 52 ENLTPDEVSKREGINAEQIVIKITDQGYVTSFGDHYHYNGVPPYDAITSEELMKDPNY 111

RESULT 26
AAU84087

ID AAU84087 standard; Peptide; 819 AA.

XX AAU84087;

DT 08-MAY-2002 (first entry)

DE Truncated variant of S. pneumoniae BVH-11-2, BVH-

XX BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;

KM pneumonia; streptococcal bacterial infection; mutant; murein.

XX Streptococcus pneumoniae.

PN WO200198334-A2.

PD 27-DEC-2001.

PF 19-JUN-2001; 2001WO-CA00908.

PR 20-JUN-2000; 2000US-212683P.

PA (SHIR-) SHIRE BIOCHEM INC.

PI Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;

DR WPI; 2002-122272/16.

PT New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
PT epitope-bearing polypeptides, useful as vaccine components for treating
PT or preventing streptococcal infections such as otitis media,
PT meningitis, and bacteraemia -

PS Example 1; Page -; 113pp; English.

XX The invention describes an isolated polypeptide (I) with 70-90%
CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC comprising (I) is useful for therapeutic or prophylactic treatment of
CC meningitis, otitis media, bacteraemia or pneumonia infection in an
CC individual susceptible to these disorders. (II) is also useful for
CC therapeutic or prophylactic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. novacardia or
CC Streptococcus aureus) in an individual susceptible to the infection.
CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for S. pneumoniae infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating S. pneumonia nucleic acid in a sample for
CC diagnosing streptococcal infections. This sequence represents a truncate
CC of a Streptococcus pneumoniae gene used to obtain antigenic peptides,
CC described in the method of the invention.
CC Note: This sequence does not appear in the specification but has
CC been created according to information given in the invention.

XX Sequence 819 AA;

Query Match 7.5%; Score 60; DB 23; Length 819;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 ENLTPDEVSKREGINAEQIVIKITDQGYVTSFGDHYHYNGVPPYDAITSEELMKDPNY 90
Db 33 ENLTPDEVSKREGINAEQIVIKITDQGYVTSFGDHYHYNGVPPYDAITSEELMKDPNY 92

RESULT 27
ABU01597

ID ABU01597 standard; Protein; 819 AA.

XX ABU01597;

DT 11-FEB-2003 (first entry)

DE S. pneumoniae type 4 strain protein from coding region #1173.

XX Bacterial meningitis; pneumonia; sepsis; otitis media;

KM ear infection; antiinflammatory; antibacterial; immunostimulant;

XX auditory; respiratory; gene therapy; vaccine.

OS Streptococcus pneumoniae type 4 strain.

PN WO200277021-A2.

PD 03-OCT-2002.

PF 27-MAR-2002; 2002WO-IB02163.

PR 27-MAR-2001; 2001GB-0007658.

PA (CHIR-) CHIRON SPA.

PI (GENO-) INST GENOMIC RES.

DR WPI; 2003-040579/03.

PT New proteins and nucleic acid molecules from Streptococcus pneumoniae,
PT useful as medicaments for treating or preventing a disease or infection
PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
PT or ear infection -

PS Claim 1; SEQ ID No 2346; 56pp; English.

XX The invention relates to a protein comprising or having at least 50%
CC identity to any of the 2469 amino acid sequences, identified in the
CC specification (available on a computer readable format), or its fragment,
CC expressed from 2469 of 2489 identified DNA coding regions from the
CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
CC ABS6454. Also included are an antibody which binds one of the
CC proteins, treating a patient by administering the protein, DNA or
CC antibody (in a composition), a kit comprising first and second primers,
CC which are the nucleic acid cited above or fragments between nucleotides
CC 8-100 of a sequence not defined in the specification, for amplifying a
CC target sequence contained within a Streptococcus nucleic acid sequence,
CC where the first primer is substantially complementary to the target
CC sequence and the second primer is substantially complementary to the
CC complement of the target sequence, and where the parts of the primers
CC having substantial complementarity define the termini of the target
CC sequence to be amplified, assay comprising contacting a test compound
CC with the protein, and determining whether the test compound binds to the
CC protein and a Streptococcus pneumoniae bacterium, where one or more
CC genes encoding the proteins has been rendered inactive. The proteins,
CC nucleic acid molecules, antibody and compositions are useful as
CC medicaments for treating or preventing a disease or infection due to
CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia,
CC sepsis, otitis media or ear infection. They are also useful in developing
CC vaccines, diagnostics and antibiotics. The methods are useful for
CC identifying immunodominant proteins. The present sequence is one of
CC the 2469 proteins expressed by the identified coding regions from the
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic

CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

SO Sequence 819 AA;

Query Match 7.5%; Score 60; DB 24; Length 819;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 ENLTPDEVSKREGINAEQIVIKITDQGYVTSBGHGHYHYNGKVPYDAIISSELMKDPNY 90
|||
DB 52 ENLTPDEVSKREGINAEQIVIKITDQGYVTSBGHGHYHYNGKVPYDAIISSELMKDPNY 111

RESULT 28

ID AAB12755 standard; Protein; 820 AA.

AC AAB12755;

DT 21-NOV-2000 (first entry)

DE Streptococcus pneumoniae strain JNR7/87 BVH-11-2 protein antigen.

XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;

KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;

KM otitis media; pneumonia; immunisation; bactericidal.

XX Streptococcus pneumoniae.

PN WO200039299-A2.

PD 06-JUL-2000.

XX 20-DEC-1999; 99WO-CA01218.

PR 23-DEC-1998; 98US-0113800.

PA (BIOC-) BIOCHEM PHARMA INC.

PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;

XX WPI; 2000-452397/39.

PT Streptococcal antigens useful for vaccinating against e.g. meningitis,

PT otitis media, bacteraemia and/or pneumonia.

XX Disclosure; Fig 12; 106pp; English.

CC The present invention describes nucleic acids (I) encoding protein

CC antigens (II) from Streptococcus pneumoniae. The protein antigens

CC have bactericidal activity. The nucleic acids, encoding the protein

CC antigens, may be used for the recombinant production of the proteins

CC they encode. The protein antigens may then be used as vaccines for the

CC prevention and treatment of Streptococcal infections in mammals

CC (especially humans) which result in, e.g. meningitis, otitis media,

CC bacteraemia and/or pneumonia. The present sequence represents a

CC S. pneumoniae BVH-11-2 protein antigen, from the present invention.

XX Sequence 820 AA;

Query Match 7.5%; Score 60; DB 21; Length 820;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 ENLTPDEVSKREGINAEQIVIKITDQGYVTSBGHGHYHYNGKVPYDAIISSELMKDPNY 90
|||
DB 33 ENLTPDEVSKREGINAEQIVIKITDQGYVTSBGHGHYHYNGKVPYDAIISSELMKDPNY 92

RESULT 29

AAV91939 standard; Protein; 826 AA.

XX AAV91939;

AC AAV91939 (first entry)

DT 19-JUL-2000

DE S. pneumoniae 92 kDa human C3-degrading protein.

KW Human C3-degrading protein; 92 kDa; immunostimulatory; vaccine;

XX inhibitor; inflammation; organ rejection; xenotransplantation.

OS Streptococcus pneumoniae.

PN WO200017370-A1.

PD 30-MAR-2000.

XX 24-SEP-1999; 99WO-US22362.

PR 24-SEP-1998; 98US-0101736.

XX 31-MAR-1999; 99US-0283094.

PA (MNU) UNIV MINNESOTA.

XX (AMCY) AMERICAN CYANAMID CO.

PI Hostetter MK, Finkel DJ, Cheng Q, Green BA, Masi AW;

XX WPI; 2000-283594/24.

DR N-PSDB; AAA08557.

PT Isolated polypeptide is used to stimulate immune system and immunize or

PT treat a mammalian subject against Streptococcus pneumoniae infection or

XX colonization

PS Claim 8; Page 55-57; 63pp; English.

XX The present sequence, isolated from Streptococcus pneumoniae, is a

CC human C3-degrading protein of about 92 kDa. This sequence may encompass

CC a smaller, approximately 20 kDa protein (see AAV91938), also having

CC human C3-degrading activity. The DNA sequences (AAA08556-57) can be

CC used for producing an immune response to Streptococcus pneumoniae in a

CC mammal. Antibodies against the proteins can be used to inhibit

CC S. pneumoniae-mediated C3 degradation. C3-mediated inflammation and

CC rejection in xenotransplantation can be inhibited by expressing the

CC nucleic acid sequences on the surface of an organ of an animal. In

CC particular, the polypeptides are useful for stimulating the immune

CC system and are effective to immunize or treat a mammalian subject

CC against Streptococcus pneumoniae infection or colonization.

XX Sequence 826 AA;

Query Match 7.5%; Score 60; DB 21; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 ENLTPDEVSKREGINAEQIVIKITDQGYVTSBGHGHYHYNGKVPYDAIISSELMKDPNY 90
|||
DB 52 ENLTPDEVSKREGINAEQIVIKITDQGYVTSBGHGHYHYNGKVPYDAIISSELMKDPNY 111

RESULT 30

AAV81662 standard; Protein; 827 AA.

XX AAV81662;

XX 24-MAY-2000 (first entry)

DE Streptococcus pneumoniae protein sequence ID311.

XX Streptococcus pneumoniae; vaccine; screening; protein antigen;

KW antibacterial; antiinflammatory; meningitis; infection; diagnosis;

XX pneumococcal disease.

XX	Streptococcus pneumoniae.
XX	WO200006737-A2.
PX	
PN	10-FEB-2000.
PD	
XX	
PF	27-JUL-1999; 99WO-GB02451.
XX	
PR	27-JUL-1998; 98GB-0016337.
XX	
PR	19-MAR-1999; 99US-0125164.
XX	
PA	(MICR-) MICROBIAL TECHNICS LTD.
XX	
PI	Gilbert CFG, Hansbro PM;
XX	
DR	WPI; 2000-195300/17.
XX	
PT	New Streptococcal protein, useful as a vaccine, for diagnosis of
XX	pneumococcal diseases and for screening agents capable of antagonizing
PT	or inhibiting expression of the protein -
PS	Claim 2, Page 99-100; 108pp; English.
XX	
CC	AAV81501 to AAV81679 represent specifically claimed protein sequences
CC	isolated from Streptococcus pneumoniae. AA05407 to AA05590 represent
CC	specifically claimed nucleotide sequences isolated from S. pneumoniae.
CC	The sequences have antibacterial and antiinflammatory properties.
CC	The protein sequences, and fragments of them, are useful as immunogens
CC	and/or antigens. The nucleotide sequences can be used in vaccines and in
CC	diagnostic assays. The proteins and nucleotides can be useful for the
CC	detection and diagnosis of S. pneumoniae. The protein sequences are also
CC	useful for screening an agent capable of antagonising, inhibiting or
CC	interfering with the function or expression of the proteins in which the
CC	agent is useful for treatment or prophylaxis of S. pneumoniae infection
CC	and meningitis. AA05591 to AA05614 represent primers used in the
CC	exemplification of the present invention.
SQ	
XX	Sequence 827 AA;
Query Match	7.5%; Score 60; DB 21; Length 827;
Best Local Similarity	100.0%; Pred. No. 1.2e-48;
Matches	60; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Dy	31 ENLTPDEVSKREGINAEQIVIKITDGYVTSHGDHYHHYNGKVPYDAIISEELMKDPNY 90 52 ENLTPDEVSKREGINAEQIVIKITDGYVTSHGDHYHHYNGKVPYDAIISEELMKDPNY 111
RESULT 31	
AAB12759	
ID	AAB12759 standard; Protein; 834 AA.
AC	AAB12759;
XX	
DT	21-NOV-2000 (first entry)
DE	Streptococcus pneumoniae strain RX1 BVH-11-2 protein antigen.
XX	
KM	Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW	prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
XX	otitis media; pneumonia; immunisation; bactericidal.
OS	Streptococcus pneumoniae.
XX	
PN	WO200039299-A2.
XX	
PD	06-JUL-2000.
XX	
PF	20-DEC-1999; 99WO-CA01218.
XX	
PR	23-DEC-1998; 98US-0113800.
XX	
PA	(BIOC-) BIOCHEM PHARMA INC.

XX	Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
PI	WPI; 2000-452397/39.
XX	
DR	Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT	otitis media, bacteraemia and/or pneumonia -
XX	
XX	Disclosure; Fig 12; 106pp; English.
XX	
CC	The present invention describes nucleic acids (I) encoding protein
CC*	antigens (II) from Streptococcus pneumoniae. The protein antigens
CC	have bactericidal activity. The nucleic acids, encoding the protein
CC	antigens, may be used for the recombinant production of the proteins
CC	they encode. The protein antigens may then be used as vaccines for the
CC	(prevention and treatment of Streptococcal infections in mammals
CC	especially humans) which result in, e.g. meningitis, otitis media,
CC	bacteraemia and/or pneumonia. The present sequence represents a
CC	S. pneumoniae BVH-11-2 protein antigen, from the present invention.
XX	
SO	Sequence 834 AA;
Query Match	7.5%; Score 60; DB 21; Length 834;
Best Local Similarity	100.0%; Pred. No. 1.2e-48;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	31 ENLTPDEVSKREGINAEQIVIKINDGCVYTSHGHHYNGKVPYDAIISELLMKDPNY 90 33 ENLPFDEVSKEGINAGQIVIKINDGCVYISHGHYHYNGKVYPYDAIISELLMKDPNY 92
Dd	
RESULT 32	
AAB12720	
ID	AAB12720 standard; Protein; 838 AA.
XX	
AC	AAB12720;
XX	
DT	21-NOV-2000 (first entry)
XX	
DE	Streptococcus pneumoniae BVH-11-2 protein antigen SEQ ID NO:14.
XX	
KM	Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW	prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
XX	otitis media; pneumonia; immunisation; bactericidal.
OS	Streptococcus pneumoniae.
XX	
FN	WO200039289-A2.
PD	06-JUL-2000.
XX	
PF	20-DEC-1999; 99WO-CA01218.
XX	
PR	23-DEC-1998; 98US-0113800.
PA	(BIOC-) BIOCHEM PHARMA INC.
PI	
PI	Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
XX	
DR	WPI; 2000-452397/39.
DR	N-PSDB; AAA65737.
PT	Streptococcal antigens useful for vaccinating against e.g. meningitis,
OT	otitis media, bacteraemia and/or pneumonia -
XX	
PS	Claim 18; Fig 17; 106pp; English.
XX	
CC	The present invention describes nucleic acids (I) encoding protein
CC	antigens (II) from Streptococcus pneumoniae. The protein antigens
CC	have bactericidal activity. The nucleic acids, encoding the protein
CC	antigens, may be used for the recombinant production of the proteins
CC	they encode. The protein antigens may then be used as vaccines for the
CC	(prevention and treatment of Streptococcal infections in mammals
CC	especially humans) which result in, e.g. meningitis, otitis media,
CC	bacteraemia and/or pneumonia. The present sequence represents a
CC	S. pneumoniae BVH-11-2 protein antigen, from the present invention.

CC (especially humans) which result in, e.g. meningitis, otitis media,
CC bacteraemia and/or pneumonia. The present sequence represents the
CC S. pneumoniae BVH-11-2 protein antigen.

XX Sequence 838 AA;

Query Match 7.5%; Score 60; DB 21; Length 838;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 31 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGHHYHYNGKVPYDAIISEELMKDPNY 90
Db 52 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGHHYHYNGKVPYDAIISEELMKDPNY 111

RESULT 33

AAB01466 standard; Protein; 838 AA.

XX AAB01466;

DT 20-OCT-2000 (first entry)

XX Recombinant variant of Sp36 (Sp36D) of S. pneumoniae.

XX Streptococcus pneumoniae; infection; vaccine; coiled coil region;

KW histidine triad residue; Sp36; antibody; otitis media;

KW nasopharyngeal infection; bronchial infection; bronchitis; sepsis;

KW meningitis; lobar pneumonia.

OS Streptococcus pneumoniae.

XX Key location/Qualifiers

FT Region 64..69 /label= Histidine triad residue

FT Region 188..193 /label= Histidine triad residue

FT Region 296..301 /label= Histidine triad residue

FT Region 541..546 /label= Histidine triad residue

FT Region 625..630 /label= Histidine triad residue

XX WO200037105-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US30390.

XX 21-DEC-1998; 98US-0113048.

XX (MEDI-) MEDIMMUNE INC.

XX Johnson LS, Koenig S, Adamou JE;

XX MPI: 2000-452129/39.

XX N-PSDB; AAA47602.

XX Vaccine useful for prophylaxis and treatment of pneumococcal infections

XX such as otitis media, nasopharyngeal and bronchial infections,

XX comprises Streptococcus pneumoniae proteins

XX Claim 1; Page 54-57; 70pp; English.

XX Although a number of proteins have been suggested as being involved
CC in the pathogenicity of Streptococcus pneumoniae, there still remains
CC a need to identify polypeptides having epitopes in common from
CC various strains of S. pneumoniae in order to utilise such
CC polypeptides in vaccines to protect against a wide variety of
CC S. pneumoniae. New vaccine compositions are described which comprise a
CC Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino
CC acids in length that comprise at least one histidine triad residue

CC (HxxHxx) or a coiled-coil region, or an antibody directed against
CC these features. The vaccine is useful in protecting against infection
CC by Streptococcus pneumoniae. The vaccine composition comprising
CC antibodies to its useful for passive immunization for treating
CC pneumococcal infections which includes otitis media, nasopharyngeal
CC and bronchial infections.

XX Sequence 838 AA;

Query Match 7.5%; Score 60; DB 21; Length 838;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 31 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGHHYHYNGKVPYDAIISEELMKDPNY 90
Db 52 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGHHYHYNGKVPYDAIISEELMKDPNY 111

RESULT 34

AU75934 standard; Protein; 838 AA.

XX AU75934;

DT 08-MAY-2002 (first entry)

XX Streptococcus pneumoniae BVH-11-2 protein.

XX BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;

KW pneumonia; streptococcal bacterial infection; BVH-11-2.

OS Streptococcus pneumoniae.

XX WO200198334-A2.

XX 27-DEC-2001.

XX 19-JUN-2001; 2001WO-CA00908.

XX 20-JUN-2000; 2000US-212683P.

XX (SHIR-) SHIRE BIOCHEM INC.

XX Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;

XX MPI: 2002-122272/16.

XX N-PSDB; ABK15104.

XX New Streptococcus pneumoniae BVH-3 and BVH-11 variant and

XX epitope-bearing polypeptides, useful as vaccine components for treating

XX or preventing streptococcal infections such as otitis media,

XX meningitis, and bacteraemia

XX Example 1; Fig 8; 113pp; English.

XX The invention describes an isolated polypeptide (I) with 70-90%
CC identity to Streptococcus pneumoniae protein BVH-3, BVH-11, variants of
CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC comprising (I) is useful for therapeutic or prophylactic treatment of
CC meningitis, otitis media, bacteraemia or pneumonia infection in an
CC individual susceptible to these disorders. (II) is also useful for
CC therapeutic or prophylactic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. novae or
CC Streptococcus pneumoniae) in an individual susceptible to the infection.
CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for S. pneumoniae infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating S. pneumonia nucleic acid in a sample for
CC diagnosing streptococcal infections. This is the amino acid sequence of

CC Streptococcus pneumoniae protein BVH-11-2, used to create the antigenic
 CC peptides described in the method of the invention.

XX Sequence 838 AA;

Query Match 7.5%; Score 60; DB 23; Length 838;
 Best Local Similarity 100.0%; Pred. No. 1.2e-48;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 ENLTPDEVSKREGINAEOIVIKITDQGYVTSBGDHYHYNGKVPYDAITSEBLMKDPNY 90
 DB 52 ENLTPDEVSKREGINAEOIVIKITDQGYVTSBGDHYHYNGKVPYDAITSEBLMKDPNY 111

RESULT 35

ABU01418 standard; Protein; 839 AA.

XX ABU01418;

DT 11-FEB-2003 (first entry)

DE S. pneumoniae type 4 strain protein from coding region #993.

XX Bacterial meningitis; pneumonia; sepsis; otitis media;

KW ear infection; antiinflammatory; antibacterial; immunostimulant;

KW auditory; respiratory; gene therapy; vaccine.

OS Streptococcus pneumoniae type 4 strain.

PN WO200277021-A2.

XX 03-OCT-2002.

PF 27-MAR-2002; 2002WO-IB02163.

PR 27-MAR-2001; 2001GB-0007658.

PA (CHIR-) CHIRON SPA.

PI (GENO-) INST GENOMIC RES.

DR MPI; 2003-040579/03.

XX N-PSDB; ABX06705.

PT New proteins and nucleic acid molecules from Streptococcus pneumoniae,
 PT useful as medicaments for treating or preventing a disease or infection
 PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
 PT or ear infection

PS Claim 1; SEQ ID No 1986; 56pp; English.

XX The invention relates to a protein comprising or having at least 50%
 CC identity to any of the 2469 amino acid sequences, identified in the
 CC specification (available on a computer readable format), or its fragment,
 CC expressed from 2469 of 2489 identified DNA coding regions from the
 CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
 CC AB556453. Also included are an antibody which binds one of the
 CC antibody, treating a patient by administering the protein, DNA or
 CC antibody (in a composition), a kit comprising first and second primers,
 CC which are the nucleic acid cited above or fragments between nucleotides
 CC 8-100 of a sequence not defined in the specification, for amplifying a
 CC target sequence contained within a Streptococcus nucleic acid sequence,
 CC where the first primer is substantially complementary to the target
 CC sequence and the second primer is substantially complementary to the
 CC complement of the target sequence, and where the parts of the primers
 CC having substantial complementarity define the termini of the target
 CC sequence to be amplified, assay comprising contacting a test compound
 CC with the protein, and determining whether the test compound binds to the
 CC protein and a Streptococcus pneumoniae bacterium, where one or more
 CC genes encoding the proteins has been rendered inactive. The proteins,
 CC nucleic acid molecules, antibody and compositions are useful as

CC medicaments for treating or preventing a disease or infection due to
 CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia,
 CC sepsis, otitis media or ear infection. They are also useful in developing
 CC vaccines, diagnostics and antibiotics. The methods are useful for
 CC identifying immunodominant proteins. The present sequence is one of
 CC the 2469 proteins expressed by the identified coding regions from the
 CC genomic sequence.

CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 839 AA;

Query Match 7.5%; Score 60; DB 24; Length 839;
 Best Local Similarity 100.0%; Pred. No. 1.2e-48;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 ENLTPDEVSKREGINAEOIVIKITDQGYVTSBGDHYHYNGKVPYDAITSEBLMKDPNY 90
 DB 52 ENLTPDEVSKREGINAEOIVIKITDQGYVTSBGDHYHYNGKVPYDAITSEBLMKDPNY 111

RESULT 36

AAB12730 standard; Protein; 613 AA.

XX AAB12730;

DT 21-NOV-2000 (first entry)

DE Streptococcus pneumoniae BVH-11C protein antigen SHQ ID NO:63.

XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-26; antigen; vaccine;

KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;

KW otitis media; pneumonia; immunisation; bactericidal.

OS Streptococcus pneumoniae.

PN WO200039299-A2.

XX 06-JUL-2000.

PF 20-DEC-1999; 99WO-CA01218.

PR 23-DEC-1998; 98US-0113800.

PA (BIOC-) BIOCHEM PHARMA INC.

PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;

DR MPI; 2000-452397/39.

XX Streptococcal antigens useful for vaccinating against e.g. meningitis,
 PT otitis media, bacteraemia and/or pneumonia

PS Claim 18; Fig 28; 106pp; English.

XX The present invention describes nucleic acids (I) encoding protein
 CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein
 CC antigens, may be used for the recombinant production of the proteins
 CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals
 CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence represents the
 CC S. pneumoniae BVH-11C protein antigen.

XX Sequence 613 AA;

Query Match 7.0%; Score 56; DB 21; Length 613;
 Best Local Similarity 100.0%; Pred. No. 5.7e-45;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 234 RTNWPSVSNPGTNTNTSNTNSQASQSDNDIDSLKQLYKPLSQRHVESDGL 289
 DB 27 RTNWPSVSNPGTNTNTSNTNSQASQSDNDIDSLKQLYKPLSQRHVESDGL 82

RESULT 37
 ID AAU84029 standard; Peptide; 613 AA.
 AC AAU84029;
 DT 08-MAY-2002 (first entry)
 DE Truncated variant of S. pneumoniae BVH-11, BVH- version #2.
 DE BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
 KW pneumonia; streptococcal bacterial infection; mutant; mutein.
 OS Streptococcus pneumoniae.
 OS Synthetic.
 PN WO200198334-A2.
 PD 27-DEC-2001.
 PE 19-JUN-2001; 2001WO-CA00908.
 PR 20-JUN-2000; 2000US-212683P.
 PA (SHIR-) SHIRE BIOCHEM INC.
 PI Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
 DR WPI: 2002-122272/16.
 PT New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
 PT epitope-bearing polypeptides, useful as vaccine components for treating
 PT or preventing streptococcal infections such as otitis media,
 PT meningitis, and bacteraemia -
 PT
 PS Example 1; Page -, 113pp; English.
 XX The invention describes an isolated polypeptide (I) with 70-90%
 CC identity to Streptococcus pneumoniae protein BVH-3, BVH-11, variants of
 CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
 CC comprising (I) is useful for therapeutic or prophylactic treatment of
 CC meningitis, otitis media, bacteraemia or pneumonia infection in an
 CC individual susceptible to these disorders. (II) is also useful for
 CC therapeutic or prophylactic treatment of any streptococcal bacterial
 CC infection (e.g., caused by Streptococcus pneumoniae, group A
 CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
 CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardiae or
 CC Staphylococcus aureus) in an individual susceptible to the infection.
 CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
 CC techniques. The Streptococcus polypeptides are useful in a diagnostic
 CC test for S. pneumoniae infection. (III) is useful for designing DNA
 CC probes for use in detecting the presence of Streptococcus in a biological
 CC sample suspected of containing the bacteria. The DNA probes may also be
 CC used for detecting circulating S. pneumoniae nucleic acid in a sample for
 CC diagnosing streptococcal infections. This sequence represents a truncate
 CC of Streptococcus pneumoniae gene used to obtain antigenic peptides,
 CC described in the method of the invention.
 CC Note: This sequence does not appear in the specification but has
 CC been created according to information given in the invention.
 XX
 SQ Sequence 613 AA;

OY Query Match 7.0%; Score 56; DB 23; Length 613;
 Best Local Similarity 100.0%; Pred. No. 6,7e-45;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

234 RTNWPSVSNPGTNTNTSNTNSQASQSDNDIDSLKQLYKPLSQRHVESDGL 289

DB 27 RTNWPSVSNPGTNTNTSNTNSQASQSDNDIDSLKQLYKPLSQRHVESDGL 82

RESULT 38
 ID AAY05753 standard; Protein; 721 AA.
 AC AAY05753;
 DT 19-JUL-1999 (first entry)
 DE Streptococcus pneumoniae 79 kDa complement C3-degrading protease.
 DE Human complement C3-degrading protease; vaccine; infection;
 KW meningitis; pneumonia; xerotransplantation; transplant rejection;
 KW inflammation.
 OS Streptococcus pneumoniae.
 OS
 FH Key Location/Qualifiers
 FT Protein 170..227
 FT /note="claimed protein of Claim 14"
 FT Protein 258..300
 FT /note="claimed protein of Claim 15"
 PN WO9915675-A1.
 PD 01-APR-1999.
 PE 24-SEP-1998; 98WO-US20186.
 PR 24-SEP-1997; 97US-0059907.
 PA (AMCY) AMERICAN CYANAMID CO.
 PA (MINU) UNIV MINNESOTA.
 PI Cheng Q, Finkel DJ, Green BA, Hostetter MK, Masi AW;
 DR WPI: 1999-254719/21.
 DR N-PSDB; AAX25394.
 XX
 PT New isolated human complement C3-degrading proteinase
 PS Claim 59; Page 54-58; 66pp; English.
 XX The present sequence is a 79 kDa protein of Streptococcus pneumoniae
 CC serotype 4 that is capable of degrading human complement protein C3
 CC (HCP3). The sequence was deduced from the open reading frame of
 CC an isolated gene (see AAX25394). A smaller (20 kDa) HCP3 protease
 CC is encoded by an open reading frame of S. pneumoniae serotype 3,
 CC and this open reading frame may be part of a larger open reading
 CC frame corresponding to the present sequence from the S. pneumoniae
 CC serotype 4 genome. Amino acids 1-58 and 90-132 of the 20 kDa
 CC protein have substantial sequence identity with amino acids 170-227
 CC and 258-300 of the 79 kDa protein. Proteins and peptides or
 CC polypeptides containing these regions, and DNA sequences encoding
 CC them, are claimed. HCP3 proteases and polypeptides can be used as
 CC immune system stimulating compositions (claimed). They can produce
 CC an immune response against S. pneumoniae to immunize or treat a
 CC mammalian subject against infection or colonization (claimed).
 CC CC epithelial cell response, or an endothelial cell response
 CC (claimed). The expression of the proteins on the surface of an
 CC organ of an animal used in xenotransplantation can be used to
 CC inhibit C3-mediated inflammation and rejection.
 XX
 SQ Sequence 721 AA;

OY Query Match 6.4%; Score 51; DB 20; Length 721;
 Best Local Similarity 100.0%; Pred. No. 5.2e-40;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 QGRYTTDDGYIFNADIIEDTGDAYIVPHGDHYHYPKNELASSELAAEA 210
 DB 74 QGRYTTDDGYIFNADIIEDTGDAYIVPHGDHYHYPKNELASSELAAEA 124

RESULT 39

ID AAM55095 standard; Protein; 763 AA.

AC AAM55095;

DT 02-OCT-1998 (first entry)

DE Streptococcus pneumoniae SP0042 protein.

KW Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
 detection; pneumonia; otitis media; meningitis.

OS Streptococcus pneumoniae.

FT Key Location/Qualifiers

FT Misc-difference 51 //label= unknown

FT Misc-difference 469 //note= "encoded by ATN"

FT Misc-difference 477 //label= "encoded by NCA"

FT Misc-difference 477 //note= "encoded by GAN"

PN WO9818930-A2.

PD 07-MAY-1998.

PF 30-OCT-1997; 97WO-US19422.

PR 31-OCT-1996; 96US-0023960.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Choi GH, Hromockyj A, Johnson LS, Kunsch CA;

DR WPI; 1998-272224/24.

DR N-PSDB; AAV27356.

PT Nucleic acid encoding antigenic peptide(s) from Streptococcus
 pneumoniae - or their epitope-containing fragments, useful in
 protective or therapeutic vaccines, and for diagnosis

PS Claim 11; Page 62; 118pp; English.

CC The present sequence represents a protein from Streptococcus pneumoniae.
 CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein
 CC can be useful in vaccines for inducing protective antibodies against
 CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.
 CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid
 CC are used to detect Streptococcus infection (by usual hybridisation or
 CC amplification methods), also for isolating Streptococcus genes or their
 CC allelic variants. The protein can be used similarly to detect specific
 CC antibodies in standard immunoassays, especially for diagnosing or
 CC monitoring infections. Antibodies which bind the protein are used to
 CC detect corresponding antigens, to purify the protein and for passive
 CC immunisation (optionally coupled to a toxin). Vaccines are administered,
 CC e.g. by injection, orally or through the skin, typically at 0.01-1000
 CC (especially 10-300) mu g/ml per dose.

SQ Sequence 763 AA;

Query Match 6.4%; Score 51; DB 19; Length 763;
 Best Local Similarity 100.0%; Pred. No. 5.5e-40;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 QGRYTTDDGYIFNADIIEDTGDAYIVPHGDHYHYPKNELASSELAAEA 210
 DB 159 QGRYTTDDGYIFNADIIEDTGDAYIVPHGDHYHYPKNELASSELAAEA 209

RESULT 40

ID ABP54589

AC ABP54589 standard; Protein; 763 AA.

DT 04-SEP-2002 (first entry)

DE S. pneumoniae SP042 protein sequence SEQ ID NO:66.

KW Streptococcus pneumoniae; epitope; vaccine; antigenic protein;
 antibacterial; Streptococcal infection; detection.

OS Streptococcus pneumoniae.

PN US2002061545-A1.

PD 23-MAY-2002.

PF 22-JAN-2001; 2001US-0765272.

PR 30-OCT-1997; 97US-0961083.

PA (CHOI/) CHOI G H.

PA (KUNS/) KUNSCH C A.

PA (BARA/) BARASH S C.

PA (DILL/) DILLON P J.

PA (DOUG/) DOUGHERTY B.

PA (FANN/) FANNON M R.

PA (ROSE/) ROSEN C A.

PI Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR;

DR WPI; 2002-479261/51.

DR N-PSDB; AB084824.

PT New Streptococcus pneumoniae antigens, useful for detecting
 Streptococcus and for preventing or attenuating disease caused by
 Streptococcus infection -

PS Claim 11; Page 29; 70pp; English.

CC AB084792 to AB084904 represents nucleic acids which encode the
 CC Streptococcus pneumoniae antigens given in ABP54557 to ABP54669;
 CC The S. pneumoniae antigens have antibacterial activity and can be
 CC used in vaccines. The S. pneumoniae antigens can also be used to
 CC prevent or attenuate a Streptococcal infection in an animal. The
 CC polynucleotides encoding the S. pneumoniae antigens can be used to
 CC detect Streptococcus nucleic acids. AB084905 to AB085130 represent
 CC primers used in the cloning of S. pneumoniae ORFs (open reading frames)
 CC which are used in an example from the present invention.

SQ Sequence 763 AA;

Query Match 6.4%; Score 51; DB 23; Length 763;
 Best Local Similarity 100.0%; Pred. No. 5.5e-40;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 QGRYTTDDGYIFNADIIEDTGDAYIVPHGDHYHYPKNELASSELAAEA 210
 DB 159 QGRYTTDDGYIFNADIIEDTGDAYIVPHGDHYHYPKNELASSELAAEA 209

RESULT 41

ID AA083828

XX AA083828 standard; Peptide; 42 AA.

PI Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
XX
XX WPI; 2002-122272/16.
DR
XX New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
PT epitope-bearing polypeptides, useful as vaccine components for treating
PT or preventing streptococcal infections such as otitis media,
PT meningitis, and bacteraemia
XX
XX Example 1; Page -; 113pp; English.
XX
XX The invention describes an isolated polypeptide (I) with 70-90%
CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC comprising (I) is useful for therapeutic or prophylactic treatment of
CC meningitis, otitis media, bacteraemia or pneumonia infection in an
CC individual susceptible to these disorders. (II) is also useful for
CC therapeutic or prophylactic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nodocidia or
CC Streptococcus aureus) in an individual susceptible to the infection.
CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for S. pneumoniae infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating S. pneumonia nucleic acid in a sample for
CC diagnosing streptococcal infections. This sequence represents a truncate
CC of a Streptococcus pneumoniae gene used to obtain antigenic peptides,
CC described in the method of the invention.
CC Note: This sequence does not appear in the specification but has
CC been created according to information given in the invention.
XX

SEQ Sequence 205 AA;

Query Match 4.0%; Score 32; DB 23; Length 205;
Best Local Similarity 100.0%; Pred. No. 3.7e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AEOIVIKITDQGVYVTSBGHGHYHYNGKVPYDA 77
DB 47 AEOIVIKITDQGVYVTSBGHGHYHYNGKVPYDA 78

RESULT 44
ID AAM61228 standard; Protein; 447 AA.
XX
XX AAM61228;
AC
XX
XX 02-OCT-1998 (first entry)
DT
XX
XX Streptococcus pneumoniae SPI03 protein.
DE
XX
XX Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
KM detection; pneumonia; otitis media; meningitis.
XX
XX Streptococcus pneumoniae.
OS
XX
XX WO98189310-A2.
PN
XX
XX 07-MAY-1998.
PD
XX
XX 30-OCT-1997; 97WO-US19422.
PF
XX
XX 31-OCT-1996; 96US-0029960.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Choi GH, Hromockyj A, Johnson LS, Kunsch CA;
PI
XX
XX WPI; 1998-272224/24.

DR N-PSDB; AAV27414.
XX
XX Nucleic acid encoding antigenic peptide(s) from Streptococcus
PT pneumoniae - or their epitope-containing fragments, useful in
PT protective or therapeutic vaccines, and for diagnosis
XX
XX Claim 11; Page 85; 118pp; English.
PS
XX

CC The present sequence represents a protein from Streptococcus pneumoniae.
CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein
CC can be useful in vaccines for inducing protective antibodies against
CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.
CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid
CC are used to detect Streptococcus infection (by usual hybridisation or
CC amplification methods), also for isolating Streptococcus genes or their
CC allelic variants. The protein can be used similarly to detect specific
CC antibodies in standard immunoassays, especially for diagnosing or
CC monitoring infections. Antibodies which bind the protein are used to
CC detect corresponding antigens, to purify the protein and for passive
CC immunisation (optionally coupled to a toxin). Vaccines are administered,
CC e.g. by injection, orally or through the skin, typically at 0.01-1000
CC (especially 10-300) mu g/ml per dose.

SEQ Sequence 447 AA;

Query Match 4.0%; Score 32; DB 19; Length 447;
Best Local Similarity 100.0%; Pred. No. 7.4e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AEOIVIKITDQGVYVTSBGHGHYHYNGKVPYDA 77
DB 43 AEOIVIKITDQGVYVTSBGHGHYHYNGKVPYDA 74

RESULT 45
ID ABP54647 standard; Protein; 447 AA.
XX
XX ABP54647;
AC
XX
XX 04-SEP-2002 (first entry)
DT
XX
XX S. pneumoniae SPI03 protein sequence SEQ ID NO:182.
DE
XX
XX Streptococcus pneumoniae; epitope; vaccine; antigenic protein;
KM antibacterial; Streptococcal infection; detection.
XX
XX Streptococcus pneumoniae.
OS
XX
XX US2002061545-A1.
PN
XX
XX 23-MAY-2002.
PD
XX
XX 22-JAN-2001; 2001US-0765272.
PF
XX
XX 30-OCT-1997; 97US-0961083.
PR
XX
XX (CHOI/) CHOI G H.
PA (KUNS/) KUNSCH C A.
PA (BARA/) BARASH S C.
PA (DILL/) DILLON P J.
PA (DOUG/) DOUGHERTY B.
PA (FANN/) FANNON M R.
PA (ROSE/) ROSEN C A.
XX
XX Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR;
PI Rosen CA;
XX
XX WPI; 2002-479261/51.
DR N-PSDB; ABQ84882.
XX
XX New Streptococcus pneumoniae antigens, useful for detecting
PT Streptococcus and for preventing or attenuating disease caused by

PT Streptococcus infection -
 XX
 PS Claim 11; Page 45; 70pp; English.
 XX
 CC AB084792 to AB084904 represents nucleic acids which encode the
 CC Streptococcus pneumoniae antigens given in ABP54557 to ABP54669.
 CC The S. pneumoniae antigens have antibacterial activity and can be
 CC used in vaccines. The S. pneumoniae antigens can also be used to
 CC prevent or attenuate a Streptococcus infection in an animal. The
 CC polynucleotides encoding the S. pneumoniae antigens can be used to
 CC detect Streptococcus nucleic acids. AB084905 to AB085130 represent
 CC primers used in the cloning of S. pneumoniae ORFs (open reading frames)
 CC which are used in an example from the present invention.
 XX
 SQ Sequence 447 AA;
 Query Match 4.0%; Score 32; DB 23; Length 447;
 Best Local Similarity 100.0%; Pred. No. 7.4e-22;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 46 AEOIVIKITDGGYVTSHGDIHYNGKVPYDA 77
 ||||||||||||||||||||||||||||
 Db 43 AEOIVIKITDGGYVTSHGDIHYNGKVPYDA 74
 RESULT 46
 AAB12718
 ID AAB12718 standard; Protein; 484 AA.
 AC AAB12718;
 XX
 DT 21-NOV-2000 (first entry)
 XX
 DE Streptococcus pneumoniae BVH-3A protein antigen SEQ ID NO:8.
 XX
 KW Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
 KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
 KW otitis media; pneumonia; immunisation; bactericidal.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN WO200039299-A2.
 XX
 PD 06-JUL-2000.
 XX
 PF 20-DEC-1999; 99WO-CA01218.
 XX
 PR 23-DEC-1998; 98US-0113800.
 XX
 PA (BIOC-) BIOCHEM PHARMA INC.
 XX
 PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
 XX
 DR WPI; 2000-452397/39.
 DR N-PSDB; AAA65733.
 XX
 PT Streptococcal antigens useful for vaccinating against e.g. meningitis,
 PT otitis media, bacteraemia and/or pneumonia -
 XX
 PS Claim 18; Fig 8; 106pp; English.
 XX
 CC The present invention describes nucleic acids (I) encoding protein
 CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein
 CC antigens, may be used for the recombinant production of the proteins
 CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals
 CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence represents the
 CC S. pneumoniae BVH-3A protein antigen.
 CC
 SQ Sequence 484 AA;

Query Match 4.0%; Score 32; DB 21; Length 484;
 Best Local Similarity 100.0%; Pred. No. 8e-22;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 46 AEOIVIKITDGGYVTSHGDIHYNGKVPYDA 77
 ||||||||||||||||||||||||||||
 Db 67 AEOIVIKITDGGYVTSHGDIHYNGKVPYDA 98
 RESULT 47
 AAB01467
 ID AAB01467 standard; Protein; 484 AA.
 AC AAB01467;
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE Recombinant variant of Sp36 (Sp36E) of S. pneumoniae.
 XX
 KW Streptococcus pneumoniae; infection; vaccine; coiled coil region;
 KW histidine triad residue; Sp36; antibody; otitis media;
 KW nasopharyngeal infection; bronchial infection; bronchitis; sepsis;
 KW meningitis; lobar pneumonia.
 XX
 OS Streptococcus pneumoniae.
 XX
 FH Key Location/Qualifiers
 FT Region 63..68
 FT /label= Histidine triad residue
 FT Region 120..140
 FT /label= Coiled coil region
 FT Region 185..190
 FT /label= Histidine triad residue
 FT Region 289..294
 FT /label= Histidine triad residue
 FT Region 376..381
 FT /label= Histidine triad residue
 FT Region 441..446
 FT /label= Histidine triad residue
 FT Region 750..772
 FT /label= Coiled coil region
 XX
 PN WO200037105-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 21-DEC-1999; 99WO-US30390.
 XX
 PR 21-DEC-1998; 98US-0113048.
 XX
 PA (MEDI-) MEDIMUNE INC.
 XX
 PI Johnson LS, Koenig S, Adamou JE;
 XX
 DR WPI; 2000-452129/39.
 DR N-PSDB; AAA47603.
 XX
 PT Vaccine useful for prophylaxis and treatment of pneumococcal infections
 PT such as otitis media, nasopharyngeal and bronchial infections,
 PT comprises Streptococcus pneumoniae proteins
 XX
 PS Claim 1; Page 58-60; 70pp; English.
 XX
 CC Although a number of proteins have been suggested as being involved
 CC in the pathogenicity of Streptococcus pneumoniae, there still remains
 CC a need to identify polypeptides having epitopes in common from
 CC various strains of S. pneumoniae in order to utilise such
 CC polypeptides in vaccines to protect against a wide variety of
 CC S. pneumoniae. New vaccine compositions are described which comprise a
 CC Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino
 CC acids in length that comprise at least one histidine triad residue
 CC (HxxHxx) or a coiled-coil region, or an antibody directed against
 CC these features. The vaccine is useful in protecting against infection

CC by Streptococcus pneumoniae. The vaccine composition comprising
CC antibodies to is useful for passive immunization for treating
CC Pneumococcal infections which includes otitis media, nasopharyngeal
CC and bronchial infections.

XX Sequence 484 AA;

Query Match 4.0%; Score 32; DB 21; Length 484;
Best Local Similarity 100.0%; Pred. No. 8e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AEOIVIKITDQGYVTSHGPHYHYNGKVPYDA 77
|||
DB 67 AEOIVIKITDQGYVTSHGPHYHYNGKVPYDA 98

RESULT 48

AA81708
ID AAY81708 standard; Protein; 484 AA.

XX AAY81708;

XX 02-JUN-2000 (first entry)

DE Streptococcus pneumoniae protein sequence ID128.

XX Streptococcus pneumoniae infection; immunogen; antigen; diagnosis; AIDS;
KW bacterial pneumonia; asplenia; heart disease; lung disease; alcoholism;
KW kidney disease; diabetes; immunosuppressive disorder; otitis media;
KW pneumococcal septicemia; sinusitis; meningitis; therapy.

OS Streptococcus pneumoniae.

PN WO200006738-A2.

PD 10-FEB-2000.

PF 27-JUL-1999; 99WO-GB02452.

PR 27-JUL-1998; 98GB-0016336.

PR 19-MAR-1999; 99US-0125329.

PA (MICR-) MICROBIAL TECHNIQS LTD.

PI Le Page RWF, Wells JM, Hanniffy SB, Hansbro PM;

DR WPI; 2000-195301/17.

DR N-PSDB; AA231804.

PT Streptococcal proteins and polynucleotides useful for diagnosis,
PT treatment and prophylaxis of bacterial infections -
XX Claim 1, Page 39; 76pp; English.

XX This sequence represents a Streptococcus pneumoniae protein of the
CC invention. The proteins (or their homologues, derivatives and/or
CC fragments) are useful as immunogens or antigens. Immunogenic or antigenic
CC compositions comprising the proteins are useful as vaccines and also in
CC diagnostic assays. The sequences are useful for the detection or
CC diagnosis of S. pneumoniae infection, by contacting a sample to be tested
CC with them. Agents capable of antagonising, inhibiting or interfering with
CC the function or expression of the protein or polypeptide are useful in
CC medical compositions in the treatment or prophylaxis of S. pneumoniae
CC infection. As the sequences can be used to treat S. pneumoniae infection,
CC they can be used to treat bacterial pneumonia, which has high rates in
CC young children, the elderly, and in patients with predisposing conditions
CC such as asplenia, heart, lung and kidney disease, diabetes, alcoholism,
CC or with immunosuppressive disorders, especially AIDS. They can also be
CC used to treat pneumococcal septicemia, otitis media, sinusitis, and
CC meningitis.

XX Sequence 484 AA;

Query Match 4.0%; Score 32; DB 21; Length 484;
Best Local Similarity 100.0%; Pred. No. 8e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AEOIVIKITDQGYVTSHGPHYHYNGKVPYDA 77
|||
DB 67 AEOIVIKITDQGYVTSHGPHYHYNGKVPYDA 98

RESULT 49

AA81538
ID AAY81538 standard; Protein; 485 AA.

XX AAY81538;

XX 24-MAY-2000 (first entry)

DE Streptococcus pneumoniae type 4 protein sequence #38.

XX Streptococcus pneumoniae; vaccine; screening; protein antigen;
KW antibacterial; antiinflammatory; meningitis; infection; diagnosis;
KW pneumococcal disease.

OS Streptococcus pneumoniae.

PN WO200006737-A2.

PD 10-FEB-2000.

PF 27-JUL-1999; 99WO-GB02451.

PR 27-JUL-1998; 98GB-0016337.

PR 19-MAR-1999; 99US-0125164.

PA (MICR-) MICROBIAL TECHNIQS LTD.

PI Gilbert CFG, Hansbro PM;

DR WPI; 2000-195300/17.

PT New Streptococcal protein, useful as a vaccine, for diagnosis of
PT pneumococcal diseases and for screening agents capable of antagonizing
PT or inhibiting expression of the protein -
XX Claim 1, Page 76; 108pp; English.

XX AAY81501 to AAY81679 represent specifically claimed protein sequences
CC isolated from Streptococcus pneumoniae. AA05407 to AA05590 represent
CC specifically claimed nucleotide sequences isolated from S. pneumoniae.
CC The sequences have antibacterial and antiinflammatory properties.
CC The protein sequences, and fragments of them, are useful as immunogens
CC and/or antigens. The nucleotide sequences can be used in vaccines and in
CC diagnostic assays. The proteins and nucleotides can be useful for the
CC detection and diagnosis of S. pneumoniae. The protein sequences are also
CC useful for screening an agent capable of antagonising, inhibiting or
CC interfering with the function or expression of the proteins in which the
CC agent is useful for treatment or prophylaxis of S. pneumoniae infection
CC and meningitis. AA05591 to AA05614 represent primers used in the
CC exemplification of the present invention.

XX Sequence 485 AA;

Query Match 4.0%; Score 32; DB 21; Length 485;
Best Local Similarity 100.0%; Pred. No. 8e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AEOIVIKITDQGYVTSHGPHYHYNGKVPYDA 77
|||
DB 67 AEOIVIKITDQGYVTSHGPHYHYNGKVPYDA 98

RESULT 50

AAB12723

ID AAB12723 standard; Protein; 489 AA.
 XX AAB12723;
 AC
 XX 21-NOV-2000 (first entry)
 DT
 XX Streptococcus pneumoniae BVH-3AD protein antigen SEQ ID NO:56.
 DE
 XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
 KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
 KM otitis media; pneumonia; immunisation; bactericidal.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN WO200039299-A2.
 PD
 XX 06-JUL-2000.
 PF
 XX 20-DEC-1999; 99WO-CA01218.
 PR
 XX 23-DEC-1998; 98US-0113800.
 PA (BIOC-) BIOCHEM PHARMA INC.
 PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
 DR WPI, 2000-452397/39.
 XX Streptococcal antigens useful for vaccinating against e.g. meningitis,
 PT otitis media, bacteraemia and/or pneumonia -
 PS
 XX Claim 18; Fig 21; 106pp; English.
 CC The present invention describes nucleic acids (I) encoding protein
 CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein
 CC antigens, may be used for the recombinant production of the proteins
 CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals
 CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence represents the
 CC S. pneumoniae BVH-3AD protein antigen.
 XX
 SQ Sequence 489 AA;
 Query Match 4.0%; Score 32; DB 21; Length 489;
 Best Local Similarity 100.0%; Pred. No. 8.1e-22;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 46 AEOIVIKITDGGYVTSHGDIHYNGKVPYDA 77
 ||||||||||||||||||||||||||||||||
 Db 47 AEOIVIKITDGGYVTSHGDIHYNGKVPYDA 78
 ||||||||||||||||||||||||||||||||
 RESULT 51
 ID AAB12724 standard; Protein; 489 AA.
 XX AAB12724;
 AC
 XX 08-MAY-2002 (first entry)
 DT
 XX Truncated variant of S. pneumoniae BVH-3, BVH-3AD.
 DE
 XX BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
 KW pneumonia; streptococcal bacterial infection; mutant; mutein.
 KM
 XX Streptococcus pneumoniae.
 OS
 XX Synthetic.
 PN WO200198334-A2.
 PD
 XX 27-DEC-2001.

XX 19-JUN-2001; 2001WO-CA00908.
 PF
 XX 20-JUN-2000; 2000US-212683P.
 PR
 XX (SHIR-) SHIRE BIOCHEM INC.
 PA
 XX Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
 PI WPI, 2002-122272/16.
 DR
 XX New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
 PT epitope-bearing polypeptides, useful as vaccine components for treating
 PT or preventing streptococcal infections such as otitis media,
 PT meningitis, and bacteraemia -
 XX
 PS Example 1; Page -, 113pp; English.
 XX
 CC The invention describes an isolated polypeptide (I) with 70-90%
 CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
 CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
 CC comprising (I) is useful for therapeutic or prophylactic treatment of
 CC meningitis, otitis media, bacteraemia or pneumonia infection in an
 CC individual susceptible to these disorders. (II) is also useful for
 CC therapeutic or prophylactic treatment of any streptococcal bacterial
 CC infection (e.g., caused by Streptococcus pneumoniae, group A
 CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
 CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. norcardia or
 CC Streptococcus aureus) in an individual susceptible to the infection.
 CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
 CC techniques. The Streptococcus polypeptides are useful in a diagnostic
 CC test for S. pneumoniae infection. (III) is useful for designing DNA
 CC probes for use in detecting the presence of Streptococcus in a biological
 CC sample suspected of containing the bacteria. The DNA probes may also be
 CC used for detecting circulating S. pneumonia nucleic acid in a sample for
 CC diagnosing streptococcal infections. This sequence represents a truncate
 CC of a Streptococcus pneumoniae gene used to obtain antigenic peptides,
 CC described in the method of the invention.
 CC Note: This sequence does not appear in the specification but has
 CC been created according to information given in the invention.
 XX
 SQ Sequence 489 AA;
 Query Match 4.0%; Score 32; DB 23; Length 489;
 Best Local Similarity 100.0%; Pred. No. 8.1e-22;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 46 AEOIVIKITDGGYVTSHGDIHYNGKVPYDA 77
 ||||||||||||||||||||||||||||||||
 Db 47 AEOIVIKITDGGYVTSHGDIHYNGKVPYDA 78
 ||||||||||||||||||||||||||||||||
 RESULT 52
 ID AAB12724 standard; Protein; 509 AA.
 XX AAB12724;
 AC
 XX 21-NOV-2000 (first entry)
 DT
 XX Streptococcus pneumoniae L-BVH-3-AD protein antigen SEQ ID NO:57.
 DE
 XX Streptococcus pneumoniae; BVH-3; BVH-11; antigen; vaccine;
 KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
 KM otitis media; pneumonia; immunisation; bactericidal.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN WO200039299-A2.
 PD
 XX 06-JUL-2000.
 PF 20-DEC-1999; 99WO-CA01218.

CC The present invention describes nucleic acids (I) encoding protein
CC antigens (II) from *Streptococcus pneumoniae*. The protein antigens
CC have bactericidal activity. The nucleic acids, encoding the protein
CC antigens, may be used for the recombinant production of the proteins
CC they encode. The protein antigens may then be used as vaccines for the
CC prevention and treatment of streptococcal infections in mammals
CC (especially humans) which result in, e.g. meningitis, otitis media,
CC bacteraemia and/or pneumonia. The present sequence represents the

RESULT 57
AAU76151
ID AAU76151 standard; Protein; 840 AA

[illegible][illegible]

PA (BIOC-) BIOCHEM PHARMA INC.
 XX Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
 XX WPI, 2000-452397/39.
 DR Streptococcal antigens useful for vaccinating against e.g. meningitis,
 XX otitis media, bacteremia and/or pneumonia -
 XX
 PS Disclosure; Fig 11; 106pp; English.
 CC The present invention describes nucleic acids (I) encoding protein
 CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein
 CC antigens, may be used for the recombinant production of the proteins
 CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals
 CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence represents a
 CC S. pneumoniae BVH-3 protein antigen, from the present invention.
 XX
 SQ Sequence 1019 AA;
 Query Match 4.0%; Score 32; DB 21; Length 1019;
 Best Local Similarity 100.0%; Pred. No. 1.6e-21;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 46 AEQIVIKITDGGYVTSHGHDHYHYNGKVPYDA 77
 |||||||
 Db 47 AEQIVIKITDGGYVTSHGHDHYHYNGKVPYDA 78
 |||||||
 RESULT 60
 AAB12749
 ID AAB12749 standard; Protein; 1019 AA.
 XX
 AC AAB12749;
 XX
 DT 21-NOV-2000 (first entry)
 XX
 DE Streptococcus pneumoniae strain RX1 BVH-3 protein antigen.
 XX
 XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
 KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
 KM otitis media; pneumonia; immunisation; bactericidal.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN WO200039299-A2.
 XX
 PD 06-JUL-2000.
 XX
 PF 20-DEC-1999; 99WO-CA01218.
 XX
 PR 23-DEC-1998; 98US-0113800.
 XX
 PA (BIOC-) BIOCHEM PHARMA INC.
 XX Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
 PI WPI, 2000-452397/39.
 DR Streptococcal antigens useful for vaccinating against e.g. meningitis,
 XX otitis media, bacteremia and/or pneumonia -
 XX
 PS Disclosure; Fig 11; 106pp; English.
 CC The present invention describes nucleic acids (I) encoding protein
 CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein
 CC antigens, may be used for the recombinant production of the proteins
 CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals

CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence represents a
 CC S. pneumoniae BVH-3 protein antigen, from the present invention.
 XX
 SQ Sequence 1019 AA;
 Query Match 4.0%; Score 32; DB 21; Length 1019;
 Best Local Similarity 100.0%; Pred. No. 1.6e-21;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 46 AEQIVIKITDGGYVTSHGHDHYHYNGKVPYDA 77
 |||||||
 Db 47 AEQIVIKITDGGYVTSHGHDHYHYNGKVPYDA 78
 |||||||
 RESULT 61
 AAB12750
 ID AAB12750 standard; Protein; 1019 AA.
 XX
 AC AAB12750;
 XX
 DT 21-NOV-2000 (first entry)
 XX
 DE Streptococcus pneumoniae strain JNR7/87 BVH-3 protein antigen.
 XX
 XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
 KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
 KM otitis media; pneumonia; immunisation; bactericidal.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN WO200039299-A2.
 XX
 PD 06-JUL-2000.
 XX
 PF 20-DEC-1999; 99WO-CA01218.
 XX
 PR 23-DEC-1998; 98US-0113800.
 XX
 PA (BIOC-) BIOCHEM PHARMA INC.
 XX Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
 PI WPI, 2000-452397/39.
 DR Streptococcal antigens useful for vaccinating against e.g. meningitis,
 XX otitis media, bacteremia and/or pneumonia -
 XX
 PS Disclosure; Fig 11; 106pp; English.
 CC The present invention describes nucleic acids (I) encoding protein
 CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein
 CC antigens, may be used for the recombinant production of the proteins
 CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals
 CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence represents a
 CC S. pneumoniae BVH-3 protein antigen, from the present invention.
 XX
 SQ Sequence 1019 AA;
 Query Match 4.0%; Score 32; DB 21; Length 1019;
 Best Local Similarity 100.0%; Pred. No. 1.6e-21;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 46 AEQIVIKITDGGYVTSHGHDHYHYNGKVPYDA 77
 |||||||
 Db 47 AEQIVIKITDGGYVTSHGHDHYHYNGKVPYDA 78
 |||||||
 RESULT 62
 AAB12751

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ID  AAB12751 standard; Protein; 1019 AA.
XX
XX  AAB12751;
AC
XX
XX  21-NOV-2000 (first entry)
DT
XX
XX  Streptococcus pneumoniae strain SP64 BVH-3 protein antigen.
DE
XX
XX  Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW  prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
XX  otitis media; pneumonia; immunisation; bactericidal.
XX
OS  Streptococcus pneumoniae.
XX
XX  WO200039299-A2.
XX
XX  06-JUL-2000.
XX
XX  20-DEC-1999; 99WO-CA01218.
XX
XX  23-DEC-1998; 98US-0113800.
XX
XX  (BIOC-) BIOCHEM PHARMA INC.
XX
XX  Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
PI  WPI; 2000-452397/39.
XX
XX  Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT  otitis media, bacteraemia and/or pneumonia -
XX
XX  Disclosure; Fig 11; 106pp; English.
XX
XX
XX  The present invention describes nucleic acids (I) encoding protein
CC  antigens (II) from Streptococcus pneumoniae. The protein antigens
CC  have bactericidal activity. The nucleic acids, encoding the protein
CC  antigens, may be used for the recombinant production of the proteins
CC  they encode. The protein antigens may then be used as vaccines for the
CC  prevention and treatment of Streptococcal infections in mammals
CC  (especially humans) which result in, e.g. meningitis, otitis media,
CC  bacteraemia and/or pneumonia. The present sequence represents a
CC  S. pneumoniae BVH-3 protein antigen, from the present invention.
XX
XX
SQ  Sequence 1019 AA;
XX
XX
XX  Query Match 4.0%; Score 32; DB 21; Length 1019;
XX  Best Local Similarity 100.0%; Pred. No. 1.6e-21;
XX  Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX  46 AEOIVIKITDQGYVTSBGDHYHYNGKVPYDA 77
XX  ||||||||||||||||||||||||||||||||
XX  47 AEOIVIKITDQGYVTSBGDHYHYNGKVPYDA 78
XX
XX
XX  RESULT 63
XX  AAB12752
XX  ID  AAB12752 standard; Protein; 1019 AA.
XX
XX  AAB12752;
AC
XX
XX  21-NOV-2000 (first entry)
DT
XX
XX  Streptococcus pneumoniae strain P4241 BVH-3 protein antigen.
DE
XX
XX  Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW  prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
XX  otitis media; pneumonia; immunisation; bactericidal.
XX
XX  Streptococcus pneumoniae.
XX
XX  WO200039299-A2.
XX
XX  06-JUL-2000.
XX

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XX
XX  20-DEC-1999; 99WO-CA01218.
XX
XX  23-DEC-1998; 98US-0113800.
XX
XX  (BIOC-) BIOCHEM PHARMA INC.
XX
XX  Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
PI  WPI; 2000-452397/39.
XX
XX  Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT  otitis media, bacteraemia and/or pneumonia -
XX
XX  Disclosure; Fig 11; 106pp; English.
XX
XX
XX  The present invention describes nucleic acids (I) encoding protein
CC  antigens (II) from Streptococcus pneumoniae. The protein antigens
CC  have bactericidal activity. The nucleic acids, encoding the protein
CC  antigens, may be used for the recombinant production of the proteins
CC  they encode. The protein antigens may then be used as vaccines for the
CC  prevention and treatment of Streptococcal infections in mammals
CC  (especially humans) which result in, e.g. meningitis, otitis media,
CC  bacteraemia and/or pneumonia. The present sequence represents a
CC  S. pneumoniae BVH-3 protein antigen, from the present invention.
XX
XX
SQ  Sequence 1019 AA;
XX
XX
XX  Query Match 4.0%; Score 32; DB 21; Length 1019;
XX  Best Local Similarity 100.0%; Pred. No. 1.6e-21;
XX  Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX  46 AEOIVIKITDQGYVTSBGDHYHYNGKVPYDA 77
XX  ||||||||||||||||||||||||||||||||
XX  47 AEOIVIKITDQGYVTSBGDHYHYNGKVPYDA 78
XX
XX
XX  RESULT 64
XX  AAB12753
XX  ID  AAB12753 standard; Protein; 1019 AA.
XX
XX  AAB12753;
AC
XX
XX  21-NOV-2000 (first entry)
DT
XX
XX  Streptococcus pneumoniae strain A66 BVH-3 protein antigen.
DE
XX
XX  Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW  prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
XX  otitis media; pneumonia; immunisation; bactericidal.
XX
XX  Streptococcus pneumoniae.
XX
XX  WO200039299-A2.
XX
XX  06-JUL-2000.
XX
XX  20-DEC-1999; 99WO-CA01218.
XX
XX  23-DEC-1998; 98US-0113800.
XX
XX  (BIOC-) BIOCHEM PHARMA INC.
XX
XX  Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
PI  WPI; 2000-452397/39.
XX
XX  Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT  otitis media, bacteraemia and/or pneumonia -
XX
XX  Disclosure; Fig 11; 106pp; English.
XX
XX
XX  The present invention describes nucleic acids (I) encoding protein
CC

```

CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein
 CC antigens, may be used for the recombinant production of the proteins
 CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals
 CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence represents a
 CC S. pneumoniae BVH-3 protein antigen, from the present invention.

XX Sequence 1019 AA:

Query Match 4.0%; Score 32; DB 21; Length 1019;
 Best Local Similarity 100.0%; Pred. No. 1.6e-21;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 46 AEQIVIKITDGGYVTSKGDHYYNGKVPYDA 77
 |||||
 Db 47 AEQIVIKITDGGYVTSKGDHYYNGKVPYDA 78

RESULT 65

AAU84021
 ID AAB12715 standard; Peptide; 1019 AA.

XX AAU84021;

DT 08-MAY-2002 (first entry)

DE Truncated variant of S. pneumoniae BVH-3, BVH-3M.

KW BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
 KM pneumoniae; streptococcal bacterial infection; mutant; mucin.

XX Streptococcus pneumoniae.

OS Synthetic.

PN WO200198334-A2.

XX 27-DEC-2001.

PF 19-JUN-2001; 2001WO-CA00908.

PR 20-JUN-2000; 2000US-212683P.

XX (SHR-) SHIRE BIOCHEM INC.

PI Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;

DR WPI; 2002-122272/16.

PT New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
 PT epitope-bearing polypeptides, useful as vaccine components for treating
 PT or preventing streptococcal infections such as otitis media,
 PT meningitis, and bacteraemia

PS Example 1; Page -; 113pp; English.

XX The invention describes an isolated polypeptide (I) with 70-90%
 CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
 CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
 CC comprising (I) is useful for therapeutic or prophylactic treatment of
 CC meningitis, otitis media, bacteraemia or pneumonia infection in an
 CC individual susceptible to these disorders. (II) is also useful for
 CC therapeutic or prophylactic treatment of any streptococcal bacterial
 CC infection (e.g., caused by Streptococcus pneumoniae, group A
 CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
 CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. novardi or
 CC Streptococcus aureus) in an individual susceptible to the infection.
 CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
 CC techniques. The Streptococcus polypeptides are useful for designing DNA
 CC probes for use in detecting the presence of Streptococcus in a biological
 CC sample suspected of containing the bacteria. The DNA probes may also be

CC used for detecting circulating S. pneumonia nucleic acid in a sample for
 CC diagnosing streptococcal infections. This sequence represents a truncate
 CC of a Streptococcus pneumoniae gene used to obtain antigenic peptides,
 CC described in the method of the invention.
 CC Note: This sequence does not appear in the specification but has
 CC been created according to information given in the invention.

XX Sequence 1019 AA:

Query Match 4.0%; Score 32; DB 23; Length 1019;
 Best Local Similarity 100.0%; Pred. No. 1.6e-21;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 46 AEQIVIKITDGGYVTSKGDHYYNGKVPYDA 77
 |||||
 Db 47 AEQIVIKITDGGYVTSKGDHYYNGKVPYDA 78

RESULT 66

AAB12715
 ID AAB12715 standard; Protein; 1039 AA.

XX AAB12715;

DT 21-NOV-2000 (first entry)

DE Streptococcus pneumoniae BVH-3 protein antigen SEQ ID NO:2.

KW Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
 KM prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
 XX otitis media; pneumonia; immunisation; bactericidal.

XX Streptococcus pneumoniae.

PN WO200039299-A2.

XX 06-JUL-2000.

PF 20-DEC-1999; 99WO-CA01218.

PR 23-DEC-1998; 98US-0113800.

XX (BIOC-) BIOCHEM PHARMA INC.

PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;

DR WPI; 2000-452397/39.

DR N-PSDB; AAA65730.

PT Streptococcal antigens useful for vaccinating against e.g. meningitis,
 PT otitis media, bacteraemia and/or pneumonia

PS Claim 18; Fig 2; 106pp; English.

XX The present invention describes nucleic acids (I) encoding protein
 CC antigens (II) from Streptococcus pneumoniae. The protein antigens
 CC have bactericidal activity. The nucleic acids, encoding the protein
 CC antigens, may be used for the recombinant production of the proteins
 CC they encode. The protein antigens may then be used as vaccines for the
 CC prevention and treatment of Streptococcal infections in mammals
 CC (especially humans) which result in, e.g. meningitis, otitis media,
 CC bacteraemia and/or pneumonia. The present sequence represents the
 CC S. pneumoniae BVH-3 protein antigen.

XX Sequence 1039 AA:

Query Match 4.0%; Score 32; DB 21; Length 1039;
 Best Local Similarity 100.0%; Pred. No. 1.6e-21;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 46 AEQIVIKITDGGYVTSKGDHYYNGKVPYDA 77
 |||||
 Db 67 AEQIVIKITDGGYVTSKGDHYYNGKVPYDA 98

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 AEOIVIKITDQGYTSHGDHYHYNGKVPYDA 77
 DB 67 AEOIVIKITDQGYTSHGDHYHYNGKVPYDA 98

RESULT 69

ID AUB4094 standard; Peptide: 294 AA.

AC AUB4094;

DT 08-MAY-2002 (first entry)

DE Truncated variant of S. pneumoniae BVH-11-2, NEM18.

KW BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;

KW pneumoniae; streptococcal bacterial infection; mutant; mutein.

OS Streptococcus pneumoniae.

PN WO200198334-A2.

PD 27-DEC-2001.

PF 19-JUN-2001; 2001WO-CA00908.

PR 20-JUN-2000; 2000US-212683P.

XX (SHIR-) SHIRE BIOCHEM INC.

PI Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;

DR WPI; 2002-122272/16.

PT New Streptococcus pneumoniae BVH-3 and BVH-11 variant and

PT epitope-bearing polypeptides, useful as vaccine components for treating

PT or preventing streptococcal infections such as otitis media,

PT meningitis, and bacteraemia -

PS Example 1; Page -; 113pp; English.

XX The invention describes an isolated polypeptide (I) with 70-90%

CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of

CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)

CC comprising (I) is useful for therapeutic or prophylactic treatment of

CC meningitis, otitis media, bacteraemia or pneumonia infection in an

CC individual susceptible to these disorders. (II) is also useful for

CC therapeutic or prophylactic treatment of any streptococcal bacterial

CC infection (e.g., caused by Streptococcus pneumoniae, group A

CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such

CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardiae or

CC Streptococcus aureus) in an individual susceptible to the infection.

CC A polynucleotide (III) encoding (I) is useful in DNA immunisation

CC techniques. The Streptococcus polypeptides are useful in a diagnostic

CC test for S. pneumoniae infection. (III) is useful for designing DNA

CC probes for use in detecting the presence of Streptococcus in a biological

CC sample suspected of containing the bacteria. The DNA probes may also be

CC used for detecting circulating S. pneumonia nucleic acid in a sample for

CC diagnosing streptococcal infections. This sequence represents a truncate

CC of a Streptococcus pneumoniae gene used to obtain antigenic peptides,

CC described in the method of the invention.

CC Note: This sequence does not appear in the specification but has

CC been created according to information given in the invention.

CC

XX

SQ Sequence 294 AA;

Query Match 3.4%; Score 27; DB 23; Length 294;

Best Local Similarity 100.0%; Pred. No. 3.4e-17;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 326 RIARILPLRYSRNMHWVPSRPEQSPQ 352

DB 106 RIARILPLRYSRNMHWVPSRPEQSPQ 132

RESULT 70

ID ABP26208 standard; Protein: 466 AA.

AC ABP26208;

DT 02-JUL-2002 (first entry)

DE Streptococcus polypeptide SEQ ID NO 1592.

KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

KW group A streptococcus; Streptococcus pyogenes; antibacterial;

OS Streptococcus agalactiae.

PN WO200234771-A2.

PD 02-MAY-2002.

PF 29-OCT-2001; 2001WO-GB04789.

PR 27-OCT-2000; 2000GB-0026333.

PR 24-NOV-2000; 2000GB-0028727.

PR 07-MAR-2001; 2001GB-0005640.

XX (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

PI Telford J, Massignani V, Margarit Ros YI, Grandi G, Fraser C;

DR Tectelin H;

DR WPI; 2002-352536/38.

DR N-PSDB; ABN66839.

PT New Streptococcus protein for the treatment or prevention of infection

PT or disease caused by Streptococcus bacteria, such as meningitis, and

PT for detecting a compound that binds to the protein -

PS Claim 1; Page 3310; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B

CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS

CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in

CC the specification. The proteins have antibacterial and anti-inflammatory

CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and

CC antibodies that bind (I) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by

CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

CC Nucleic acids encoding (I) are used to detect Streptococcus in a

CC biological sample. (I) is used to determine whether a compound binds to

CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be

CC used as a vaccine or diagnostic composition. The disease caused by

CC Streptococcus that is prevented or treated may be meningitis. Nucleic

CC acid encoding (I) may be used to recombinantly produce (I) and may be

CC used in gene therapy. Antibodies to (I) are used for affinity

CC chromatography, immunoassays, and distinguishing/identifying

CC Streptococcus proteins.

XX

SQ Sequence 466 AA;

Query Match 3.4%; Score 27; DB 23; Length 466;

Best Local Similarity 100.0%; Pred. No. 5.2e-17;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 57 GYVTSBGDHYHYNGKVPYDAIISEEL 83

DB 81 GYVTSBGDHYHYNGKVPYDAIISEEL 107

```
RESULT 71
AAB12743
ID AAB12743 standard; Protein; 473 AA.
XX
AC AAB12743;
XX
DT 21-NOV-2000 (first entry)
XX
DE Streptococcus pneumoniae NEW12 protein antigen SEQ ID NO:77.
XX
KM Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
XX
XX ctitis media; pneumonia; immunisation; bactericidal.
XX
OS Streptococcus pneumoniae.
XX
PN WO200039299-A2.
XX
PD 06-JUL-2000.
XX
PF 20-DEC-1999; 99WO-CA01218.
XX
PR 23-DEC-1998; 98US-0113800.
XX
PA (BIOC-) BIOCHEM PHARMA INC.
XX
PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
DR WPI; 2000-452397/39.
XX
PT Streptococcal antigens useful for vaccinating against e.g. meningitis,
XX
XX ctitis media, bacteraemia and/or pneumonia -
XX
PS Claim 18; Fig 42; 106pp; English.
XX
CC The present invention describes nucleic acids (I) encoding protein
CC antigens (II) from Streptococcus pneumoniae. The protein antigens
CC have bactericidal activity. The nucleic acids, encoding the proteins
CC antigens, may be used for the recombinant production of the proteins
CC they encode. The protein antigens may then be used as vaccines for the
CC prevention and treatment of Streptococcal infections in mammals
CC (especially humans) which result in, e.g. meningitis, ctitis media,
CC bacteraemia and/or pneumonia. The present sequence represents the
CC S. pneumoniae NEW14 protein antigen.
XX
SQ Sequence 473 AA;
XX
Query Match 3.4%; Score 27; DB 21; Length 473;
Best Local Similarity 100.0%; Pred. No. 5.3e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 326 RIARIIPLRYSNHWVDSRPEQSPQ 352
DB 106 RIARIIPLRYSNHWVDSRPEQSPQ 132
XX
RESULT 72
AAB12741
ID AAB12741 standard; Peptide; 473 AA.
XX
AC AAB12741;
XX
DT 08-MAY-2002 (first entry)
XX
DE Truncated variant of S. pneumoniae BVH-11-2, NEW14.
XX
KM BVH-3; BVH-11; vaccine; meningitis; ctitis media; bacteraemia;
XX
XX pneumonia; streptococcal bacterial infection; mutant; mtein.
XX
OS Streptococcus pneumoniae.
XX
PN WO200198334-A2.
```

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XX
PD 27-DEC-2001.
XX
PF 19-JUN-2001; 2001WO-CA00908.
XX
PR 20-JUN-2000; 2000US-212683P.
XX
PA (SHIR-) SHIRE BIOCHEM INC.
XX
PI Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
DR WPI; 2002-122272/16.
XX
PT New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
XX
XX epitope-bearing polypeptides, useful as vaccine components for treating
XX
XX or preventing streptococcal infections such as ctitis media,
XX
XX meningitis, and bacteraemia -
XX
XX Example 1; Page -, 113pp; English.
XX
CC The invention describes an isolated polypeptide (I) with 70-90%
CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC comprising (I) is useful for therapeutic or prophylactic treatment of
CC meningitis, ctitis media, bacteraemia or pneumonia infection in an
CC individual susceptible to these disorders. (II) is also useful for
CC therapeutic or prophylactic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. novacardia or
CC Staphylococcus aureus) in an individual susceptible to the infection.
CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for S. pneumoniae infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating S. pneumonia nucleic acid in a sample for
CC diagnosing streptococcal infections. This sequence represents a truncate
CC of a Streptococcus pneumoniae gene used to obtain antigenic peptides,
CC described in the method of the invention.
CC Note: This sequence does not appear in the specification but has
CC been created according to information given in the invention.
XX
SQ Sequence 473 AA;
XX
Query Match 3.4%; Score 27; DB 23; Length 473;
Best Local Similarity 100.0%; Pred. No. 5.3e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 326 RIARIIPLRYSNHWVDSRPEQSPQ 352
DB 106 RIARIIPLRYSNHWVDSRPEQSPQ 132
XX
RESULT 73
AAB12741
ID AAB12741 standard; Protein; 568 AA.
XX
AC AAB12741;
XX
DT 21-NOV-2000 (first entry)
XX
DE Streptococcus pneumoniae NEW10 protein antigen SEQ ID NO:74.
XX
KM Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
XX
XX prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
XX
XX ctitis media; pneumonia; immunisation; bactericidal.
XX
OS Streptococcus pneumoniae.
XX
PN WO200039299-A2.
XX
PD 06-JUL-2000.
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XX 20-DEC-1999; 99WO-CA01218.
XX
XX 23-DEC-1998; 98US-0113800.
XX
XX (BIOC-) BIOCHEM PHARMA INC.
XX
XX Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N,
XX WPI; 2000-452397/39.
XX
XX Streptococcal antigens useful for vaccinating against e.g. meningitis,
XX otitis media, bacteraemia and/or pneumonia -
XX
XX Claim 18; Fig 39; 106pp; English.
XX
XX The present invention describes nucleic acids (I) encoding protein
XX antigens (II) from Streptococcus pneumoniae. The protein antigens
XX have bactericidal activity. The nucleic acids, encoding the protein
XX antigens, may be used for the recombinant production of the proteins
XX they encode. The protein antigens may then be used as vaccines for the
XX prevention and treatment of Streptococcal infections in mammals
XX (especially humans) which result in, e.g. meningitis, otitis media,
XX bacteraemia and/or pneumonia. The present sequence represents the
XX S. pneumoniae NEW10 protein antigen.
XX
XX Sequence 568 AA;
SQ

Query Match 3.4%; Score 27; DB 21; Length 568;
Best Local Similarity 100.0%; Pred. No. 6,2e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 326 RIARIIPLRYSNHWVPSRPEQSPQ 352
Db 62 RIARIIPLRYSNHWVPSRPEQSPQ 88

RESULT 74
AAU84088
ID AAU84088 standard; Peptide; 568 AA.
XX
XX AAU84088;
AC
XX 08-MAY-2002 (first entry)
DT
XX Truncated variant of S. pneumoniae BVH-11-2, NEW10.
DE
XX BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
KW pneumonia; streptococcal bacterial infection; mutant; mutein.
XX
XX Streptococcus pneumoniae.
OS
XX WO200198334-A2.
PN
XX 27-DEC-2001.
PD
XX 19-JUN-2001; 2001WO-CA00908.
PF
XX 20-JUN-2000; 2000US-212683P.
PR
XX (SHIR-) SHIRE BIOCHEM INC.
PA
XX Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
PI WPI; 2002-122272/16.
DR
XX New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
XX epitope-bearing polypeptides, useful as vaccine components for treating
XX or preventing streptococcal infections such as otitis media,
XX meningitis, and bacteraemia -
XX
XX Example 1; Page -, 113pp; English.
XX

CC The invention describes an isolated polypeptide (I) with 70-90%
CC identity to Streptococcus pneumoniae protein BVH-3, BVH-11, variants of
CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC comprising (I) is useful for therapeutic or prophylactic treatment of
CC meningitis, otitis media, bacteraemia or pneumonia infection in an
CC individual susceptible to these disorders. (II) is also useful for
CC therapeutic or prophylactic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. novarcia or
CC Streptococcus aureus) in an individual susceptible to the infection.
CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for S. pneumoniae infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating S. pneumonia nucleic acid in a sample for
CC diagnosing streptococcal infections. This sequence represents a truncate
CC of a Streptococcus pneumoniae gene used to obtain antigenic peptides,
CC described in the method of the invention.
CC Note: This sequence does not appear in the specification but has
CC been created according to information given in the invention.
XX
XX Sequence 568 AA;
SQ

Query Match 3.4%; Score 27; DB 23; Length 568;
Best Local Similarity 100.0%; Pred. No. 6,2e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 326 RIARIIPLRYSNHWVPSRPEQSPQ 352
Db 62 RIARIIPLRYSNHWVPSRPEQSPQ 88

RESULT 75
AAU84031
ID AAU84031 standard; Peptide; 612 AA.
XX
XX AAU84031;
AC
XX 08-MAY-2002 (first entry)
DT
XX Truncated variant of S. pneumoniae BVH-11, NEW24.
DE
XX BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
KW pneumonia; streptococcal bacterial infection; mutant; mutein.
XX
XX Streptococcus pneumoniae.
OS
XX WO200198334-A2.
PN
XX 27-DEC-2001.
PD
XX 19-JUN-2001; 2001WO-CA00908.
PF
XX 20-JUN-2000; 2000US-212683P.
PR
XX (SHIR-) SHIRE BIOCHEM INC.
PA
XX Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
PI WPI; 2002-122272/16.
DR
XX New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
XX epitope-bearing polypeptides, useful as vaccine components for treating
XX or preventing streptococcal infections such as otitis media,
XX meningitis, and bacteraemia -
XX
XX Example 1; Page -, 113pp; English.
XX
XX The invention describes an isolated polypeptide (I) with 70-90%
XX identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC

CC meningitis, otitis media, bacteraemia or pneumonia infection in an
CC individual susceptible to these disorders. (II) is also useful for
CC therapeutic or prophylactic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardiae or
CC Streptococcus aureus) in an individual susceptible to the infection.
CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for S. pneumoniae infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating S. pneumonia nucleic acid in a sample for
CC diagnosing streptococcal infections. This sequence represents a chimeric
CC gene created from fragments and variant fragments of Streptococcus
CC pneumoniae genes, described in the method of the invention.
CC Note: This sequence does not appear in the specification but has
CC been created according to information given in the invention.

SQ Sequence 1378 AA;

Query Match 3.4%; Score 27; DB 23; Length 1378;
Best Local Similarity 100.0%; Pred. No. 1,4e-16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 326 RIARIIPRYRSNMWVPDSRPEQSPQ 352

Db 63 RIARIIPRYRSNMWVPDSRPEQSPQ 89

RESULT 78
AAV91938
ID AAV91938 standard; Protein; 168 AA.

AC AAV91938;

DT 19-JUL-2000 (first entry)

DE S. pneumoniae 20 kDa human C3-degrading protein.

XX Human C3-degrading protein; 20 kDa; immunostimulatory; vaccine;
XX inhibitor; inflammation; organ rejection; xenotransplantation.

OS Streptococcus pneumoniae.

PN WO200017370-A1.

PD 30-MAR-2000.

PF 24-SEP-1999; 99WO-US22362.

PR 24-SEP-1998; 98US-0101736.

PR 31-MAR-1999; 99US-0283094.

PA (MINU) UNIV MINNESOTA.

PA (AMCY) AMERICAN CYANAMID CO.

PI Hostetter MK, Finkel DJ, Cheng Q, Green BA, Masi AW;

DR WPI; 2000-283594/24.

DR N-PSDB; AAA08556.

PT Isolated polypeptide is used to stimulate immune system and immunize or

PT treat a mammalian subject against Streptococcus pneumoniae infection or

PT colonization

PS Claim 8; Page 54-55; 63pp; English.

CC The present sequence, isolated from Streptococcus pneumoniae, is a
CC human C3-degrading protein of about 20 kDa. This sequence may be part
CC of a larger, approximately 92 kDa protein (see AAV91939), also having
CC human C3-degrading activity. The DNA sequences (AAA08556-57) can be
CC used for producing an immune response to Streptococcus pneumoniae in a

CC mammal. Antibodies against the proteins can be used to inhibit
CC S. pneumoniae-mediated C3 degradation. C3-mediated inflammation and
CC rejection in xenotransplantation can be inhibited by expressing the
CC nucleic acid sequences on the surface of an organ of an animal. In
CC particular, the polypeptides are useful for stimulating the immune
CC system and are effective to immunize or treat a mammalian subject
CC against Streptococcus pneumoniae infection or colonization.

SQ Sequence 168 AA;

Query Match 3.1%; Score 25; DB 21; Length 168;
Best Local Similarity 100.0%; Pred. No. 1,8e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 328 ARIIPRYRSNMWVPDSRPEQSPQ 352

Db 62 ARIIPRYRSNMWVPDSRPEQSPQ 86

RESULT 79
AAB12738
ID AAB12738 standard; Protein; 226 AA.

AC AAB12738;

DT 21-NOV-2000 (first entry)

DE Streptococcus pneumoniae NEM8 protein antigen SEQ ID NO:71.

XX Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
XX prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
XX otitis media; pneumonia; immunisation; bactericidal.

OS Streptococcus pneumoniae.

PN WO200039299-A2.

PD 06-JUL-2000.

PF 20-DEC-1999; 99WO-CA01218.

PR 23-DEC-1998; 98US-0113800.

PA (BIOC-) BIOCHEM PHARMA INC.

PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;

DR WPI; 2000-452397/39.

PT Streptococcal antigens useful for vaccinating against e.g. meningitis,

PT otitis media, bacteraemia and/or pneumonia -

PS Claim 18; Fig 36; 106pp; English.

CC The present invention describes nucleic acids (I) encoding protein
CC antigens (II) from Streptococcus pneumoniae. The protein antigens
CC have bactericidal activity. The nucleic acids, encoding the proteins
CC antigens, may be used for the recombinant production of the proteins
CC they encode. The protein antigens may then be used as vaccines for the
CC prevention and treatment of Streptococcal infections in mammals
CC (especially humans) which result in, e.g. meningitis, otitis media,
CC bacteraemia and/or pneumonia. The present sequence represents the
CC S. pneumoniae NEM8 protein antigen.

SQ Sequence 226 AA;

Query Match 3.0%; Score 24; DB 21; Length 226;
Best Local Similarity 100.0%; Pred. No. 2,1e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 266 DIDLKQLYKPLPSQRHVESDGL 289

Db 1 DIDLKQLYKPLPSQRHVESDGL 24

RESULT 80

ID AAB12735 standard; Protein; 428 AA.

XX AC AAB12735;

XX DT 21-NOV-2000 (first entry)

XX DE Streptococcus pneumoniae NEWS protein antigen SEQ ID NO:68.

XX KW Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;

XX KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;

XX KW otitis media; pneumonia; immunisation; bactericidal.

XX OS Streptococcus pneumoniae.

XX PN WO200039299-A2.

XX PD 06-JUL-2000.

XX PF 20-DEC-1999; 99WO-CA01218.

XX PR 23-DEC-1998; 98US-0113800.

XX PA (BIOC-) BIOCHEM PHARMA INC.

XX PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N,

XX DR WPI; 2000-452397/39.

XX PT Streptococcal antigens useful for vaccinating against e.g. meningitis,

XX PT otitis media, bacteraemia and/or pneumonia -

XX PS Claim 18; Fig 33; 106pp; English.

XX CC The present invention describes nucleic acids (I) encoding protein

XX CC antigens (II) from Streptococcus pneumoniae. The protein antigens

XX CC have bactericidal activity. The nucleic acids, encoding the protein

XX CC antigens, may be used for the recombinant production of the proteins

XX CC they encode. The protein antigens may then be used as vaccines for the

XX CC prevention and treatment of Streptococcal infections in mammals

XX CC (especially humans) which result in, e.g. meningitis, otitis media,

XX CC bacteraemia and/or pneumonia. The present sequence represents the

XX CC S. pneumoniae NEWS protein antigen.

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX AC AAB12735;

XX DT 21-NOV-2000 (first entry)

XX DE Streptococcus pneumoniae NEWS protein antigen SEQ ID NO:68.

XX KW Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;

XX KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;

XX KW otitis media; pneumonia; immunisation; bactericidal.

XX OS Streptococcus pneumoniae.

XX PN WO200039299-A2.

XX PD 06-JUL-2000.

XX PF 20-DEC-1999; 99WO-CA01218.

XX PR 23-DEC-1998; 98US-0113800.

XX PA (BIOC-) BIOCHEM PHARMA INC.

XX PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N,

XX DR WPI; 2000-452397/39.

XX PT Streptococcal antigens useful for vaccinating against e.g. meningitis,

XX PT otitis media, bacteraemia and/or pneumonia -

XX PS Claim 18; Fig 33; 106pp; English.

XX CC The present invention describes nucleic acids (I) encoding protein

XX CC antigens (II) from Streptococcus pneumoniae. The protein antigens

XX CC have bactericidal activity. The nucleic acids, encoding the protein

XX CC antigens, may be used for the recombinant production of the proteins

XX CC they encode. The protein antigens may then be used as vaccines for the

XX CC prevention and treatment of Streptococcal infections in mammals

XX CC (especially humans) which result in, e.g. meningitis, otitis media,

XX CC bacteraemia and/or pneumonia. The present sequence represents the

XX CC S. pneumoniae NEWS protein antigen.

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

RESULT 81

ID AAB12735 standard; Peptide; 226 AA.

XX AC AAB12735;

XX DT 08-MAY-2002 (first entry)

XX DE Truncated variant of S. pneumoniae BVH-11, NEWS.

XX KW BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;

XX KW pneumonia; streptococcal bacterial infection; mutant; mutein.

XX OS Streptococcus pneumoniae.

XX PN WO200198334-A2.

XX PD 27-DEC-2001.

XX PF 19-JUN-2001; 2001WO-CA00908.

XX PR 20-JUN-2000; 2000US-212683P.

XX PA (SHIR-) SHIRE BIOCHEM INC.

XX PI Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;

XX DR WPI; 2002-122272/16.

XX PT New Streptococcus pneumoniae BVH-3 and BVH-11 variant and

XX PT epitope-bearing polypeptides, useful as vaccine components for treating

XX PT meningitis, and bacteraemia -

XX PS Example 1; Page -; 113pp; English.

XX CC The invention describes an isolated polypeptide (I) with 70-90%

XX CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of

XX CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)

XX CC comprising (I) is useful for therapeutic or prophylactic treatment of

XX CC meningitis, otitis media, bacteraemia or pneumonia infection in an

XX CC individual susceptible to these disorders. (II) is also useful for

XX CC therapeutic or prophylactic treatment of any streptococcal bacterial

XX CC infection (e.g., caused by Streptococcus pneumoniae, group A

XX CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such

XX CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. novae or

XX CC Streptococcus aureus) in an individual susceptible to the infection.

XX CC A polynucleotide (III) encoding (I) is useful in DNA immunisation

XX CC techniques. The Streptococcus polypeptides are useful in a diagnostic

XX CC test for S. pneumoniae infection. (III) is useful for designing DNA

XX CC probes for use in detecting the presence of Streptococcus in a biological

XX CC sample suspected of containing the bacteria. The DNA probes may also be

XX CC used for detecting circulating S. pneumonia nucleic acid in a sample for

XX CC diagnosing streptococcal infections. This sequence represents a truncate

XX CC of a Streptococcus pneumoniae gene used to obtain antigenic peptides,

RESULT 82

ID AAB12735 standard; Peptide; 428 AA.

XX AC AAB12735;

XX DT 08-MAY-2002 (first entry)

XX DE Truncated variant of S. pneumoniae BVH-11, NEWS.

XX KW BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;

XX KW pneumonia; streptococcal bacterial infection; mutant; mutein.

XX OS Streptococcus pneumoniae.

XX PN WO200198334-A2.

XX PD 27-DEC-2001.

XX PF 19-JUN-2001; 2001WO-CA00908.

XX PR 20-JUN-2000; 2000US-212683P.

XX PA (SHIR-) SHIRE BIOCHEM INC.

XX PI Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;

XX DR WPI; 2002-122272/16.

XX PT New Streptococcus pneumoniae BVH-3 and BVH-11 variant and

XX PT epitope-bearing polypeptides, useful as vaccine components for treating

XX PT meningitis, and bacteraemia -

XX PS Example 1; Page -; 113pp; English.

XX CC The invention describes an isolated polypeptide (I) with 70-90%

XX CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of

XX CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)

XX CC comprising (I) is useful for therapeutic or prophylactic treatment of

XX CC meningitis, otitis media, bacteraemia or pneumonia infection in an

XX CC individual susceptible to these disorders. (II) is also useful for

XX CC therapeutic or prophylactic treatment of any streptococcal bacterial

XX CC infection (e.g., caused by Streptococcus pneumoniae, group A

XX CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such

XX CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. novae or

XX CC Streptococcus aureus) in an individual susceptible to the infection.

XX CC A polynucleotide (III) encoding (I) is useful in DNA immunisation

XX CC techniques. The Streptococcus polypeptides are useful in a diagnostic

XX CC test for S. pneumoniae infection. (III) is useful for designing DNA

XX CC probes for use in detecting the presence of Streptococcus in a biological

XX CC sample suspected of containing the bacteria. The DNA probes may also be

XX CC used for detecting circulating S. pneumonia nucleic acid in a sample for

XX CC diagnosing streptococcal infections. This sequence represents a truncate

XX CC of a Streptococcus pneumoniae gene used to obtain antigenic peptides,

PD		27-DEC-2001.	
XX	PF	19-JUN-2001; 2001WO-CA00908.	
PR	XX	20-JUN-2000; 2000US-212683P.	
XX	PA	(SHIR-) SHIRE BIOCHEM INC.	
XX	PI	Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;	
XX	DR	WPI; 2002-122272/16.	
XX	PT	New Streptococcus pneumoniae BVH-3 and BVH-11 variant and	
XX	PT	epitope-bearing polypeptides, useful as vaccine components for treating	
XX	PT	or preventing streptococcal infections such as otitis media,	
XX	PT	meningitis, and bacteraemia	
PS		Example 1; Page -; 113pp; English.	
XX	CC	The invention describes an isolated polypeptide (I) with 70-90%	
XX	CC	identity to Streptococcus pneumonia protein BVH-3, BVH-11,' variants of	
XX	CC	BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)	
XX	CC	comprising (I) is useful for therapeutic or prophylactic treatment of	
XX	CC	meningitis, otitis media, bacteraemia or pneumonia infection in an	
XX	CC	individual susceptible to these disorders. (II) is also useful for	
XX	CC	therapeutic or prophylactic treatment of any streptococcal bacterial	
XX	CC	infection (e.g., caused by Streptococcus pneumoniae, group A	
XX	CC	Streptococcus such as Streptococcus pyogenes, group B Streptococcus such	
XX	CC	as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. norcardia or	
XX	CC	Staphylococcus aureus) in an individual susceptible to the infection.	
XX	CC	A polynucleotide (III) encoding (I) is useful in DNA immunisation	
XX	CC	techniques. The Streptococcus polypeptides are useful in diagnostic	
XX	CC	tests for S. pneumoniae infection. (III) is useful for designing DNA	
XX	CC	probes for use in detecting the presence of Streptococcus in a biological	
XX	CC	sample suspected of containing the bacteria. The DNA probes may also be	
XX	CC	used for detecting circulating S. pneumonia nucleic acid in a sample for	
XX	CC	diagnosing streptococcal infections. This sequence represents a truncate	
XX	CC	of a Streptococcus pneumoniae gene used to obtain antigenic peptides,	
XX	CC	described in the method of the invention.	
XX	CC	Note: This sequence does not appear in the specification but has	
XX	CC	been created according to information given in the invention.	
SQ		Sequence 428 AA.	
QY		Query Match 3.0%; Score 24; DB 23; Length 428;	
Dd		Best Local Similarity 100.0%; Pred. No. 3.8e-14;	
		Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
		266 DIDSLKOLYKLPISORHVESGGL 289	
		1 DIDSLKOLYKLPISORHVESDGL 24	
RESULT 83			
ID		AAB12734	
AC		AAB12734 standard; Protein; 555 AA.	
XX		AAB12734;	
XX		21-NOV-2000 (first entry)	
DE		Streptococcus pneumoniae NEW4 protein antigen SRQ ID NO:67.	
XX		Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; Vaccine;	
KW		prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;	
XX		otitis media; pneumonia; immunisation; bactericidal.	
OS		Streptococcus pneumoniae.	
XX			
FN		WO200039299-A2.	
XX			
PD		06-JUL-2000.	

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PF      20-DEC-1999;    99WO-CA01218.
XX      XX
BR      23-DEC-1998;    98US-0113800.
XX      XX
PA      (BIOC-) BIOCHEM PHARMA INC.
XX      XX
PI      Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
XX      DR
XX      WPI; 2000-452397/39.
XX      XX
PS      Claim 18; Fig 32; 106pp; English.
XX      XX
CC      The present invention describes nucleic acids (I) encoding protein
CC      antigens (II) from Streptococcus pneumoniae. The protein antigens
CC      have bactericidal activity. The nucleic acids, encoding the proteins
CC      antigens, may be used for the recombinant production of the proteins
CC      they encode. The protein antigens may then be used as vaccines for the
CC      prevention and treatment of Streptococcal infections in mammals
CC      (especially humans) which result in, e.g. meningitis, otitis media,
CC      bacteraemia and/or pneumonia. The present sequence represents the
CC      S. pneumoniae NEW4 protein antigen.
XX      CC
SQ      Sequence    555 AA;

Query Match          3.0%; Score 24; DB 21; Length 555;
Best Local Similarity 100.0%; Pred. No. 4,8e-14;
Matches   24; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

QY      266 DIDSILKQLYKLPISQRHVESDGL 289
        ||| ||||| ||||| ||||| |||
DB      1 DIDSILKQLYKLPISQRHVESDGL 24

RESULT 84
AAU84047
ID      AAU84047 standard; Peptide; 555 AA.
XX      AC
XX      AAU84047;
XX      DT
XX      DT      08-MAY-2002 (first entry)
DE      Truncated variant of S. pneumoniae BVH-11, NEW4.
XX      KW
XX      BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
KW      pneumonia; streptococcal bacterial infection; mutant; mutein.
XX      OS
XX      Streptococcus pneumoniae.
OS      Synthetic.
XX      PN
XX      WO200198334-A2.
XX      PD
XX      PD      27-DEC-2001.
XX      PF
XX      PF      19-JUN-2001; 2001WO-CA00908.
XX      PR
XX      PR      20-JUN-2000; 2000US-212683P.
PA      (SHIR-) SHIRE BIOCHEM INC.
XX      PI
XX      PI      Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;
XX      DR
XX      DR      WPI; 2002-122272/16.
XX      PT
XX      PT      New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
PT      epitope-bearing polypeptides, useful as vaccine components for treating
PT      or preventing streptococcal infections such as otitis media,
PT      meningitis, and bacteraemia -
XX      XX
XX      Example 1; Page -, 113pp; English.

```


CC The invention describes an isolated polypeptide (I) with 70-90%
CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC comprising (I) is useful for therapeutic or prophylactic treatment of
CC meningitis, otitis media, bacteraemia or pneumonia infection in an
CC individual susceptible to these disorders. (II) is also useful for
CC therapeutic or prophylactic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. novardi or
CC Streptococcus aureus) in an individual susceptible to the infection.
CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for S. pneumoniae infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating S. pneumonia nucleic acid in a sample for
CC diagnosing streptococcal infections. This sequence represents a truncate
CC of a Streptococcus pneumoniae gene used to obtain antigenic peptides,
CC described in the method of the invention.
CC Note: This sequence does not appear in the specification but has
CC been created according to information given in the invention.

SQ Sequence 555 AA:

Query Match 3.0%; Score 24; DB 23; Length 555;
Best Local Similarity 100.0%; Pred. No. 4.8e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 266 DIDSLLKQLYKPLSQRHVESDGL 289
DB 1 DIDSLLKQLYKPLSQRHVESDGL 24
|||||

RESULT 85

AAU84051 standard; Peptide; 999 AA.

AC AAU84051;

DT 08-MAY-2002 (first entry)

DE S. pneumoniae derived chimeric peptide, NEW17.

KV BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;

KW pneumonia; streptococcal bacterial infection; mutant; mutein;

KM BVH-11-2.

XX Streptococcus pneumoniae.

OS Synthetic.

XX WO200198334-A2.

PN 27-DEC-2001.

PD 19-JUN-2001; 2001WO-CA00908.

PF 20-JUN-2000; 2000US-212683P.

PR (SHIR-) SHIRE BIOCHEM INC.

PI Hamel J, Quillet C, Charland N, Martin D, Brodeur B;

PA WPI; 2002-122272/16.

DR New Streptococcus pneumoniae BVH-3 and BVH-11 variant and

XX PT epitope-bearing polypeptides, useful as vaccine components for treating

XX PT or preventing streptococcal infections such as otitis media,

XX PT meningitis, and bacteraemia

XX PS Example 1; Page -; 113pp; English.

XX CC The invention describes an isolated polypeptide (I) with 70-90%

CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC comprising (I) is useful for therapeutic or prophylactic treatment of
CC meningitis, otitis media, bacteraemia or pneumonia infection in an
CC individual susceptible to these disorders. (II) is also useful for
CC therapeutic or prophylactic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. novardi or
CC Streptococcus aureus) in an individual susceptible to the infection.
CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for S. pneumoniae infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating S. pneumonia nucleic acid in a sample for
CC diagnosing streptococcal infections. This sequence represents a chimeric
CC gene created from fragments and variant fragments of Streptococcus
CC pneumoniae genes, described in the method of the invention.
CC Note: This sequence does not appear in the specification but has
CC been created according to information given in the invention.

SQ Sequence 999 AA:

Query Match 3.0%; Score 24; DB 23; Length 999;
Best Local Similarity 100.0%; Pred. No. 8.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 266 DIDSLLKQLYKPLSQRHVESDGL 289
DB 2 DIDSLLKQLYKPLSQRHVESDGL 25
|||||

RESULT 86

AAU84052 standard; Peptide; 999 AA.

AC AAU84052;

DT 08-MAY-2002 (first entry)

DE S. pneumoniae derived chimeric peptide, NEW20.

KV BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;

KW pneumonia; streptococcal bacterial infection; mutant; mutein;

KM BVH-11-2.

XX Streptococcus pneumoniae.

OS Synthetic.

XX WO200198334-A2.

PN 27-DEC-2001.

PD 19-JUN-2001; 2001WO-CA00908.

PF 20-JUN-2000; 2000US-212683P.

PR (SHIR-) SHIRE BIOCHEM INC.

PI Hamel J, Quillet C, Charland N, Martin D, Brodeur B;

PA WPI; 2002-122272/16.

DR New Streptococcus pneumoniae BVH-3 and BVH-11 variant and

XX PT epitope-bearing polypeptides, useful as vaccine components for treating

XX PT or preventing streptococcal infections such as otitis media,

XX PT meningitis, and bacteraemia

XX PS Example 1; Page -; 113pp; English.

XX CC The invention describes an isolated polypeptide (I) with 70-90%

CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of

CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC comprising (I) is useful for therapeutic or prophylactic treatment of
CC meningitis, otitis media, bacteraemia or pneumonia infection in an
CC individual susceptible to these disorders. (II) is also useful for
CC therapeutic or prophylactic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. novacardia or
CC Streptococcus aureus) in an individual susceptible to the infection.
CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for S. pneumoniae infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating S. pneumonia nucleic acid in a sample for
CC diagnosing streptococcal infections. This sequence represents a chimeric
CC gene created from fragments and variant fragments of Streptococcus
CC pneumoniae genes, described in the method of the invention.
CC Note: This sequence does not appear in the specification but has
CC been created according to information given in the invention.

SO Sequence 999 AA;

Query Match 3.0%; Score 24; DB 23; Length 999;
Best Local Similarity 100.0%; Pred. No. 8.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DIDSLLKQLYKPLSQRHVESDGL 289
Db 572 DIDSLLKQLYKPLSQRHVESDGL 595

RESULT 87

ID AAU84058 standard; Peptide; 1126 AA.

AC AAU84058;

DT 08-MAY-2002 (first entry)

DE S. pneumoniae derived chimeric peptide, NEW31.

KW BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;

KW pneumonia; streptococcal bacterial infection; mutant; mutein;

KW BVH-11-2.

OS Streptococcus pneumoniae.

OS Synthetic.

PN WO200198334-A2.

PD 27-DEC-2001.

PF 19-JUN-2001; 2001WO-CA00908.

PR 20-JUN-2000; 2000US-212683P.

PA (SHIR-) SHIRE BIOCHEM INC.

PI Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;

DR WPI; 2002-122272/16.

PT New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
PT epitope-bearing polypeptides, useful as vaccine components for treating
PT or preventing streptococcal infections such as otitis media,
PT meningitis, and bacteraemia

PS Example 1; Page -; 113pp; English.

CC The invention describes an isolated polypeptide (I) with 70-90%
CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)

CC comprising (I) is useful for therapeutic or prophylactic treatment of
CC meningitis, otitis media, bacteraemia or pneumonia infection in an
CC individual susceptible to these disorders. (II) is also useful for
CC therapeutic or prophylactic treatment of any streptococcal bacterial
CC infection (e.g., caused by Streptococcus pneumoniae, group A
CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. novacardia or
CC Streptococcus aureus) in an individual susceptible to the infection.
CC A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC techniques. The Streptococcus polypeptides are useful in a diagnostic
CC test for S. pneumoniae infection. (III) is useful for designing DNA
CC probes for use in detecting the presence of Streptococcus in a biological
CC sample suspected of containing the bacteria. The DNA probes may also be
CC used for detecting circulating S. pneumonia nucleic acid in a sample for
CC diagnosing streptococcal infections. This sequence represents a chimeric
CC gene created from fragments and variant fragments of Streptococcus
CC pneumoniae genes, described in the method of the invention.
CC Note: This sequence does not appear in the specification but has
CC been created according to information given in the invention.

SO Sequence 1126 AA;

Query Match 3.0%; Score 24; DB 23; Length 1126;
Best Local Similarity 100.0%; Pred. No. 9.1e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DIDSLLKQLYKPLSQRHVESDGL 289
Db 2 DIDSLLKQLYKPLSQRHVESDGL 25

RESULT 88

ID AAU84056 standard; Peptide; 1238 AA.

AC AAU84056;

DT 08-MAY-2002 (first entry)

DE S. pneumoniae derived chimeric peptide, NEW29.

KW BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;

KW pneumonia; streptococcal bacterial infection; mutant; mutein;

KW BVH-11-2.

OS Streptococcus pneumoniae.

OS Synthetic.

PN WO200198334-A2.

PD 27-DEC-2001.

PF 19-JUN-2001; 2001WO-CA00908.

PR 20-JUN-2000; 2000US-212683P.

PA (SHIR-) SHIRE BIOCHEM INC.

PI Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;

DR WPI; 2002-122272/16.

PT New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
PT epitope-bearing polypeptides, useful as vaccine components for treating
PT or preventing streptococcal infections such as otitis media,
PT meningitis, and bacteraemia

PS Example 1; Page -; 113pp; English.

CC The invention describes an isolated polypeptide (I) with 70-90%
CC identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC comprising (I) is useful for therapeutic or prophylactic treatment of

meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus pyogenes, group B Streptococcus such as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardiae or Streptococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a chimeric gene created from fragments and variant fragments of Streptococcus pneumoniae genes, described in the method of the invention. Note: This sequence does not appear in the specification but has been created according to information given in the invention.

Sequence 1238 AA;

Query Match 3.0%; Score 24; DB 23; Length 1238;
Best Local Similarity 100.0%; Pred. No. 9.9e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DIDSLKQLYKPLPSQRHVESDGL 289
DB 2 DIDSLKQLYKPLPSQRHVESDGL 25

RESULT 89

AAU84057
ID AAU84057 standard; Peptide; 1365 AA.

AAU84057;

08-MAY-2002 (first entry)

S. pneumoniae derived chimeric peptide, NEM30.

BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;

pneumonia; streptococcal bacterial infection; mutant; mutein;

BVH-11-2.

Streptococcus pneumoniae.

Synthetic.

WO200198334-A2.

27-DEC-2001.

19-JUN-2001; 2001WO-CA00908.

20-JUN-2000; 2000US-212683P.

(SHIR-) SHIRE BIOCHEM INC.

Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;

WPI; 2002-122272/16.

New Streptococcus pneumoniae BVH-3 and BVH-11 variant and

epitope-bearing polypeptides, useful as vaccine components for treating

or preventing streptococcal infections such as otitis media,

meningitis, and bacteraemia

Example 1; Page -; 113pp; English.

individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus pyogenes, group B Streptococcus such as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardiae or Streptococcus aureus) in an individual susceptible to the infection. A polynucleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a chimeric gene created from fragments and variant fragments of Streptococcus pneumoniae genes, described in the method of the invention. Note: This sequence does not appear in the specification but has been created according to information given in the invention.

Sequence 1365 AA;

Query Match 3.0%; Score 24; DB 23; Length 1365;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DIDSLKQLYKPLPSQRHVESDGL 289
DB 2 DIDSLKQLYKPLPSQRHVESDGL 25

RESULT 90

AAU83827
ID AAU83827 standard; Peptide; 94 AA.

AAU83827;

08-MAY-2002 (first entry)

S. pneumoniae antigenic peptide 404.9.

BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;

pneumonia; streptococcal bacterial infection.

Streptococcus pneumoniae.

WO200198334-A2.

27-DEC-2001.

19-JUN-2001; 2001WO-CA00908.

20-JUN-2000; 2000US-212683P.

(SHIR-) SHIRE BIOCHEM INC.

Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;

WPI; 2002-122272/16.

New Streptococcus pneumoniae BVH-3 and BVH-11 variant and

epitope-bearing polypeptides, useful as vaccine components for treating

or preventing streptococcal infections such as otitis media,

meningitis, and bacteraemia

Example 3; Figure 11; 113pp; English.

The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II) comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A

CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
 CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. norcardia or
 CC Streptococcus aureus) in an individual susceptible to the infection.
 CC A polynucleotide (iii) encoding (i) is useful in DNA immunisation
 CC techniques. The Streptococcus polypeptides are useful in a diagnostic
 CC test for S. pneumoniae infection. (iii) is useful for designing DNA
 CC probes for use in detecting the presence of Streptococcus in a biological
 CC sample suspected of containing the bacteria. The DNA probes may also be
 CC used for detecting circulating S. pneumonia nucleic acid in a sample for
 CC diagnosing streptococcal infections. This sequence represents an
 CC antigenic peptide derived from the S. pneumoniae genome, described in the
 CC method of the invention.

CC Sequence 94 AA;

Query Match 2.9%; Score 23; DB 23; Length 94;
 Best Local Similarity 100.0%; Pred. No. 8.8e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 DGGYVTSHGDIHYNGKVPYDA 77
 DB 1 DGGYVTSHGDIHYNGKVPYDA 23

RESULT 91
 ID AAY05752 standard; Protein; 163 AA.

AC AAY05752;
 DT 19-JUL-1999 (first entry)

DE Streptococcus pneumoniae 20 kDa complement C3-degrading protease.

KM Human complement C3-degrading protease; vaccine; infection;
 KM meningitis; pneumonia; xerodermapigmentation; transplant rejection;
 KM inflammation.

OS Streptococcus pneumoniae.

Key Location/Qualifiers

FT Protein 1..58
 FT /note="Claimed protein of Claim 12"
 FT 90..132
 FT /note="Claimed protein of Claim 13"

XX WO9915675-A1.

XX 01-APR-1999.

XX 24-SEP-1998; 98WO-US20186.

XX 24-SEP-1997; 97US-0059907.

XX (AMCY) AMERICAN CYANAMID CO.

XX (MINU) UNIV MINNESOTA.

XX Cheng Q, Finkel DJ, Green BA, Hoschetter MK, Masi AW;

XX WPI; 1999-254719/21.

XX N-PSDB; AAX25393.

XX New isolated human complement C3-degrading proteinase

XX Claim 7; Page 50; 66pp; English.

CC The present sequence is a 20 kDa protein of Streptococcus pneumoniae
 CC serotype 3 that is capable of degrading human complement protein C3
 CC (HCP3). The sequence was deduced from the open reading frame of
 CC an isolated gene (see AAX25393). Alignment of this gene sequence
 CC with the S. pneumoniae (serotype 4) genome showed that the open
 CC reading frame that codes for the 20 kDa protein may be part of a
 CC larger open reading frame, i.e. a 2163 bp (see AAX25394) in the

CC serotype 4 genome, which encodes a protein of approximately 79
 CC kDa (see AAY05753). Amino acids 1-58 and 90-132 of the 20 kDa
 CC protein have substantial sequence identity with amino acids 170-227
 CC and 258-300 of the 79 kDa protein. Proteins and peptides or
 CC polypeptides containing these regions, and DNA sequences encoding
 CC them, are claimed. HCP3 proteases and polypeptides can be used as
 CC immune system stimulating compositions (claimed). They can produce
 CC an immune response against S. pneumoniae to immunize or treat a
 CC mammalian subject against infection or colonization (claimed).
 CC They can produce a B cell response, a T cell response, an
 CC epithelial cell response, or an endothelial cell response
 CC (claimed). The expression of the proteins on the surface of an
 CC organ of an animal used in xenotransplantation can be used to
 CC inhibit C3-mediated inflammation and rejection.

CC Sequence 163 AA;

Query Match 2.1%; Score 17; DB 20; Length 163;
 Best Local Similarity 100.0%; Pred. No. 9e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 303 GVAVPHGDHYHFIPYSQ 319
 DB 37 GVAVPHGDHYHFIPYSQ 53

RESULT 92
 ID AAY91286 standard; Protein; 381 AA.

AC AAY91286;

DT 30-MAY-2000 (first entry)

DE Group B Streptococcus protein sequence SEQ ID NO:12.

KM Group B Streptococcus; Streptococcus agalactiae; protein antigen;
 KM vaccine; screening; immunogen; detection; diagnosis; infection;
 KM antibody; antibody; antibacterial.

OS Streptococcus agalactiae.

PN WO200006736-A2.

PD 10-FEB-2000.

PF 27-JUL-1999; 99WO-GB02444.

PR 27-JUL-1998; 98GB-0016335.

PR 19-MAR-1999; 99US-0125163.

PA (MICR-) MICROBIAL TECHNICS LTD.

PI Le Page RWF, Wells JM, Hamillfy SB;

XX WPI; 2000-195299/17.

XX New Group B Streptococcus protein, useful as vaccine, for diagnosis of

PT Streptococcal infections and for screening of antibodies or antibodies

PS Claim 1; Fig 1; 123pp; English.

CC AAY05803 to AAY05872 encode proteins, polypeptides and peptides (given
 CC in AAY91275 to AAY91343) isolated from Group B Streptococcus (GBS), also
 CC known as Streptococcus agalactiae. The GBS polynucleotides and
 CC polypeptides have antibacterial activity. Immunogenic compositions
 CC comprising GBS polynucleotides or polypeptides can be used as vaccines
 CC and for the treatment or prophylaxis of GBS infection. The
 CC polynucleotides and polypeptides can also be used in the detection of GBS
 CC and for screening DNA encoding bacterial cell envelope associated or
 CC secreted antigens in gram positive bacteria. AAY05873 to AAY05941
 CC represent primers used in the exemplification of the present invention.

SQ Sequence 381 AA;

Query Match 2.1%; Score 17; DB 21; Length 381;

Best Local Similarity 100.0%; Pred. No. 2e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 YNGKVPYDAIISELLM 85
 |||||
 DB 92 YNGKVPYDAIISELLM 108

RESULT 93

AAV27347

ID AAV27347 standard; protein; 793 AA.

AC AAV27347;

DT 15-NOV-1999 (first entry)

DE Group B Streptococcus (GBS) antigen (clone 3).

DE Group B Streptococcus; GBS; antigen; vaccine; Streptococcus infection;

KM sepsis; meningitis; pneumonia; immunocompromise; diabetes; liver disease;

KW cancer; velinary; mastitis.

OS Streptococcus sp.

PN WO9942588-A2.

PD 26-AUG-1999.

PF 17-FEB-1999; 99WO-CA00114.

PR 20-FEB-1998; 98US-0075425.

(BIOC-) BIOCHEM VACCINS INC.

Boyer M, Brodeur BR, Charlebois I, Hamel J, Martin D;

Roux C;

WPI; 1999-540309/45.

N-PSDB; AAX91105.

Novel group B Streptococcus antigens - useful as vaccine

compositions for prophylaxis or therapy of Streptococcus infections

Claim 26; Fig 3C; 154pp; English.

The invention provides Group B Streptococcus (GBS) antigens

(AAV27336-370) and nucleic acids (AAX91103-X91111) encoding the antigens.

The GBS antigens can be recombinantly expressed using standard

recombinant methodology. The GBS antigens of the invention can be used as

vaccine components for the treatment or prophylaxis of diseases and

syndromes mediated by Streptococcus infection, especially group A

Streptococcus (S. pyogenes), GBS or S. agalactiae, S. dysgalactiae, S.

uberis, S. nocardia, as well as Staphylococcus aureus. The vaccines are

administered to those individuals at risk of GBS infection, particularly

pregnant women and infants for sepsis, meningitis, and pneumonia, as well

as immunocompromised individuals, such as those with diabetes, liver

disease or cancer. The vaccines also have veterinary applications, such as

for the treatment of mastitis in cattle. The present sequence represents

a GBS antigen of the invention.

SQ Sequence 793 AA;

Query Match 2.1%; Score 17; DB 20; Length 793;

Best Local Similarity 100.0%; Pred. No. 3.8e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 YNGKVPYDAIISELLM 85
 |||||
 DB 63 YNGKVPYDAIISELLM 79

RESULT 94

AAV91283

ID AAV91283 standard; Protein; 822 AA.

AC AAV91283;

DT 30-MAY-2000 (first entry)

DE Group B Streptococcus protein sequence SEQ ID NO:9.

Group B Streptococcus; Streptococcus agalactiae; protein antigen;

KW vaccine; screening; immunogen; detection; diagnosis; infection;

KM antibody; antibody; antibacterial.

OS Streptococcus agalactiae.

PN WO200006736-A2.

PD 10-FEB-2000.

PF 27-JUL-1999; 99WO-GB02444.

PR 27-JUL-1998; 98GB-0016335.

PR 19-MAR-1999; 99US-0125163.

(MICR-) MICROBIAL TECHNICS LTD.

Le Page RWF, Wells JM, Hanniffy SB;

WPI; 2000-195299/17.

New Group B Streptococcus protein, useful as vaccine, for diagnosis of

Streptococcal infections and for screening of antibodies or antibodies

Claim 1; Fig 1; 123pp; English.

AAA05803 to AAA05872 encode proteins, polypeptides and peptides (given

known as Streptococcus agalactiae. The GBS polynucleotides and

polypeptides have antibacterial activity. Immunogenic compositions

comprising GBS polynucleotides or polypeptides can be used as vaccines

and for the treatment or prophylaxis of GBS infection. The

polynucleotides and polypeptides can also be used in the detection of GBS

and for screening DNA encoding bacterial cell envelope associated or

secreted antigens in gram positive bacteria. AAA05873 to AAA05941

represent primers used in the exemplification of the present invention.

SQ Sequence 822 AA;

Query Match 2.1%; Score 17; DB 21; Length 822;

Best Local Similarity 100.0%; Pred. No. 3.9e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 YNGKVPYDAIISELLM 85
 |||||
 DB 92 YNGKVPYDAIISELLM 108

RESULT 95

AAU00028

ID AAU00028 standard; Protein; 822 AA.

AC AAU00028;

DT 11-MAY-2001 (first entry)

DE Streptococcus agalactiae GBS36#1.

Group B streptococci protein 36; GBS36; immunogen; vaccine;

antibody; necrotizing fasciitis; scarlet fever; sepsis; impetigo;

bacterial meningitis; otitis media; community-acquired pneumonia.

OS	Streptococcus agalactiae.
XX	
FH	Key
FT	Region
FT	/label= Histidine triad motif
FT	/note= "Proposed to be involved in metal binding"
FT	219..224
FT	/label= Histidine triad motif
FT	/note= "Proposed to be involved in metal binding"
FT	353..358
FT	/label= Histidine triad motif
FT	/note= "Proposed to be involved in metal binding"
FT	444..449
FT	/label= Histidine triad motif
FT	/note= "Proposed to be involved in metal binding"
FT	584..589
FT	/label= Histidine triad motif
FT	/note= "Proposed to be involved in metal binding"
XX	
PN	WO200114421-A1.
PD	
PD	01-MAR-2001.
XX	
PF	25-AUG-2000; 2000WO-US23417.
XX	
PR	25-AUG-1999; 99US-0150750.
XX	
PA	(MED1-) MEDIMMUNE INC.
XX	
PI	Koenig S, Heinrichs J, Johnson LS, Adamou JE;
XX	
DR	WPI; 2001-211305/21.
DR	N-PSDB; AAS00038.
XX	
PT	New polypeptides obtained from group A or B streptococci , especially
PT	Staphylococcus aureus homologous to Sp36 protein of Streptococcus
PT	pneumoniae useful as antibacterial vaccines -
XX	
PS	Claim 4; Fig 2; 62pp; English.
XX	
CC	The sequence represents Streptococcus agalactiae Group B Streptococci
CC	protein 36, GBS36. A recombinant cell producing GAS36, GAS36(12) or
CC	GBS36 is useful as a vaccine for vaccinating an animal, preferably a
CC	human against infection by a bacterial organism such as a streptococcal
CC	or staphylococcal bacteria, and for treating a disease caused by group A
CC	streptococci, group B streptococci or Staphylococcus aureus in an animal
CC	preferably a human. Vaccines and antibodies against the proteins of the
CC	invention are useful in prophylaxis and/or treatment of diseases such as
CC	necrotizing fasciitis, scarlet fever, sepsis, impetigo, bacterial
CC	meningitis, otitis media, community-acquired pneumonia and many diseases
CC	of newborns. The proteins are also used as immunogens to stimulate the
CC	production of antibodies for use in passive immunotherapy, for use as
CC	diagnostic reagents and for use as reagents in other processes such as
CC	affinity chromatography.
XX	
SQ	Sequence 822 AA:
OY	Query Match 2.1%; Score 17; DB 22; Length 822;
ID	Best Local Similarity 100.0%; Pred. No. 3.9e-07;
MATCHES	Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0
DB	69 YNGKVPYDAISELLM 85 92 YNGKVPYDAISELLM 108
RESULT 96	
AU000030	AAU00030 standard; Protein; 822 AA.
NC	AAU00030;
XX	
DT	11-MAY-2001 (first entry)

XX	Streptococcus agalactiae GBS36#2.
DE	
XX	
KW	Group B streptococci protein 36; GBS36; immunogen; vaccine;
KM	antibody; necrotising fasciitis; scarlet fever; sepsis; impetigo;
KX	bacterial meningitis; otitis media; community-acquired pneumonia.
XX	
OS	Streptococcus agalactiae.
XX	
FH	Key
FT	Misc_feature
FT	Location/Qualifiers
FT	1
FT	/note= "Encoded by GNG using prokaryote alternative genetic code"
FT	85..90
FT	/label= Histidine triad_motif
FT	/note= "Proposed to be involved in metal binding"
FT	219..224
FT	/label= Histidine triad_motif
FT	/note= "Proposed to be involved in metal binding"
FT	353..358
FT	/label= Histidine triad_motif
FT	/note= "Proposed to be involved in metal binding"
FT	444..449
FT	/label= Histidine triad_motif
FT	/note= "Proposed to be involved in metal binding"
FT	584..589
FT	/label= Histidine triad_motif
FT	/note= "Proposed to be involved in metal binding"
FT	
Region	
PM	WO200114421-A1.
PD	01-MAR-2001.
XX	
PF	25-AUG-2000; 2000WO-US23417.
XX	
PR	25-AUG-1999; 99US-0150750.
XX	
PA	(MED1-) MEDIMMUNE INC.
PI	Koenig S, Heinrichs J, Johnson LS, Adamou JE;
DR	WPI; 2001-211305/21.
XX	N-PADB; AAS00038.
PT	New polypeptides obtained from group A or B streptococci , especially
PT	Staphylococcus aureus homologous to Sp36 protein of Streptococcus
PT	pneumoniae useful as antibacterial vaccines -
XX	
PB	Example 2; Fig 5c; 62pp; English.
XX	
CC	The sequence represents Streptococcus agalactiae Group B Streptococci
CC	protein 36, GBS36. A recombinant cell producing GAS36, GAS36(12) or
CC	GBS36 is useful as a vaccine for vaccinating an animal, preferably a
CC	human against infection by a bacterial organism such as a streptococcal
CC	or staphylococcal bacteria, and for treating a disease caused by group A
CC	streptococci, group B streptococci or Staphylococcus aureus in an animal
CC	preferably a human. Vaccines and antibodies against the proteins of the
CC	invention are useful in prophylaxis and/or treatment of diseases such as
CC	necrotising fasciitis, scarlet fever, sepsis, impetigo, bacterial
CC	meningitis, otitis media, community-acquired pneumonia and many diseases
CC	of newborns. The proteins are also used as immunogens to stimulate the
CC	production of antibodies for use in passive immunotherapy, for use as
CC	diagnostic reagents and for use as reagents in other processes such as
CC	affinity chromatography.
XX	
SQ	Sequence 822 AA;
Query Match	2.1%; Score 17; DB 22; Length 822;
Best Local Similarity	100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
69 YNKGVPYDATISELLM 85	


```

XX      20-DEC-1999;          99WO-CA01218.
PF
XX      23-DEC-1998;          98US-0113800.
PR
XX      (BIOC-) BIOCHEM PHARMA INC.
PA
XX      Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
PI
XX      WPI; 2000-452397/39.
DR
XX      N-PSDB; AAA65741.
PT      Streptococcal antigens useful for vaccinating against e.g. meningitis,
XX      otitis media, bacteraemia and/or pneumonia -
XX
XX      Claim 18; Fig 48; 106pp; English.
XX
CC      The present invention describes nucleic acids (I) encoding protein
CC      antigens (II) from Streptococcus pneumoniae. The protein antigens
CC      have bactericidal activity. The nucleic acids, encoding the proteins
CC      antigens, may be used for the recombinant production of the proteins
CC      they encode. The protein antigens may then be used as vaccines for the
CC      prevention and treatment of Streptococcal infections in mammals
CC      (especially humans) which result in, e.g. meningitis, otitis media,
CC      bacteraemia and/or pneumonia. The present sequence represents the
CC      S. pneumoniae GAS BVH-71 protein antigen.
XX
SQ      Sequence      824 AA;

Query Match                2.1%; Score 17; DB 21; Length 824;
Best local Similarity     100.0%; Pred. No. 3.9e-07;
Matches    17; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

QY      69 YNGKVPYDAIISELLM 85
       |||||
Db      92 YNGKVPYDAIISELLM 108

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 10:50:50 ; Search time 40 Seconds
(without alignments)
1913.757 Million cell updates/sec

Title: US-09-765-271-56

Perfect score: 796
Sequence: 1 SYELGLYQARTYKENVNRSY.....KLIALIKGSNPSSVSKEKIN 796

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	635	87.3	802	2 C95136	conserved domain p
2	616	77.4	828	2 E98004	hypothetical prote
3	107	13.4	855	2 D98004	histidine Motif-Co
4	60	7.5	819	2 B95136	conserved domain p
5	60	7.5	839	2 G95115	conserved hypotet
6	60	7.5	853	2 C97985	hypothetical prote
7	32	4.0	1039	2 H95115	conserved hypotet
8	32	4.0	1039	2 D97985	hypothetical prote
9	17	2.1	822	2 T46758	hypothetical prote
10	10	1.3	182	2 P97985	hypothetical 92.4K
11	9	1.1	921	2 A48184	hypothetical prote
12	9	1.1	921	2 A45183	transcription init
13	8	1.0	71	2 E72853	TBP-associated fac
14	8	1.0	284	2 S58821	AcOrf-29 protein -
15	8	1.0	284	2 S58822	tropomyosin isofor
16	8	1.0	292	2 T49361	probable transpor
17	8	1.0	294	2 T27791	hypothetical prote
18	8	1.0	448	2 S05355	hypothetical prote
19	8	1.0	484	2 F82303	probable multidrug
20	8	1.0	488	2 B89557	hypothetical prote
21	8	1.0	795	1 S73830	hypothetical prote
22	8	1.0	825	2 T00818	endopeptidase La (
23	8	1.0	840	2 C75313	hypothetical prote
24	8	1.0	945	2 A64714	probable proteinas
25	8	1.0	1289	2 B70748	helicase - Helicob
26	8	1.0	1659	2 H97926	probable smc prote
27	8	1.0	1659	2 G95057	hypothetical prote
28	7	0.9	44	2 S55073	endo-beta-N-acetyl
29	7	0.9	49	2 S55072	env polypeptide -

30	7	0.9	49	2 D70091	hypothetical prote
31	7	0.9	68	2 D87657	hypothetical prote
32	7	0.9	70	2 A75134	hypothetical prote
33	7	0.9	90	2 C90404	conserved hypotet
34	7	0.9	93	2 C75396	hypothetical prote
35	7	0.9	94	2 E75556	hypothetical prote
36	7	0.9	100	1 BVMYBA	chaperonin groES -
37	7	0.9	100	1 BVMY7B	chaperonin groES -
38	7	0.9	101	2 T38824	thioltransferase -
39	7	0.9	101	2 E83874	ribosomal protein
40	7	0.9	106	2 I64171	hypothetical prote
41	7	0.9	110	2 D87498	Hesb/Yadr/Yehf fam
42	7	0.9	110	2 C86891	hypothetical prote
43	7	0.9	117	2 AG3598	transcription regu
44	7	0.9	121	2 T44473	conserved hypotet
45	7	0.9	124	1 NRPRH	pancreatic ribonuc
46	7	0.9	128	2 H72500	hypothetical prote
47	7	0.9	129	2 T36220	mult-like protein
48	7	0.9	130	2 S76934	hypothetical prote
49	7	0.9	131	2 T35461	mult-like protein
50	7	0.9	136	2 B65240	hypothetical prote
51	7	0.9	136	2 D64964	hypothetical prote
52	7	0.9	136	2 T19240	hypothetical prote
53	7	0.9	139	2 B81286	probable membrane
54	7	0.9	143	2 A71717	hypothetical prote
55	7	0.9	145	2 AF1219	Salmonella enteric
56	7	0.9	147	2 D83261	probable transcrip
57	7	0.9	148	2 A86079	PTS system, fructo
58	7	0.9	148	2 B91232	PTS system, fructo
59	7	0.9	148	2 D48649	frvA protein - Esc
60	7	0.9	154	2 S39873	hypothetical prote
61	7	0.9	157	2 AC2947	ribonuclease H [lm
62	7	0.9	157	2 G98335	ribonuclease H PAI
63	7	0.9	157	2 AP3240	conserved hypotet
64	7	0.9	158	1 D63256	hypothetical prote
65	7	0.9	158	2 A89943	transcription elon
66	7	0.9	165	2 C83415	hypothetical prote
67	7	0.9	166	2 A86450	probable glycine c
68	7	0.9	178	2 C81235	transcription anti
69	7	0.9	179	2 H71920	adenine phosphorib
70	7	0.9	181	2 A70178	conserved hypotet
71	7	0.9	185	2 F75487	V-type ATP synthas
72	7	0.9	191	2 T35792	beta-glucosidase -
73	7	0.9	197	1 S01249	Cytochrome c-L pre
74	7	0.9	201	2 S06147	GTP-binding protei
75	7	0.9	203	2 F90658	hypothetical prote
76	7	0.9	203	2 F85509	hypothetical prote
77	7	0.9	210	2 S62443	diadenosine 5', 5'
78	7	0.9	211	2 AH0899	conserved hypotet
79	7	0.9	211	2 T01627	probable ATP bindi
80	7	0.9	213	2 F83144	conserved hypotet
81	7	0.9	219	2 B75533	hypothetical prote
82	7	0.9	226	2 D65105	hypothetical 24.8
83	7	0.9	226	2 A98133	hypothetical prote
84	7	0.9	226	2 D85978	hypothetical prote
85	7	0.9	226	2 G81894	probable integral
86	7	0.9	226	2 D81125	hypothetical prote
87	7	0.9	232	2 C83744	two-component resp
88	7	0.9	237	2 G87286	conserved hypotet
89	7	0.9	238	2 I67638	proteasome activat
90	7	0.9	240	2 D75203	hypothetical prote
91	7	0.9	241	2 C71725	transcription init
92	7	0.9	241	2 H97723	hypothetical prote
93	7	0.9	255	2 T03482	amino-acid ABC tra
94	7	0.9	257	2 I36025	hypothetical prote
95	7	0.9	260	2 D86722	keratin-like prote
96	7	0.9	261	2 G70980	hypothetical prote
97	7	0.9	264	2 D71037	transcription init
98	7	0.9	269	2 T32639	hypothetical prote
99	7	0.9	271	1 ELK12	pancreatic elastas
100	7	0.9	279	2 S62364	L-2-chlorotriptoni
101	7	0.9	281	2 T43945	ribosomal protein
102	7	0.9	284	2 A44980	tropomyosin, obliq

hypothetical prote
hypothetical prote
hypothetical prote
conserved hypotet
hypothetical prote
hypothetical prote
chaperonin groES -
thioltransferase -
ribosomal protein
hypothetical prote
Hesb/Yadr/Yehf fam
hypothetical prote
transcription regu
conserved hypotet
pancreatic ribonuc
hypothetical prote
mult-like protein
hypothetical prote
mult-like protein
hypothetical prote
hypothetical prote
probable membrane
hypothetical prote
Salmonella enteric
probable transcrip
PTS system, fructo
PTS system, fructo
frvA protein - Esc
hypothetical prote
ribonuclease H [lm
ribonuclease H PAI
conserved hypotet
hypothetical prote
transcription elon
hypothetical prote
probable glycine c
transcription anti
adenine phosphorib
conserved hypotet
V-type ATP synthas
beta-glucosidase -
Cytochrome c-L pre
GTP-binding protei
hypothetical prote
hypothetical prote
diadenosine 5', 5'
conserved hypotet
probable ATP bindi
conserved hypotet
hypothetical prote
hypothetical 24.8
hypothetical prote
hypothetical prote
probable integral
hypothetical prote
two-component resp
conserved hypotet
proteasome activat
hypothetical prote
amino-acid ABC tra
hypothetical prote
keratin-like prote
hypothetical prote
transcription init
hypothetical prote
pancreatic elastas
L-2-chlorotriptoni
ribosomal protein
tropomyosin, obliq

103	7	0.9	284	2	A33085
104	7	0.9	284	2	S38381
105	7	0.9	284	2	D82486
106	7	0.9	289	2	T25831
107	7	0.9	293	2	S66356
108	7	0.9	295	2	B95298
109	7	0.9	296	2	T20005
110	7	0.9	298	2	F90495
111	7	0.9	305	2	F84595
112	7	0.9	318	2	G87342
113	7	0.9	319	2	G75106
114	7	0.9	322	2	H83851
115	7	0.9	323	2	A54021
116	7	0.9	323	2	B54021
117	7	0.9	327	1	OKDRC
118	7	0.9	327	2	A55545
119	7	0.9	331	2	T48667
120	7	0.9	333	1	J50590
121	7	0.9	338	2	S26976
122	7	0.9	338	2	J10121
123	7	0.9	340	2	T35394
124	7	0.9	343	2	G88795
125	7	0.9	344	2	A97699
126	7	0.9	344	2	AB2925
127	7	0.9	347	2	G87449
128	7	0.9	372	2	AG1896
129	7	0.9	373	2	F84396
130	7	0.9	379	2	F71533
131	7	0.9	381	2	H69367
132	7	0.9	383	2	S51327
133	7	0.9	384	2	D69411
134	7	0.9	386	1	KMECPW
135	7	0.9	386	2	B95906
136	7	0.9	386	2	F91061
137	7	0.9	387	2	H65132
138	7	0.9	399	2	C87387
139	7	0.9	399	2	F87547
140	7	0.9	402	2	H86649
141	7	0.9	405	2	H88930
142	7	0.9	405	2	A46699
143	7	0.9	406	2	H70670
144	7	0.9	416	2	S63221
145	7	0.9	416	2	D72456
146	7	0.9	423	2	AB2021
147	7	0.9	423	2	D81248
148	7	0.9	424	2	S78610
149	7	0.9	425	2	T15959
150	7	0.9	430	2	C84190
151	7	0.9	432	2	G72456
152	7	0.9	444	2	B83891
153	7	0.9	445	2	T31581
154	7	0.9	446	1	UBZPG
155	7	0.9	447	2	G84001
156	7	0.9	450	2	S00950
157	7	0.9	451	1	UBHUG
158	7	0.9	451	1	UBXUG
159	7	0.9	452	2	A10779
160	7	0.9	453	2	AB1665
161	7	0.9	455	2	T15622
162	7	0.9	455	2	E90316
163	7	0.9	457	2	B96037
164	7	0.9	457	2	J01413
165	7	0.9	461	1	A35356
166	7	0.9	462	2	S53084
167	7	0.9	462	2	G87534
168	7	0.9	462	2	T25544
169	7	0.9	466	2	B9186
170	7	0.9	466	2	AB6033
171	7	0.9	467	2	S01943
172	7	0.9	469	2	UC5798
173	7	0.9	471	2	S01937
174	7	0.9	479	1	VGBEF2
175	7	0.9	480	2	A56694

tropomyosin - bioo
 tropomyosin - Cali
 probable lipase ac
 hypothetical prote
 mannose/glucose-bi
 Lyar family transc
 conserved hypotnet
 conserved hypotnet
 hypothetical prote
 hypothetical prote
 hypothetical prote
 hypothetical prote
 phosphotyrosyl pho
 protein kinase (EC
 F1P1 protein - yea
 dtdglucose 4,6-de
 endo-1,4-beta-xyla
 glyceraldehyde-3-p
 glyceraldehyde-3-p
 probable glycerol
 hypothetical prote
 uroporphyrinogen d
 conserved hypotnet
 hypothetical prote
 signal recognition
 hypothetical prote
 hypothetical prote
 heparin-binding gl
 probable acyl-CoA
 chorismate mutase
 chorismate mutase-
 chorismate mutase-
 hypothetical 44.3
 beta-ketoadipyl-Co
 beta-ketoadipyl-Co
 rhamnosyltransfera
 protein R1lg11.14
 translation initia
 hypothetical prote
 DNA-directed RNA p
 probable glutamyl-
 3-deoxy-D-manno-oc
 3-deoxy-D-manno-oc
 hypothetical prote
 hypothetical prote
 cytophan synthas
 probable glutamate
 intracellular alka
 hypothetical prote
 tubulin gamma chai
 glycine dehydrogen
 hypothetical prote
 tubulin gamma chai
 tubulin gamma chai
 probable n-hydroxy
 hypothetical RNA m
 hypothetical prote
 oxidoreductase (lm
 probable alpha-gal
 hypothetical 50.9K
 tumor necrosis fac
 gamma-tubulin - Bu
 UDP-N-acetylglucos
 hypothetical prote
 probable permease
 probable permease
 F0F1-ATPase (EC 3.
 hypothetical prote
 glycoprotein F - h
 keratin, type II,

176	7	0.9	483	2	T36811	probable integral
177	7	0.9	488	1	S55874	sulfite oxidase (E
178	7	0.9	490	2	B86813	xyloside transport
179	7	0.9	491	2	S05408	keratin, type II,
180	7	0.9	493	2	H83052	N utilization subs
181	7	0.9	499	2	G75600	cleavage and poly
182	7	0.9	503	2	T24985	hypothetical prote
183	7	0.9	503	2	S29094	keratin, type II,
184	7	0.9	508	1	KRSHL2	keratin type II, m
185	7	0.9	508	2	S41877	readthrough protei
186	7	0.9	508	2	S41879	readthrough protei
187	7	0.9	508	2	S41875	readthrough protei
188	7	0.9	508	2	S03551	hypothetical prote
189	7	0.9	508	2	S24594	hypothetical prote
190	7	0.9	510	2	C97232	GMP synthase (limp
191	7	0.9	512	1	TVHUX	protein-tyrosine k
192	7	0.9	512	2	G91200	type III secretion
193	7	0.9	512	2	180311	sepc (protein - Esc
194	7	0.9	512	2	C86047	escC (imported) -
195	7	0.9	520	2	T04591	ferulate-5-hydroxy
196	7	0.9	524	2	C37222	cytochrome P450 1A
197	7	0.9	534	2	S31300	regulatory protein
198	7	0.9	538	2	S67766	kna-export mediat
199	7	0.9	540	2	AG2161	GMP synthase (gut
200	7	0.9	542	2	S76358	GMP synthase (gut

ALIGNMENTS

RESULT 1

C95136
 conserved domain protein SP1175 (imported) - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae
 C:Date: 03-Aug-2001 #sequence: revision 03-Aug-2001 #text_change 24-Aug-2001

C:Accession: C95136

R:Terrellin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,

son, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: C95136

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-802 <KOR>

A:Cross-references: GB:AE005672; PIDN:AAK75284.1; PID:gi14972655; GSPDB:GN00164; TIGR:SP4

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP1175

C:Superfamily: Streptococcus agalactiae hypothetical 92.4K protein

Query Match 87.3%; Score 695; DB 2; Length 802;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	SYELGLVQARTVKNNRVS	YIDGKQATOKTEN	LPDEVSREGINAOIVIKIDOGVYT	60
DB	7	SYELGLVQARTVKNNRVS	YIDGKQATOKTEN	LPDEVSREGINAOIVIKIDOGVYT	66
QY	61	SHGHHYNGKGVYDAI	ISEELMKDPNYKLKED	IVNEVKGGVYIKVDKGVVYLKDA	120
DB	67	SHGHHYNGKGVYDAI	ISEELMKDPNYKLKED	IVNEVKGGVYIKVDKGVVYLKDA	126
QY	121	AHADNVTKKEINRQKH	SGHREGGTPRNDGAVAL	ARSQGRYTTDDGYIFNA5DIIDT	180
DB	127	AHADNVTKKEINRQKH	SGHREGGTPRNDGAVAL	ARSQGRYTTDDGYIFNA5DIIDT	186
QY	181	GDATVYHGHYHIIIPK	ELASASFLAFLSGRGL	SLNSRTYRRONSNDTSRTNWPS	240
DB	187	GDATVYHGHYHIIIPK	ELASASFLAFLSGRGL	SLNSRTYRRONSNDTSRTNWPS	246

QY 241 VSNPGTTNTNTSNTNSQASQASNDIDSLIKQYKPLSQRHVESDGLVFDPAQITTSRT 300
DB 247 VSNPGTTNTNTSNTNSQASQASNDIDSLIKQYKPLSQRHVESDGLVFDPAQITTSRT 306
QY 301 ARGVAAPHGDHFIYISQMSLEERLARIIPLRYSNMWVPDSREQSPQPTPEPSPG 360
DB 307 AKVAAPHGDHFIYISQMSLEERLARIIPLRYSNMWVPDSREQSPQPTPEPSPG 366
QY 361 POPAPNLKIDSNSLVSQVRAKYGEGVFEKGISRYFAKDPSETVKLSEKLSKQES 420
DB 367 POPAPNLKIDSNSLVSQVRAKYGEGVFEKGISRYFAKDPSETVKLSEKLSKQES 426
QY 421 VSHITLAKKENVAPRODFYDKAYNLLTEAHKALFXNKGNSDPQALDKLERLNDSTN 480
DB 427 VSHITLAKKENVAPRODFYDKAYNLLTEAHKALFXNKGNSDPQALDKLERLNDSTN 486
QY 481 KEKLVDDLAFAPITHPERLGRPNQIETDEVRIAQLADKTTSDGYTFDEHDIISD 540
DB 487 KEKLVDDLAFAPITHPERLGRPNQIETDEVRIAQLADKTTSDGYTFDEHDIISD 546
QY 541 EGDAYVTPHMGSHWIGKDSLSDKEKVAQAAYTKERGIIPSPDADVKANPTGDSAAAT 600
DB 547 EGDAYVTPHMGSHWIGKDSLSDKEKVAQAAYTKERGIIPSPDADVKANPTGDSAAAT 606
QY 601 NRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPKDHVHNKFAFPDHTYKAPNGYTLBD 660
DB 607 NRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPKDHVHNKFAFPDHTYKAPNGYTLBD 666
QY 661 LPATIKYVEHPERHSNDGCMNASEHVLGKKHSDPKNFKADEEPVEETPAEPDVP 720
DB 667 LPATIKYVEHPERHSNDGCMNASEHVLGKKHSDPKNFKADEEPVEETPAEPDVP 726
QY 721 QVETEKVAEQKAEVLLAKVTDSLKANATETLAGLRNNLTLOIMDNNSIMAEKELIA 780
DB 727 QVETEKVAEQKAEVLLAKVTDSLKANATETLAGLRNNLTLOIMDNNSIMAEKELIA 786
QY 781 LKGSNPSVSKEKIN 796
DB 787 LKGSNPSVSKEKIN 802

RESULT 2

E98004
hypothetical protein phtA [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #ext_change 02-Nov-2001
C:Accession: E98004
R:Hostins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A>Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: E98004
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-828 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK99865.1; PID:g15458683; GSPDB:GN00174
C:Genetics:
A:Gene: phtA
C:Superfamily: Streptococcus agalactiae hypothetical 92.4K protein

Query Match 77.4%; Score 616; DB 2; Length 828;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 716; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 80 SEELAKDPYKXKDDIVNEVKGYYIKVDGYYVYLKDAHADNVRTKEEINRQKOE 139
DB 112 SEELAKDPYKXKDDIVNEVKGYYIKVDGYYVYLKDAHADNVRTKEEINRQKOE 171
QY 140 SQHREGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYPKNE 199

DB 172 SQHREGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYPKNE 231
QY 200 LSASELAAREAFPLSGRGNLSNGRTYRRONSDNTSRNWPVSNGCTNTNTSNTNS 259
DB 232 LSASELAAREAFPLSGRGNLSNGRTYRRONSDNTSRNWPVSNGCTNTNTSNTNS 291
QY 260 QASQNDIDSLIKQYKPLSQRHVESDGLVFDPAQITTSRTARGAVAPHGDHFIYISQ 319
DB 292 QASQNDIDSLIKQYKPLSQRHVESDGLVFDPAQITTSRTARGAVAPHGDHFIYISQ 351
QY 320 MSELERLARIIPLRYSNMWVPDSREQSPQPTPEPSPGPOAPNLKIDSNSLVSQ 379
DB 352 MSELERLARIIPLRYSNMWVPDSREQSPQPTPEPSPGPOAPNLKIDSNSLVSQ 411
QY 380 VRVKGEVFEKGISRYFAKDPSETVKNLSEKLSKQESVSHITLAKKENVAPRODF 439
DB 412 VRVKGEVFEKGISRYFAKDPSETVKNLSEKLSKQESVSHITLAKKENVAPRODF 471
QY 440 YKAVNLLTEAHKALFXNKGNSDPQALDKLERLNDSTNKEKLVDDLAFAPITHP 499
DB 472 YKAVNLLTEAHKALFXNKGNSDPQALDKLERLNDSTNKEKLVDDLAFAPITHP 531
QY 500 RLKGNQIETDEVRIAQLADKTTSDGYTFDEHDIISDEGDAYVTPHMGSHWIGK 559
DB 532 RLKGNQIETDEVRIAQLADKTTSDGYTFDEHDIISDEGDAYVTPHMGSHWIGK 591
QY 560 SLSDKEKVAQAAYTKERGIIPSPDADVKANPTGDSAAATYRVKGEKRIPLVRLPYME 619
DB 592 SLSDKEKVAQAAYTKERGIIPSPDADVKANPTGDSAAATYRVKGEKRIPLVRLPYME 651
QY 620 HTVEVNGNLIIPKDHVHNKFAFPDHTYKAPNGYTLBDLPATIKYVEHPERPHSN 679
DB 652 HTVEVNGNLIIPKDHVHNKFAFPDHTYKAPNGYTLBDLPATIKYVEHPERPHSN 711
QY 680 DCMNASEHVLGKKHSDPKNFKADEEPVEETPAEPDVPQVETEKVAEQKAEVLLA 739
DB 712 DCMNASEHVLGKKHSDPKNFKADEEPVEETPAEPDVPQVETEKVAEQKAEVLLA 771
QY 740 KYTDSLKANATETLAGLRNNLTLOIMDNNSIMAEKELIALKGSNPSVSKEKIN 796
DB 772 KYTDSLKANATETLAGLRNNLTLOIMDNNSIMAEKELIALKGSNPSVSKEKIN 828

RESULT 3

D98004
histidine Motif-Containing protein [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #ext_change 02-Nov-2001
C:Accession: D98004
R:Hostins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A>Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: D98004
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-855 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK99864.1; PID:g15458682; GSPDB:GN00174
C:Genetics:
A:Gene: phtA
C:Superfamily: Streptococcus agalactiae hypothetical 92.4K protein

Query Match 13.4%; Score 107; DB 2; Length 855;
Best Local Similarity 100.0%; Pred. No. 1.8e-99;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 102 KGGYIKVDGKYVYLKDAHADNVRTKEEINRQKQSHREGTPRNDGAVALARSQ 161
DB 133 KGGYIKVDGKYVYLKDAHADNVRTKEEINRQKQSHREGTPRNDGAVALARSQ 192

Oy 162 RYTTDDGYIFNASDIIEDTGDAYIVHGHDHYIIPKNELSASELAA 208
|||
Db 193 RYTDDGXYIFNASDIIEDTGDAYIVHGHDHYIIPKNELSASELAA 239

RESULT 4
B95136
conserved domain protein SP1174 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001

R. Tetteletijn, H. Nelsson, K. E. Poulsen, I. T. Eisen, J. A. Read, T. D. Peterson, S. J. Halsey, and J. D. Umayah, L. A. White, O. Salzberg, S. L. Lewis, M. R. Radune, D. Holtzapfel, Nelson, T. Hickey, E. K. Holt, I. E. Science 293, 498-506, 2001

A. Authors: Lotius, B. J., Yang, F., Smith, H. O., Venter, J. C., Dougherty, B. A., Morrison, A. Title: Complete Genome Sequence of a Virulent Isolate of *Streptococcus pneumoniae*. Reference number: A95000; MUID:21357209; PMID:11463196

C:\Superfamily: Streptococcus agalactiae hypothetical 92.4K protein
 Query Match 7.5%; Score 60; DB 2; Length 819;
 Best Local Similarity 100.0%; Pred. No. 7.7e-52;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0

[illegible]

RESULT 5
G95115
conserved hypothetical protein SPI003 [imported] - Streptococcus pneumoniae (strain TIGR4)
C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C/Accession: G95115
R/Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umeyama, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Raduane, D.; Holtzapfel,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001

A:Title: Complete Genome Sequence of a Virulent Isolate of *Streptococcus pneumoniae*.
A:Authors: Lotefus, B.U.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.;
A:Reference number: A95000; MUID:21357209; PMID:11463916

C:Superfamily: Streptococcus agalactiae hypothetical 92.4K protein

Query Match	7.5%	Score 60	DB 2	Length 839
Best Local Similarity	100.0%	Pred. No. 7.8e-52		
Matches	60	Conservative	0	Mismatches 0
			Indels	0
			Gaps	0

Dy . 31 ENLTDEVSKREGINAEQIVIKITDQGVTSHGHGHHYYNGKVPIDAIISELLMKDPNY 900
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 52 ENLTDEVSKREGINAEQIVIKITDQGVTSHGHGHHYYNGKVPIDAIISELLMKDPNY 111

RESULT 6
C97985
hypothetical protein phd (imported) - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #ext_change 02-Nov-2001
C:Accession: C97985
R:Hoskins, J.A.; Alborn, Jr., W.; Arnold, J.; Blaszczyk, L.; Burgett, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Du, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5711, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Balaz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.
A:Reference number: A97872; MUID: A1429245; PMID:11544234

C:Superfamily: Streptococcus agalactiae hypothetical 92.4K protein

[illegible]

R. T. Retzelin, H. Nelson, K. E. Paulsen, I. T. Eissen, J. A. Raad, T. D. Peterson, S. J. Heston, J. D. Umayam, L. A. White, O. J. Salzb erg, S. L. Lewis, M. R. Radune, D. J. Holtzap ple, J. D. Hick ey, E. K. Holt, I. E. S. A. Authors: Loftus, B. J.; Yang, F.; Smith, H. O.; Venter, J. C.; Dougherty, B. A.; Morrison, A. Title: Complete Genome Sequence of a Virulent Isolate of *Streptococcus pneumoniae*. Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: AY5113
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1038 <RUR>
A:Cross-references: GB:AE005672; PID:AAK75121.1; PID:G14972477; GSPDR:G000164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI004

Query Match	4.0%	Score 32	DB 2	length 1039
Best Local Similarity	100.0%	Pred. NO.	2.3e-23	
Matches 32	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Oy	46	AEOIYIKITDQGYVTSHGHHYYNGKVYPDA	77
Db	67	AEQIVIKITDQGYVTSHGHHYYNGKVYPDA	98

RESULT 8
D97985
hypothetical protein phtE [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #ext_change 22-Oct-2001
C:Accession: D97985
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Buggett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: D97985
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-1039 <KUR>
A:Cross-References: GB:AE007317; PIDN:AAK99712.1; PID:g15458515; GSPDB:GN00174
C:Genetics:
A:Gene: phcE

Query Match 4.0%; Score 32; DB 2; Length 1039;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AEOIVIKIDGCVTSHGDHYHYNGKVPYDA 77
DB 67 AEOIVIKITDQGVTVSHGDHYHYNGKVPYDA 98

RESULT 9

T46758
hypothetical 92.4K protein - Streptococcus agalactiae

C:Species: Streptococcus agalactiae
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
C:Accession: T46758

R:Spellerberg, B.; Rozdzinski, E.; Martin, S.; Weber-Heynemann, J.; Schuttzler, N.; Luet
Infect. Immun. 67, 871-878, 1999
A:Title: Lmb, a protein with similarities to the Lrai adhesin family, mediates attachment
A:Reference number: Z24091; MUID:99115568; PMID:9916102

A:Accession: T46758
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA

A:Residues: 1-822 <SPB>
A:Cross-References: EMBL:AF062533; NID:g4249622; PIDN:AAD13797.1; PID:g4249624
A:Experimental source: strain R268
C:Superfamily: Streptococcus agalactiae hypothetical 92.4K protein

Query Match 2.1%; Score 17; DB 2; Length 822;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 YNGKVPYDAIISEELM 85
DB 92 YNGKVPYDAIISEELM 108

RESULT 10

F97985
hypothetical protein phE-truncation [imported] - Streptococcus pneumoniae (strain R6)

C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C:Accession: F97985

R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; F
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: F97985
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-182 <KUR>
A:Cross-References: GB:AE007317; PIDN:AAK99714.1; PID:g15458517; GSPDB:GN00174
C:Genetics:
A:Gene: phE-truncation

Query Match 1.3%; Score 10; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 HGDHYHYIPK 197
DB 35 HGDHYHYIPK 44

RESULT 11

A48184
transcription initiation factor IID 110K chain - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999
C:Accession: A48184
R:Okubo, T.; Gong, D.W.; Roeder, R.G.; Horikoshi, M.; Nakatani, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 5896-5900, 1993
A:Title: The Drosophila 110-kDa transcription factor TFIID subunit directly interacts wi
A:Reference number: A48184; MUID:9317591; PMID:8327460

A:Accession: A48184
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-921 <KOK>
A:Cross-References: GB:S63550; NID:g398432; PID:g398433

A:Experimental source: embryo nuclear extract
A>Note: sequence extracted from NCBI backbone (NCBIN:134863, NCBI:134864)
C:Genetics:
A:Gene: FlyBase:Tafl10
A:Cross-References: FlyBase:FBgn0010280

C:Keywords: transcription initiation

Query Match 1.1%; Score 9; DB 2; Length 921;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 TTNNSNNT 257
DB 178 TTNNSNNT 186

RESULT 12

A45183
TBP-associated factor TFIID - fruit fly (Drosophila sp.)

C:Species: Drosophila sp.
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C:Accession: A45183
R:Hoey, T.; Weinzierl, R.O.; Gill, G.; Chen, J.L.; Dynlacht, B.D.; Tijan, R.
Cell 72, 247-260, 1993

A:Title: Molecular cloning and functional analysis of Drosophila TAF110 reveal propertie
A:Reference number: A45183; MUID:93145326; PMID:7678780
A:Accession: A45183
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid

A:Residues: 1-921 <HOE>
A:Experimental source: embryo
A>Note: sequence extracted from NCBI backbone (NCBIP:123832)
C:Genetics:
A:Gene: FlyBase:Tafl10
A:Cross-References: FlyBase:FBgn0010280

Query Match 1.1%; Score 9; DB 2; Length 921;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 TTNNSNNT 257
DB 178 TTNNSNNT 186

RESULT 13

E72853
AcOrf-29 protein - Autographa californica nuclear polyhedrosis virus

C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A>Note: dsDNA virus
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
C:Accession: E72853

R:AYres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus
A:Reference number: A72850; MUID:94303173; PMID:8030224
A:Accession: E72853
A:Status: preliminary
A:Molecule type: DNA

RESULT 14

A:Residues: 1-71 <AVR>
A:Cross-references: GB:L22858; NID:9510708; PIDN:AAA6659.1; PID:9559098
C:Genetics:
A:Gene: ACO-f-29

Query Match 1.0%; Score 8; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 130 EFINRQKQ 137
DB 20 EFINRQKQ 27

RESULT 14
S58921
tropomyosin isoform TMI - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text_change 20-Jun-2000
C:Accession: S58921; S62127; S58918
R:Kagawa, H.; Sugimoto, K.; Matsumoto, H.; Inoue, T.; Imadzu, H.; Takuwa, K.; Sakube, Y.
J. Mol. Biol. 251, 603-613, 1995
A>Title: Genome structure, mapping and expression of the tropomyosin gene tmy-1 of Caenc
A:Reference number: S58918; MUID:95395840; PMID:7666414
A:Accession: S58921

A:Molecule type: mRNA
A:Residues: 1-284 <KAG>
A:Cross-references: EMBL:D38540; NID:91208412; PIDN:BA07543.1; PID:91208413
A:Accession: S62127
A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-276, 'NLP', 280-284 <KAF>
A:Cross-references: EMBL:D38539; NID:9871835; PIDN:BA07540.1; PID:91208409
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
A:Accession: S58918
A:Molecule type: protein
A:Residues: 11-49; 171-211 <KAW>
C:Genetics:

A:Gene: tmy-1
A:introns: 15/3; 61/3; 80/3; 125/2; 164/3; 188/2; 234/3; 258/1
C:Superfamily: tropomyosin
C:Keywords: alternative splicing

Query Match 1.0%; Score 8; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 727 VEAQLKEA 734
DB 144 VEAQLKEA 151

RESULT 15
S58922

tropomyosin isoform TMI - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: S58922; S62128; S58918
R:Kagawa, H.; Sugimoto, K.; Matsumoto, H.; Inoue, T.; Imadzu, H.; Takuwa, K.; Sakube, Y.
J. Mol. Biol. 251, 603-613, 1995
A>Title: Genome structure, mapping and expression of the tropomyosin gene tmy-1 of Caenc
A:Reference number: S58918; MUID:95395840; PMID:7666414
A:Accession: S58922

A:Molecule type: mRNA
A:Residues: 1-284 <KAG>

A:Cross-references: EMBL:D38541; NID:9871837; PIDN:BA07544.1; PID:91208414
A:Accession: S62128
A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-284 <KAW>
A:Cross-references: EMBL:D38539; NID:9871835; PIDN:BA07541.1; PID:91208410
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
A:Accession: S58918

A:Molecule type: protein
A:Residues: 11-49; 171-211 <KAF>
C:Genetics:
A:Gene: tmy-1
A:introns: 15/3; 61/3; 80/3; 125/2; 164/3; 188/2; 234/3; 258/1
C:Superfamily: tropomyosin
C:Keywords: alternative splicing

Query Match 1.0%; Score 8; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 727 VEAQLKEA 734
DB 144 VEAQLKEA 151

RESULT 16
T49361

probable transport vesicle fusion protein SEC17 [imported] - Neurospora crassa

N:Alternate names: protein B1D.150
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49361
R:Schulte, U.; Algen, V.; Hohlseil, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: 225022
A:Accession: T49361

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-292 <SCH>
A:Cross-references: EMBL:AL355927; GSPDB:GN00116; NCSP:B1D1.150

A:Experimental source: BAC clone B1D1, strain OK74A
C:Genetics:

A:Gene: NCSP:B1D1.150
A:Map position: 6
A:introns: 11/3; 53/1; 155/2

Query Match 1.0%; Score 8; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 NDGAVALLA 157
DB 150 NDGAVALLA 157

RESULT 17
T27791

hypothetical protein ZK228.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T27791

R:Baaham, V.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20419

A:Accession: T27791
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-294 <WLL>
A:Cross-references: EMBL:Z82086; PIDN:CAB04996.1; GSPDB:GN00023; CESP:ZK228.4

A:Experimental source: clone ZK228
C:Genetics:

A:Gene: CESP:ZK228.4
A:Map position: 5

A:introns: 38/1; 99/1; 143/3; 181/3; 250/2
C:Superfamily: Caenorhabditis elegans hypothetical protein F31F7.1

Query Match 1.0%; Score 8; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 11 TVKENNRV 18

DB 262 TVKENNRV 269
|||||
RESULT 18
S05355
hypothetical protein (clone AAC11) - slime mold (Dictyostelium discoideum) (fragment)
C:Species: Dictyostelium discoideum
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 29-Oct-1999
C:Accession: S05355
R:Shaw, D.R.; Richter, H.; Giorda, R.; Ohmachi, T.; Ennis, H.L.
Mol. Gen. Genet. 218, 453-459, 1999
A:Title: Nucleotide sequences of Dictyostelium discoideum developmentally regulated cdna
A:Reference number: S05355; MUID:90066348; PMID:2511421
A:Accession: S05355
A:Molecule type: mRNA
A:Residues: 1-448 <SHA>
A:Cross-references: EMBL:X16522; NID:g7173; PIDD:CAA34529.1; PID:g7174
Query Match
1.0%; Score 8; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 250 NTSNMSNT 257
|||||
DB 378 NTSNMSNT 385
RESULT 19
F82203
probable multidrug resistance protein VC1409 [imported] - Vibrio cholerae (strain N16961)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: F82203
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Glimm, M.L.; Dodson, R.J.;
Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Baas, S.; Qin, H.; Dragol, I.; Sellers, F.
L. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10952301
A:Accession: F82203
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-484 <HE1>
A:Cross-references: GB:AE004219; GB:AE003852; NID:G9655899; PIDD:AAF94566.1; GSPDB:GN001
C:Genetic: A:Experimental source: serogroup O1, strain N16961, biotype El Tor
A:Gene: VC1409
A:Map position: 1
Query Match
1.0%; Score 8; DB 2; Length 484;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 203 SELAAEA 210
|||||
DB 169 SELAAEA 176
RESULT 20
B89957
hypothetical protein ptaA [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: B89957
R:Ruuda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: AB9758; MUID:21311952; PMID:11418146
A:Accession: B89957
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-488 <KUR>
A:Cross-references: GB:BA000018; PID:g13701521; PIDD:BA842815.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetic: A:Gene: ptaA
C:Superfamily: phosphotransferase system glucose-specific enzyme II, factor II; phosphot
Query Match
1.0%; Score 8; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 150 NDGAVALA 157
|||||
DB 72 NDGAVALA 79
RESULT 21
S73830
endopeptidase Ia (EC 3.4.21.53) - Mycoplasma pneumoniae (strain ATCC 29342)
N:Alternate names: ATP-dependent proteinase Ipn; ATP-dependent serine proteinase Ia; hyl
N:contains: adenosinetriphosphatase (EC 3.6.1.3)
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 19-Jan-2001
C:Accession: S73830
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirk, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A:Reference number: S73327; MUID:97105885; PMID:8948633
A:Accession: S73830
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-795 <HIM>
A:Cross-references: EMBL:AE000050; GB:U00089; NID:g1674197; PIDD:AAB96152.1; PID:g167419
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Comment: This enzyme catalyzes the hydrolysis of large proteins in the presence of ATF
C:Genetic: A:Gene: Ipn; F10 orf795
A:Genetic code: GCG3
C:Superfamily: ATP-dependent serine proteinase Ia
C:Keywords: ATP; DNA binding; heat shock; hydrolase; nucleotide binding; P-loop; serine
F:379-386/Region: nucleotide-binding motif A (P-loop)
F:442-447/Region: nucleotide-binding motif B
F:702/Active site: Ser #status predicted
Query Match
1.0%; Score 8; DB 1; Length 795;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 466 ALDKLLER 473
|||||
DB 127 ALDKLLER 134
RESULT 22
T00818
hypothetical protein At2g41620 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T32G6.14
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
C:Accession: T00818; AB4844
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, November 1997
A:Description: Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence.
A:Reference number: Z14163
A:Accession: T00818
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-825 <ROU>
A:Cross-references: EMBL:AC002510; NID:g2618683; PID:g2618698
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koc, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; Nuss, D.; Niernman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A:Reference number: A84420; MUID:20083487; PMID:1061197

A:Accession: A84844

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-825 <STO>

A:Cross-references: GB:AE002093; NID:g2618698; PIDN:AAB84345.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g41620; T32G6.14

A:Map position: 2

A:Introns: 43/3; 74/2; 96/3; 116/3; 146/3; 234/3; 311/3; 329/3; 368/3; 669/3; 725

A:Notes: T32G6.14

C:Superfamily: Arabidopsis thaliana hypothetical protein At2g41620

Query Match 1.0%; Score 8; DB 2; Length 825;

Best Local Similarity 100.0%; Pred. No. 40;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 REGINAEO 48

DB 78 REGINAEO 85

RESULT 23

C75313

Probable proteinase - *Deinococcus radiodurans* (strain R1)

C:Species: *Deinococcus radiodurans*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: C75313

R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vanathavan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A>Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A:Reference number: A75250; MUID:20036896; PMID:1056266

A:Accession: C75313

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-840 <WHI>

A:Cross-references: GB:AE002047; GB:AE000513; NID:g6459915; PIDN:AAFL1680.1; PID:g645992

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2130

A:Map position: 1

Query Match 1.0%; Score 8; DB 2; Length 840;

Best Local Similarity 100.0%; Pred. No. 41;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 287 DGLVDPDA 294

DB 332 DGLVDPDA 339

RESULT 24

A64714

Helicase - *Helicobacter pylori* (strain 26695)

C:Species: *Helicobacter pylori*

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

C:Accession: A64714

R.Tomb, J.F.; White, O.; Kertavagge, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L. Nature 388, 533-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpe, P.D.; Smith, H.O.; Fraser, C.

A>Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: A64714

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-945 <TOM>

A:Cross-references: GB:AE000653; GB:AE000511; NID:g2314733; PIDN:AD08593.1; PID:g231473

Query Match 1.0%; Score 8; DB 2; Length 945;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 499 ERLGKPN 506

DB 657 ERLGKPN 664

RESULT 25

B70748

probable smc protein - *Mycobacterium tuberculosis* (strain H37RV)

C:Species: *Mycobacterium tuberculosis*

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: B70748

R.Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamilton, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A>Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: B70748

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1289 <COL>

A:Cross-references: GB:B74697; GB:AL123456; NID:g3361602; PIDN:CAA98982.1; PID:g1405958

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: smc

C:Superfamily: chromosome segregation protein SMCI

Query Match 1.0%; Score 8; DB 2; Length 1289;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 203 SELMAEA 210

DB 756 SELMAEA 763

RESULT 26

H97926

hypothetical protein sp10440 [imported] - *Streptococcus pneumoniae* (strain R6)

C:Species: *Streptococcus pneumoniae*

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001

C:Accession: H97926

R.Hockings, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E. e. R.; LeBlanc, D.J.; Lee, H.N.; Lefkowitz, E.J.; Lu, Y.; Matsushima, P.; McAnren, S.; M. y. P.; Sun, P.M.; Winkler, M.E. J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.

A>Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.

A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: H97926

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1659 <KUR>

A:Cross-references: GB:AE007317; PIDN:AAK99244.1; PID:g15458007; GSPDB:GN00174

C:Genetics:

A:Gene: sp10440

Query Match 1.0%; Score 8; DB 2; Length 1659;

Best Local Similarity 100.0%; Pred. No. 76;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 447 LTEAHKAL 454

DB 1292 LTEAHKAL 1299

RESULT 27
G95057
endo-beta-N-acetylglucosaminidase, probable [imported] - Streptococcus pneumoniae (strain
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #ext_change 03-Aug-2001
C:Accession: G95057
R:Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
non, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Sequence of a Virulent Isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1659 <KUR>
A:Cross-references: GB:A0005672; PIDN:AAK74656.1; PID:g14971970; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0498
Query Match 1.0%; Score 8; DB 2; Length 1659;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 447 LFEAKAL 454
| | | | |
Db 1292 LFEAKAL 1299
RESULT 28
S55073
env polypeptide - simian immunodeficiency virus STVmac (strain macC8) (fragment)
C:Species: simian immunodeficiency virus STVmac
A:Variety: strain macC8
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #ext_change 26-Aug-1999
C:Accession: S55073
R:Whitmore, A.; Cook, N.; Hall, G.; Sharpe, S.; Rud, E.; Cranage, M.
submitted to the EMBL Data Library, April 1995
A:Description: Repair and evolution of nef in vivo modulates SIV virulence.
A:Reference number: S54796
A:Accession: S55073
A:Molecule type: DNA
A:Residues: 1-44 <WHA>
A:Cross-references: EMBL:X86728; NID:g840891; PIDN:CAA60402.1; PID:g861124
A:Experimental source: strain macC8; week 33 after infection
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; immunodeficiency; polypeptide
Query Match 0.9%; Score 7; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 750 ATETLAG 756
| | | | |
Db 6 ATETLAG 12
RESULT 29
S55072
env polypeptide - simian immunodeficiency virus STVmac (strain macC8) (fragment)
C:Species: simian immunodeficiency virus STVmac
A:Variety: strain macC8
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #ext_change 26-Aug-1999
C:Accession: S55072
R:Whitmore, A.; Cook, N.; Hall, G.; Sharpe, S.; Rud, E.; Cranage, M.
submitted to the EMBL Data Library, April 1995
A:Description: Repair and evolution of nef in vivo modulates SIV virulence.
A:Reference number: S54796

A:Accession: S55072
A:Molecule type: DNA
A:Residues: 1-49 <WHA>
A:Cross-references: EMBL:X86727; NID:g840890; PIDN:CAA60400.1; PID:g861122
A:Experimental source: strain macC8; week 25 after infection
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; immunodeficiency; polypeptide
Query Match 0.9%; Score 7; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 750 ATETLAG 756
| | | | |
Db 11 ATETLAG 17
RESULT 30
D70091
hypothetical protein yydF - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #ext_change 15-Oct-1999
C:Accession: D70091
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteri
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Eyring, J.; Fabre, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Oawa, K.; Ogawa, A.; Oudega, B.; Park, S.H.; Paro, V.; Pohl, T.M.; Portet
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeder, R.; Scifone, F.; Sekiguchi, J.; Sekowska, A.; Seto
akuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumeit, E.; Yoshikawa, H.; Dancho, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D70091
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-49 <KUN>
A:Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16055.1; PID:e1184744,
A:Experimental source: strain 168
C:Genetics:
A:Gene: yydF
Query Match 0.9%; Score 7; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 406 ETVKNLE 412
| | | | |
Db 9 ETVKNLE 15
RESULT 31
D87657
hypothetical protein CC3294 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #ext_change 20-Apr-2001
C:Accession: D87657
R:Niemann, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc Natl Acad Sci U S A 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: D87657
A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-68 <STO>
 A:Cross-references: GB:AE005673; NID:g13424988; PIDN:AAK5256.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC3294

Query Match 0.9%; Score 7; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 322 EMBEIRA 328
 |||||
 Db 31 EMBEIRA 37

RESULT 32

A75134
 Hypothetical protein PAB8218 - Pyrococcus abyssi (strain Orsay)
 C:Species: Pyrococcus abyssi
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: A75134
 R:Anonymous, Genoscope
 Submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
 A:Reference number: A75001
 A:Accession: A75134
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-70 <RAM>
 A:Cross-references: GB:A0248285; GB:AL096836; NID:gs458067; PIDN:CAB49786.1; PID:el51568
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: PAB8218

Query Match 0.9%; Score 7; DB 2; Length 70;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 478 STNKEKL 484
 |||||
 Db 34 STNKEKL 40

RESULT 33

C90404
 Conserved hypothetical protein [imported] - Sulfolobus solfataricus
 C:Species: Sulfolobus solfataricus
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
 C:Accession: C90404
 R:She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.
 arrett, R.A.; Regan, M.A.; Senses, C.W.; Van der Oost, J.
 Submitted to GenBank, April 2001
 A:Description: Sulfolobus solfataricus complete genome.
 A:Reference number: A99139
 A:Accession: C90404
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-90 <RUR>
 A:Cross-references: GB:AE006641; NID:g13815638; PIDN:AAK42490.1; GSPDB:GN00155
 C:Genetics:
 A:Gene: SSO10237

Query Match 0.9%; Score 7; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 111 GKYYVYL 117
 |||||
 Db 18 GKYYVYL 24

RESULT 34

C75396
 Hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: C75396
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma-
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: C75396
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-93 <WHI>
 A:Cross-references: GB:AE001987; GB:AE000513; NID:g6459180; PIDN:AAFI1000.1; PID:g645918
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR1421
 A:Map position: 1

Query Match 0.9%; Score 7; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 487 DLAFILA 493
 |||||
 Db 6 DLAFILA 12

RESULT 35

E75556
 Hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: E75556
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma-
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: E75556
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-94 <WHI>
 A:Cross-references: GB:AE001875; GB:AE000513; NID:g6457790; PIDN:AAF09721.1; PID:g645779
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR0124
 A:Map position: 1

Query Match 0.9%; Score 7; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 322 EMBEIRA 328
 |||||
 Db 81 EMBEIRA 87

RESULT 36

BYMYBA
 Chaperonin groES - Mycobacterium tuberculosis
 N:Alternate names: 10K antigen; BCG-a homolog; Cpn10; heat shock protein 10K (hsp10); im
 C:Species: Mycobacterium tuberculosis
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jun-2000
 C:Accession: S01381; A37166; S02727; A47292; G70737; A46481; S18040
 R:Baird, P.N.; Hall, L.M.C.; Coates, A.R.M.
 Nucleic Acids Res. 16, 9047, 1988
 A:Title: A major antigen from Mycobacterium tuberculosis which is homologous to the heat
 A:Reference number: S01381; MUID:89015584; PMID:2902558
 A:Accession: S01381

A:Molecule type: DNA
A:Residues: 1-100 <BA1>
A:Cross-references: EMBL:X12598; NID:g44551; PID:g581338
R:BaIRD, P.N.; Hall, L.M.C.; Coates, A.R.W.
J:Gen. Microbiol. 135, 931-939, 1989
A:Title: Cloning and sequence analysis of the 10 kDa antigen gene of Mycobacterium tuberculosis
A:Reference number: A37166; MUID:90095443; PMID:2480990
A:Accession: A37166
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 'V', 2-100 <BA2>
A:Cross-references: GB:M25258; GB:X12598
R:Shimnick, T.M.; Plikavets, B.B.; Hyche, A.D.; van Landingham, R.M.; Walker, L.L.
Nucleic Acids Res. 17, 1254, 1989
A:Title: The Mycobacterium tuberculosis BCG-a protein has homology with the Escherichia
A:Reference number: S02727; MUID:89160258; PMID:2564178
A:Accession: S02727
A:Molecule type: DNA
A:Residues: 1-100 <SH1>
A:Cross-references: EMBL:X13739; NID:g44571; PIDN:CAA32003.1; PID:g581360
R:Kong, T.H.; Coates, A.R.; Butcher, P.D.; Hickman, C.J.; Shimnick, T.M.
Proc. Natl. Acad. Sci. U.S.A. 90, 2608-2612, 1993
A:Title: Mycobacterium tuberculosis expresses two chaparonin-60 homologs.
A:Reference number: A47292; MUID:93219332; PMID:7681982
A:Accession: A47292
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-100 <KON>
A:Cross-references: EMBL:X60350; NID:g44599; PIDN:CAA42908.1; PID:g581363
R:Kong, T.H.; Coates, A.R.; Butcher, P.D.; Hickman, C.J.; Shimnick, T.M.
Proc. Natl. Acad. Sci. U.S.A. 90, 2608-2612, 1993
A:Title: Sequence extracted from NCBI backbone (NCBIN:128605, NCBIPI:128607)
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295587; PMID:9634230
A:Accession: G70737
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-100 <COL>
A:Cross-references: GB:277165; GB:AL123456; NID:g3261609; PIDN:CAB01005.1; PID:g1449369
A:Experimental source: strain H37Rv
R:BaIRD, P.F.; Mehra, V.; Rivoltre, B.; Fong, S.J.; Brennan, P.J.; Voegtline, M.S.; Minco
J. Immunol. 148, 1835-1840, 1992
A:Title: Immunoreactivity of a 102-kDa antigen of Mycobacterium tuberculosis.
A:Reference number: A46481; MUID:92176646; PMID:1371791
A:Accession: A46481
A:Status: preliminary
A:Molecule type: protein
A:Residues: 2-16 <BAR>
A:Note: sequence extracted from NCBI backbone (NCBIPI:87128)
C:Genetics:
A:Gene: groES; cpn10
A:Start codon: GTG
C:Function:
A:Description: mediates protein folding and renaturation
C:Superfamily: ATP; heat shock; molecular chaperone; stress-induced protein
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
P:2-100/Product: chaparonin groES #status experimental <MAT>

Chapteron groES - Mycobacterium bovis
 N:Alernaite names: heat shock protein, 10K (hspl0) ; immunogenic protein MPB57
 C:Species: Mycobacterium bovis
 C:Date: 31-Mar-1991 #sequence revision 31-Mar-1991 #text_change 16-Jul-1999
 C:Accession: S01784; A37534; C60278
 R:Yamaguchi, R.; Matsuo, K.; Yamazaki, A.; Negai, S.; Terasaka, K.; Yamada, T.
 FEBS Lett. 240, 115-117, 1998
 A>Title: Immunogenic protein MPB57 from Mycobacterium bovis BCG: molecular cloning, nuc-
 A:Reference number: S01784; MUID:89052868; PMID:3056744
 A:Accession: S01784
 A:Molecule type: DNA
 A:Residues: 1-100 <YAM>
 A:Cross-references: EMBL:X13970; NID:G44190; PIDN:CAA3149.1; PID:G581313
 A:Accession: A37534
 A:Molecule type: protein
 A:Residues: 2-21 <YAM2>
 R:Flits, T.; Costopolous, C.; Radford, A.J.; Bacic, A.; Wood, P.R.
 Infect. Immun. 59, 800-807, 1991
 A>Title: Purification and characterization of major antigens from a Mycobacterium bovis
 A:Reference number: A60278; MUID:91147217; PMID:1900061
 A:Accession: C60278
 A:Molecule type: protein
 A:Residues: 2-15, 'E', 17-20 <FIF>
 C:Genetics:
 A:Gene: groES
 A:Start codon: GTG
 C:Superfamily: chaperonin groES
 C:Keywords: heat shock; molecular chaperone; stress-induced protein
 F:2-100/Product: chaperonin groES #status predicted <MAT>

Query Match	0.94	Score 71	DB 1	Length 100
Best Local Similarity	100.0%	Pred. No. 62		
Matches	7	Conservative	0	Mismatches 0; Indels 0; Gaps 0;
QY	605	GEKRIPL	611	
Db	55	GEKRIPL	61	

RESULT 38

T38824
thioltransferase - fission yeast (Schizosaccharomyces pombe)

N.Alternate names: glutaredoxin
C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text_change 20-Jun-2000
C.Accession: T38824; T43362; T50489
R.Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997

A.Reference number: Z21813
A.Accession: T38824
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-101 <CON>
A.Cross-references: EMBL:Z96980, PIDN:CA611722.1; GSPDB:GN00066; SPDB:SPAC4F10.20
A.Experimental source: strain 972h(-); cosmid c4F10
R.Kawamukai, M.
submitted to the EMBL Data Library, June 1998
A.Description: S.pombe glutaredoxin.
A.Reference number: Z22451
A.Accession: T43362
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-101 <KAW>
A.Cross-references: EMBL:AB015167; PIDN:BA28750.1
R.Kim, H.G.; Cho, Y.W.; Park, E.H.; Lim, C.J.
submitted to the EMBL Data Library, January 1999
A.Description: Characterization of cDNA encoding thioltransferase (glutaredoxin) from S.
A.Reference number: Z25091
A.Accession: T50489
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-101 <KIM>
A.Cross-references: EMBL:AF121275, PIDN:AAD5391.1

RESULT 37
BVMY7B

A; Cross-references: EMBL:AF121275; PIDN:AAD25391.1

C:Genetics:
A:Gene: gtx1; SPAC4F10.20
A:Map position: 1
A:Intons: 7/3; 25/2; 58/1
C:Superfamily: glutaredoxin; glutaredoxin homology
C:Species: electron transfer; redox-active disulfide
C:Keywords: redox-active #status predicted
F:25-28/Disulfide bonds: redox-active #status predicted

Query Match 0.9%; Score 7; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 461 NSDFQAL 467
|||
Db 82 NSDFQAL 88

RESULT 39

E82874
ribosomal protein S16 U568 [imported] - Ureaplasma urealyticum

C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: E82874

R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Helner, C.R.; Chen, E.Y.; Cassell, G.H.

submitted to GenBank, February 2000

A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir

A:Reference number: A82870

A:Accession: E82874

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-101 <GLA>

A:Cross-references: GB:AE002155; GB:AF222894; NID:G6699572; PIDN:AAF30982.1; GSPDB:GN001

C:Genetics:

A:Gene: rps16; U568

A:Genetic code: SGC3

Query Match 0.9%; Score 7; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 404 PSETVKN 410
|||
Db 66 PSETVKN 72

RESULT 40

I64171
hypothetical protein H1436 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Dec-2002

C:Accession: I64171

R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kevlavage, A.

; Gozdayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodex, A.; Kelley, J.M.; Weidman, J.

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A:Authors: Ghem, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: I64171

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-106 <TIGR>

A:Cross-references: GB:U52822; GB:I42023; NID:g1574265; PIDN:AAC3085.1; PID:g1574275; T

A:Note: best homolog was a hypothetical protein from Erwinia carotovora

C:Superfamily: uncharacterized conserved protein

Query Match 0.9%; Score 7; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 AAEAFLS 213
|||||

Db 28 AAEAFLS 34

RESULT 41

D87498
HesB/YadR/YfhF family protein [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C:Accession: D87498

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.O.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: D87498

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-110 <STO>

A:Cross-references: GB:AE005673; NID:G13423480; PIDN:AAK23984.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC2009

C:Superfamily: conserved hypothetical protein H10376

Query Match 0.9%; Score 7; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 779 LALLKGS 785
|||
Db 72 LALLKGS 78

RESULT 42

C86891
hypothetical protein ywab [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C:Accession: C86891

R:Boletijn, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich,

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp

A:Reference number: A86825; MUID:21235186; PMID:11337471

A:Accession: C86891

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-110 <STO>

A:Cross-references: GB:AE005176; PID:g12725188; PIDN:AAK06229.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: ywab

Query Match 0.9%; Score 7; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 710 VEETPAE 716
|||
Db 94 VEETPAE 100

RESULT 43

AG3598
transcription regulator [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002

C:Accession: AG3598

R:DeiVecchio, V.G.; Kaparat, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, I.

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD3252; PMID:11756688

A:Accession: AG3598

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <RUR>
A:Cross-references: GB:AE008918; PIDN:ALU53954.1; PID:G17984900; GSPDB:GN00191
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME110712
A:Map position: 11
C:Superfamily: Rhizobium plasmid pMGR234a protein y4ho

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 117;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 LSASELA 206
|||||
Db 88 LSASELA 94

RESULT 44
T44473
conserved hypothetical protein tnpG [imported] - Shigella flexneri
C:Species: Shigella flexneri
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44473
R:Moss, J.E.; Cardozo, T.J.; Zychlinsky, A.; Groisman, E.A.
Mol. Microbiol. 33, 74-83, 1999
A:title: The selC-associated SHI-2 pathogenicity island of Shigella flexneri.
A:Reference number: Z22779; MUID:99340540; PMID:10411725
A:Accession: T44473
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-121 <MOS>
A:Cross-references: EMBL:AF141323; NID:G5532445; PIDN:AD44740.1; PID:G5532456
A:Experimental source: strain M90T; serotype 5a
C:Genetics:
A:Gene: tnpG
C:Superfamily: Agrobacterium tumefaciens insertion sequence IS1312 hypothetical protein

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 121;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 ASELAAA 208
|||||
Db 70 ASELAAA 76

RESULT 45
NRPRH
pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: Antilocapra americana (pronghorn)
C:Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
C:Accession: A00813
R:Beintema, J.J.; Gastra, W.; Munnikema, J.
J. Mol. Evol. 13, 305-316, 1979
A:title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw
A:Reference number: A00813; MUID:80075014; PMID:515141
A:Accession: A00813
A:Molecule type: protein
A:Residues: 1-124 <BBI>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (asn) (covalent) (partial) #status experimental

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 124;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 785 SNPSVS 791

Db 15 SNPSVS 21
|||||

RESULT 46
H72500
hypothetical protein APE1982 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: H72500
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A:title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: H72500
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-128 <RAM>
A:Cross-references: DBJ:AP000063; NID:G5105654; PIDN:BAA0992.1; PID:G5105680
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1982
C:Superfamily: Aeropyrum pernix hypothetical protein APE1982

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 128;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 785 SNPSVS 791
|||||
Db 43 SNPSVS 49

RESULT 47
T36220
mutL-like protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Aug-2000
C:Accession: T36220
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21577
A:Accession: T36220
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-129 <OLI>
A:Cross-references: EMBL:AL049573; PIDN:CAB40318.1; GSPDB:GN00070; SCOEDB:SCB39.10
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCB39.10
C:Superfamily: unassigned mutL domain proteins; mutL domain homology

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 129;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LTPDEV 39
|||||
Db 89 LTPDEV 95

RESULT 48
S76934
hypothetical protein slr0588 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S76934
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud
DNA Res. 3, 109-136, 1996
A:title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti

5. A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76934
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-130 <KAN>
A:CROSS-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BA1846.1; PID:g165393
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: Synchocystis hypothetical protein slt0588

Query Match 0.9%; Score 7; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 268 DSLKOL 274
DB 111 DSLKOL 117

RESULT 49
T35461
mutr-like protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 26-May-2000
C:Accession: T35461
R:Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A:Reference number: Z21578
A:Accession: T35461
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-131 <MUR>
A:CROSS-references: EMBL:AL031035; PIDN:CAA19915.1; GSPDB:GN00070; SCOPDB:SC6A9.30C
C:Genetics:
A:Experimental source: strain A3(2)
A:Gene: SCOPDB:SC6A9.30C
C:Superfamily: unassigned mutr domain proteins; mutr domain homology

Query Match 0.9%; Score 7; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LTPDEV 39
DB 91 LTPDEV 97

RESULT 50
B65240
hypothetical protein, 13.4K - Escherichia coli (strain K-12) insertion sequence IS2
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 01-Mar-2002
C:Accession: B65240; F64891; B65092; S56497; JQ0039
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burlingame, V.; Riley, M.;
A.: Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: B65240
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-136 <BLAT>
A:CROSS-references: GB:AE000498; GB:U00096; NID:g2367366; PIDN:AACT7228.1; PID:g1790723;
A:Experimental source: strain K-12, substrain MGI655
A:Genetics: Y21
A:Accession: F64891
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-136 <BLAT>
A:CROSS-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AACT74485.1; PID:g1787670;
A:Experimental source: strain K-12, substrain MGI655
A:Genetics: Y22
A:Accession: H64763

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-136 <BLAT>
A:CROSS-references: GB:AE000493; GB:U00096; NID:g1786554; PIDN:AACT73463.1; PID:g1786557;
A:Experimental source: strain K-12, substrain MGI655
A:Genetics: Y11
A:Accession: B65092
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 16-136 <BLAT>
A:CROSS-references: GB:AE000386; GB:U00096; NID:g2367187; PIDN:AACT6080.1; PID:g1789423;
A:Experimental source: strain K-12, substrain MGI655
A:Genetics: Y25
A:Accession: F65069
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 16-136 <BLAT>
A:CROSS-references: GB:AE000369; GB:U00096; NID:g2367168; PIDN:AACT5900.1; PID:g1789225;
A:Experimental source: strain K-12, substrain MGI655
A:Genetics: Y24
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A:Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A:Reference number: S56314; MUID:95334362; PMID:7610040
A:Accession: S56497
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-136 <BUR>
A:CROSS-references: EMBL:U14003; NID:g1263172; PIDN:AAA97168.1; PID:g537113
A:Genetics: Y26
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R:Ronecker, H.J.; Rak, B.
Gene 59, 291-296, 1987
A:Title: Genetic organization of insertion element IS2 based on a revised nucleotide seq
A:Reference number: A91582; MUID:88137965; PMID:2830172
A:Accession: JQ0039
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 16-136 <RON>
A:CROSS-references: GB:V00279; GB:U01732; GB:M18426; NID:g41525; PIDN:CAA23542.1; PID:g4
A:Experimental source: K12, strain HB101
A:Genetics: HB1
C:Genetics: <Y21>
A:Gene: Y121
A:Molecule element: insertion sequence IS2
C:Genetics: <Y22>
A:Gene: Y121_2
A:Molecule element: insertion sequence IS2
C:Genetics: <Y11>
A:Gene: Y121.1
A:Molecule element: insertion sequence IS2
C:Genetics: <Y25>
A:Gene: Y121_5
A:Molecule element: insertion sequence IS2
C:Genetics: <Y24>
A:Gene: Y121.4
A:Molecule element: insertion sequence IS2
C:Genetics: <Y26>
A:Molecule element: insertion sequence IS2
C:Genetics: <HB1>
A:Molecule element: insertion sequence IS2
A:Start codon: GTG
C:Superfamily: Agrobacterium tumefaciens insertion sequence IS1312 hypothetical protein

Query Match 0.9%; Score 7; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 ASELAAA 208
DB 85 ASELAAA 91

RESULT 51
D64964
hypothetical protein - Escherichia coli (strain K-12) insertion sequence IS2
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-sep-1997 #ext_change 01-Mar-2002
C:Accession: D64964
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; PMID:97426617; PMID:92788503
A:Accession: D64964
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-136 <BLAT>
A:Cross-references: GB:AE000291; GB:U00096; NID:g1788298; PIDN:ACT5058.1; PID:g1788306;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: y121_3
A:Mobile element: insertion sequence IS2
C:Superfamily: Agrobacterium tumefaciens insertion sequence IS1312 hypothetical protein

Query Match 0.9%; Score 7; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 ASELAAA 208
Db 85 ASELAAA 91

RESULT 52
T19240
hypothetical protein C13G3.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 15-Oct-1999
C:Accession: T19240
R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19096
A:Accession: T19240
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-136 <WILP>
A:Cross-references: EMBL:Z74027; PIDN:CA98421.1; GSPDB:GN00023; CESP:C13G3.1
C:Genetics:
A:Gene: CESP:C13G3.1
A:Map position: 5
A:introns: 49/1

Query Match 0.9%; Score 7; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 783 KGSNPS 789
Db 96 KGSNPS 102

RESULT 53
B81286
probable membrane protein Cj1410c [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #ext_change 03-Jun-2002
C:Accession: B81286
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: AB1250; PMID:20150912; PMID:10688204
A:Accession: B81286
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-139 <PAR>
A:Cross-references: GB:AL111168; GB:AL111168; NID:g6968723; PIDN:CAB73834.1; PID:g69688;
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj1410c
C:Superfamily: Campylobacter jejuni probable membrane protein Cj1410c

Query Match 0.9%; Score 7; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 IVIKITD 55
Db 100 IVIKITD 106

RESULT 54
A71717
hypothetical protein RP082 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #ext_change 03-Nov-2000
C:Accession: A71717
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Alsmark, I
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; PMID:99039499; PMID:9823893
A:Accession: A71717
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-143 <AND>
A:Cross-references: GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CA14552.1; PID:e134239
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: RP082

Query Match 0.9%; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 NRQOEK 139
Db 106 NRQOEK 112

RESULT 55
AF1219
Salmonella enterica pduK protein homolog lmo1158 [imported] - Listeria monocytogenes (str
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #ext_change 27-Nov-2001
C:Accession: AF1219
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karsc, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, U.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; PMID:21537279; PMID:11679669
A:Accession: AF1219
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-145 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC99236.1; PID:g16410574; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1158

Query Match 0.9%; Score 7; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 722 VETKVE 728

Db 103 VETEKVE 109

RESULT 56

Problematic transcription regulator PA3067 [imported] - Pseudomonas aeruginosa (strain PAO1)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: D83261
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: D83261
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-147 <STO>
 A:Cross-references: GB:AE004731; GB:AE004091; NID:g9949171; PIDN:AA06455.1; GSPDB:GN001
 A:Experimental source: strain PAO1
 C:Genetics:
 A:Gene: PA3067
 C:Superfamily: Mycobacterium leprae hypothetical protein MLCB57.31

Query Match 0.9%; Score 7; DB 2; Length 147;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 203 SELAAE 209
 Db 54 SELAAE 60

RESULT 57

Problematic transcription regulator PA3067 [imported] - Escherichia coli (strain O157:H
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: A86079
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 M.; Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamous, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: A86079
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-148 <STO>
 A:Cross-references: GB:AE005174; NID:g12518795; PIDN:AA059093.1; GSPDB:GN00145; UMGPR:254
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: fliA
 C:Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannitol-5

Query Match 0.9%; Score 7; DB 2; Length 148;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 GVAAPHG 309
 Db 59 GVAAPHG 65

RESULT 58

Problematic transcription regulator PA3067 [imported] - Escherichia coli (strain O157
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
 C:Accession: B91232
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: B91232
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-148 <HAV>
 A:Cross-references: GB:BA000007; PIDN:BA038249.1; PID:g13364302; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RMD 0509952
 C:Genetics:
 A:Gene: EC94826
 C:Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannitol-5

Query Match 0.9%; Score 7; DB 2; Length 148;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 GVAAPHG 309
 Db 59 GVAAPHG 65

RESULT 59

Problematic transcription regulator PA3067 [imported] - Escherichia coli (strain K-12)
 N:Alternate names: hypothetical protein f147 (rhad 3' region)
 C:Species: Escherichia coli
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 01-Mar-2002
 C:Accession: D48649; G65195; S40844; S36642
 R:Moralto, P.; Egan, S.M.; Hoidalgo, E.; Aguilar, J.
 J. Bacteriol. 175, 5585-5594, 1993
 A:Title: Sequencing and characterization of a gene cluster encoding the enzymes for L-rh
 A:Reference number: A48649; MUID:93374854; PMID:8396120
 A:Accession: D48649
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-148 <MOR>
 A:Cross-references: GB:X60472; NID:g396678; PIDN:CAA43004.1; PID:g396682
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: G65195
 A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-148 <BLAT>
 A:Cross-references: GB:AE000465; GB:U00096; NID:g2367326; PIDN:AACT6882.1; PID:g2367327;
 A:Experimental source: strain K-12, substrain MG1655
 R:Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R.
 Nucleic Acids Res. 21, 3391-3398, 1993
 A:Title: Analysis of the Escherichia coli genome. III. DNA sequence of the region from 8
 A:Reference number: S40802; MUID:93347969; PMID:8346018
 A:Accession: S40844
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-80, 'G', 82-102, 'XXXX', 107, 109-148 <PLU>
 A:Cross-references: EMBL:U13201; NID:g304961; PIDN:AA03033.1; PID:g305004
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993
 C:Genetics:
 A:Gene: fliA
 C:Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannitol-5
 C:Keywords: phosphoprotein

Query Match 0.9%; Score 7; DB 2; Length 148;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 GVAAPHG 309
 Db 59 GVAAPHG 65


```
RESULT 60
S39873
hypothetical protein 154 - Streptomyces ambofaciens
C:Species: Streptomyces ambofaciens
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 26-May-2000
C:Accession: S39873; S33421
R:Hagege, J.; Perinot, J.L.; Friedmann, A.; Guerin, M.
Mol. Microbiol. 10, 799-812, 1993
A>Title: Mode and origin of replication of pSAM2, a conjugative integrating element of S
A:Reference number: S39873; PMID:95020551; PMID:7934842
A:Accession: S39873
A:Molecule type: DNA
A:Residues: 1-154 <HAG>
A:Cross-references: EMBL:Z19590; NID:G238044; PIDN:CAA79638.1; PID:G238045
A>Note: the authors translated the codon TAC for residue 81 as Thr and TAC for residue 1
C:Superfamily: unassigned mult domain proteins; mult domain homology
F:43-77/Domain: mult domain homology <MUT>

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 154;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LTPDEVS 39
|||||
114 LTPDEVS 120

RESULT 61
AC2947
ribonuclease H [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AC2947
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavina, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:21608550; PMID:11743193
A:Accession: AC2947
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-157 <KUR>
A:Cross-references: GB:AE008689; PIDN:AAL43393.1; PID:gl77441550; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: rnhA
A:Map position: linear chromosome
C:Superfamily: ribonuclease H

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 157;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 467 LDKLRL 473
|||||
117 LDKLRL 123

RESULT 62
G98335
ribonuclease H PA1815 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C:Accession: G98335
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Oncollo, B.; Goldman,
A.; Liu, F.; Mollan, C.; Allinger, M.; Doughy, D.; Scott, C.; Leppas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; PMID:21608551; PMID:11743194
A:Accession: G98335
```

```
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-157 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK90209.1; PID:gl5160220; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L_3264
A:Map position: linear chromosome
C:Superfamily: ribonuclease H

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 157;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 467 LDKLRL 473
|||||
117 LDKLRL 123

RESULT 63
AF3240
conserved hypothetical protein Atu6104 [imported] - Agrobacterium tumefaciens (strain C
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AF3240
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavina, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:21608550; PMID:11743193
A:Accession: AF3240
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-157 <KUR>
A:Cross-references: GB:AE008690; PIDN:AAL46340.1; PID:gl7744128; GSPDB:GN00189
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu6104
A:Genome: plasmid

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 157;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 489 LAFLAPI 495
|||||
5 LAFLAPI 11

RESULT 64
D69256
hypothetical protein AF0052 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: D69256
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uitterlinden, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaite, B.P.; Sykes, S
Smith, H.O.; Woese, C.R.; Venter, J.C.
A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; PMID:98049343; PMID:938475
A:Accession: D69256
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <KUR>
A:Cross-references: GB:AE001102; GB:AE000782; NID:G2689425; PIDN:AA91174.1; PID:G265055
C:Superfamily: Archaeoglobus fulgidus hypothetical protein AF2183

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 158;
```

Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 NSSLVSO 378
|||||
Db 36 NSSLVSO 42

RESULT 65
transcription elongation factor grea [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: AB99943
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: AB9758; MUID:2111952; PMID:11418146
A:Accession: AB99943
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-158 <KUR>
A:Cross-references: GB:BA000018; PID:g13701408; PIDN:BAB42702.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: greA
C:Superfamily: transcription elongation factor greb
C:Keywords: transcription factor

Query Match 0.9%; Score 7; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 IIEDTGD 182
|||||
Db 77 IIEDTGD 83

RESULT 66
C83415
hypothetical protein PA1841 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83415
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: C83415
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-165 <STO>
A:Cross-references: GB:AE004610; GB:AE004091; NID:g9947825; PIDN:AA05230.1; GSPDB:GN001
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA1841

Query Match 0.9%; Score 7; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 487 DLALFLA 493
|||||
Db 148 DLALFLA 154

RESULT 67
A86450
probable glycine cleavage system H-protein precursor - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
C:Accession: AB6450
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federici, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Stimm, P.; Southwick, A.M.; Sun, H.; Telson,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MUID:21016719; PMID:11130712
A:Accession: AB6450
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-166 <STO>
A:Cross-references: GB:AE005172; NID:g8920623; PIDN:AAF81345.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: glycine cleavage system protein H; lipoyl/biotin-binding homology

Query Match 0.9%; Score 7; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 SSVSKEK 794
|||||
Db 83 SSVSKEK 89

RESULT 68
C81235
transcription antitermination protein NusG NMB0126 [imported] - Neisseria meningitidis (C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C:Accession: C81235; AB2008
R:Terrellin, H.; Sanders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathevan, V.; Gill, J.; Scariato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755; PMID:10710307
A:Accession: C81235
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-178 <TER>
A:Cross-references: GB:AE002371; GB:AE002098; NID:g7225337; PIDN:AAF40585.1; PID:g722534
A:Experimental source: serogroup B, strain MC58
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holtroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.
A:Reference number: AB1775; MUID:20222556; PMID:10761919
A:Accession: AB2008
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-178 <PAR>
A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83462.1; PID:g737891
A:Experimental source: serogroup A, strain 22491
C:Genetics:
A:Gene: nusG; NMB0126; NMA0147
C:Superfamily: transcription antitermination factor nusG

Query Match 0.9%; Score 7; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 LEBRIAR 329
|||||
Db 22 LEBRIAR 28

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RESULT 69
H71920
adenine phosphoribosyltransferase (EC 2.4.2.7) - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Jul-1999
C:Accession: H71920
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Meberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: H71920
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-179 <ARN>
A:Cross-references: GB:AE001465; GB:AE001439; NID:g4155057; PIDN:AAD06100.1; PID:g415506
A:Experimental source: strain J99
C:Genetics:
A:Gene: apt
C:Function:
A:Pathway: purine salvage
C:Superfamily: adenine phosphoribosyltransferase
C:Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match
Best Local Similarity 0.9%; Score 7; DB 2; Length 179;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 484 LVDDLLA 490
|||||
Db 124 LVDDLLA 130

RESULT 70
A70178
conserved hypothetical protein B80626 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Dec-2002
C:Accession: A70178
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Iathigra, R.; White
son, D.; Peterson, J.; Kexlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: A70178
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-181 <KLE>
A:Cross-references: GB:AE001164; GB:AE000783; NID:g2688550; PIDN:AAC66987.1; PID:g268855
A:Experimental source: strain B31
C:Superfamily: Primase-related protein

Query Match
Best Local Similarity 0.9%; Score 7; DB 2; Length 181;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 KLLERLN 475
|||||
Db 153 KLLERLN 159

RESULT 71
F75487
v-type ATP synthase, E subunit - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: F75487
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

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, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: F75487
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-185 <WHI>
A:Cross-references: GB:AE001926; GB:AE000513; NID:g6458395; PIDN:AAF10275.1; PID:g645840
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0697
A:Map position: 1

Query Match
Best Local Similarity 0.9%; Score 7; DB 2; Length 185;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 ALDKLLE 472
|||||
Db 2 ALDKLLE 8

RESULT 72
T35792
beta-glucosidase - Streptomyces coelicolor (fragment)
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 26-May-2000
C:Accession: T35792
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A:Reference number: Z21570
A:Accession: T35792
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-191 <SEB>
A:Cross-references: EMBL:AL031013; PIDN:CAA19797.1; GSPDB:GN000070; SCOEDB:SC8A6.25
C:Genetics:
A:Experimental source: strain A312)
A:Gene: SCOEDB:SC8A6.25
C:Superfamily: Agrobacterium beta-glucosidase

Query Match
Best Local Similarity 0.9%; Score 7; DB 2; Length 191;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 484 LVDDLLA 490
|||||
Db 122 LVDDLLA 128

RESULT 73
S01249
cytochrome c-L precursor - Methylobacterium sp.
C:Species: Methylobacterium sp.
C:Date: 30-Sep-1989 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: S01249; S02658
R:Nunn, D.N.; Anthony, C.
Biochem J. 256, 673-676, 1988
A:Title: The nucleotide sequence and deduced amino acid sequence of the cytochrome c(L)
A:Reference number: S02658; MUID:89134152; PMID:2851998
A:Accession: S02658
A:Molecule type: DNA
A:Residues: 1-197 <NUN2>

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A>Note: source designated as *Methylobacterium extorquens* AM1
A>Note: part of this sequence was confirmed by protein sequencing
C:Genetics:
A:Gene: moxG
C:Function:
A:Description: electron acceptor for methanol dehydrogenase; electron donor to cytochrom
A:Pathway: methanol oxidation
C:Superfamily: cytochrome c-L; cytochrome c6 homology
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; periplasmic sp
F:1-35/Domain: signal sequence #status predicted <SIG>
F:26-197/Product: cytochrome c-L #status predicted <MAT>
F:80-153/Domain: cytochrome c6 homology <CY6>
F:90,93/Binding site: heme (Cys) (covalent) #status predicted
F:94,134/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 0.9%; Score 7; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 ENLTPDE 37
|||||
DB 139 ENLTPDE 145

RESULT 74
S06147
GFP-binding protein rab1B - rat
N:Alternate names: rat-related protein rab1B
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 02-Feb-2001
C:Accession: S06147; S03189
R:Touchot, N.; Zahraoui, A.; Viehl, E.; Tavittian, A.
FEBS Lett. 256, 79-84, 1989
A:Title: Biochemical properties of the YPT-related rab1B protein. Comparison with rab1A.
A:Reference number: S06147; MUID:90033316; PMID:2509243
A:Accession: S06147
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-201 <TOU>
R:Viehl, E.; Touchot, N.; Zahraoui, A.; Tavittian, A.
Nucleic Acids Res. 17, 1770, 1989
A:Title: Nucleotide sequence of a rat cDNA, RAB1B, encoding a RAB1-YPT related protein.
A:Reference number: S03189; MUID:89160341; PMID:2493636
A:Accession: S03189
A:Molecule type: mRNA
A:Residues: 1-95, 'YA', 98-201 <VIE>
A:Cross-references: EMBL:X13905; NID:G57005; PIDN:CAA32105.1; PID:G57006
C:Genetics:
A:Gene: rab1B
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GFP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop;
F:9-124/Domain: translation elongation factor Tu homology <ETU>
F:15-22/Region: nucleotide-binding motif A (P-loop)
F:121-124/Region: GTP-binding NKXD motif
F:151-153/Region: GTP-binding SAK/L motif
F:21-32, 40, 121, 122, 124, 151/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta
F:200,201/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

Query Match 0.9%; Score 7; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 PVLKIDS 371
|||||
DB 184 PVLKIDS 190

RESULT 75
P90658
Hypochemical protein ECG0238 [imported] - *Escherichia coli* (strain O157:H7, substrain RI
C:Species: *Escherichia coli*
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: P90658

R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: P90658
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-203 <HAV>
A:Cross-references: GB:BA000007; PIDN:BA033661.1; PID:G13359694; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECG0238

Query Match 0.9%; Score 7; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 774 EAEKLLA 780
|||||
DB 31 EAEKLLA 37

RESULT 76
P85509
Hypochemical protein Z0269 [imported] - *Escherichia coli* (strain O157:H7, substrain EDL9
C:Species: *Escherichia coli*
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: P85509
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: P85509
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-203 <STO>
A:Cross-references: GB:AE005174; NID:G12512978; PIDN:AG54538.1; GSPDB:GN00145; UWGP:202
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z0269

Query Match 0.9%; Score 7; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 774 EAEKLLA 780
|||||
DB 31 EAEKLLA 37

RESULT 77
S62443
Adenosine 5', 5''-P1, P6-hexaphosphate hydrolase [validated] - fission yeast (*Schizosa
N:Alternate names: hypothetical protein SPAC24B11.03
C:Species: *Schizosaccharomyces pombe*
C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 15-Sep-2000
C:Accession: S62443; S62548; T37649; T38330; T50491
R:Odell, C.; Bowman, S.
submitted to the EMBL Data Library, October 1995
A:Reference number: S62430
A:Accession: S62443
A:Molecule type: DNA
A:Residues: 1-210 <ODE>
A:Cross-references: EMBL:Z54308; NID:G1008985; PIDN:CAA91107.1; PID:G1008999
R:Odell, C.; Churcher, C.M.
submitted to the EMBL Data Library, November 1995
A:Reference number: S62546
A:Accession: S62546
A:Molecule type: DNA
A:Residues: 1-210 <OD2>
A:Cross-references: EMBL:Z67757; NID:G1061288; PIDN:CAA91768.1; PID:G1061291*

R.Ode11, C.; Bowman, S.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z21734
A:Accession: T37649
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-210 <OD3>
A:Cross-references: EMBL:Z54308; PIDN:CAA91107.1; GSPDB:GN00066; SPDB:SPAC136.14
A:Experimental source: strain 972h(-); cosmid c136
R.Ode11, C.; Church, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z21786
A:Accession: T38330
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-210 <OD4>
A:Cross-references: EMBL:Z6757; PIDN:CAA91768.1; GSPDB:GN00066; SPDB:SPAC24B11.03
A:Experimental source: strain 972h(-); cosmid c24B11
R.Ingram, S.W.; Stratemann, S.A.; Barnes, L.D.
Biochemistry 38, 3649-3655, 1999
A:Title: Schizosaccharomyces pombe Aps1, a diadenosine 5',5'''-P1,P6-hexaphosphate hydrolase purified enzyme.
A:Reference number: Z25093; MID:99192402; PMID:10090752
A:Accession: T50491
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-210 <ING>
A:Cross-references: EMBL:AF125215; PIDN:AAD2005.1
A:Experimental source: strain 972
C:Genetics:
A:Gene: aps1; SPAC136.14; SPAC24B11.03; SPAC24B11.03
A:Map position: 1L
C:Complex: monomer [validated, MUID:99192402]
C:Function:
A:Description: catalyzes the hydrolysis of dinucleoside oligophosphates [validated, MUID:99192402]
C:Superfamily: Saccharomycetes cerevisiae hypothetical protein YOR163w

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 210;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 773 AEAEXLL 779
|||||
Db 143 AEAEXLL 149

RESULT 78
AH0899
conserved hypothetical protein STY3451 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AH0899
R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0899
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD07790.1; PID:G16504338; GSPDB:GN00176
C:Genetics:
A:Gene: STY3451

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 211;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 YNRVKG 606

Db 122 YNRVKG 128
|||||

RESULT 79
T01627
probable ATP binding protein At2g18990 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 02-Feb-2001
C:Accession: T01627; B84571
R.Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, M.; Koo, H.; Moffat, K.S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Eues, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:1061197
A:Accession: B84571
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <STO>
A:Cross-references: GB:AE002093; MID:96598372; PIDN:AAF18603.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g18990
A:Map position: 2
A:Insertions: 7/3; 99/3; 152/3
A:Note: P19F24.19

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 211;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 LERIRAR 329
|||||
Db 169 LERIRAR 175

RESULT 80
F83144
conserved hypothetical protein PA4017 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83144
R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: F83144
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-213 <STO>
A:Cross-references: GB:AE004818; GB:AE004091; MID:9950200; PIDN:AA07404.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4017

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 213;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 YNRVKG 606
|||||

Db 125 YNRVKG6 131

RESULT 81

B75533

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000

C:Accession: B75533

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uetereback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: B75533

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-219 <MH1>

A:Cross-references: GB:AE001893; GB:AE000513; NID:g6458001; PIDN:AAF0916.1; PID:g645801

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR0333

A:Map position: 1

C:Superfamily: Deinococcus radiodurans hypothetical protein DR0333

Query Match 0.9%; Score 7; DB 2; Length 219;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 199 ELSASEL 205

105 ELSASEL 111

RESULT 82

D65105

hypothetical 24.8 kD protein in agaI-mtr intergenic region - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002

C:Accession: D65105

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A61720; MUID:97426617; PMID:9278503

A:Accession: D65105

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-226 <BLAT>

A:Cross-references: GB:AE000396; GB:U00096; NID:g1789536; PIDN:AACT6186.1; PID:g1789542;

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: yrar

Query Match 0.9%; Score 7; DB 2; Length 226;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 600 YNRVKG6 606

137 YNRVKG6 143

RESULT 83

A98133

hypothetical protein Ecs4033 [imported] - Escherichia coli (strain O157:H7, substrain R1)

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C:Accession: A98133

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Ganeswara, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno

A:Reference number: A98629; MUID:21156231; PMID:11258796

A:Accession: A98133

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-226 <HAV>

A:Cross-references: GB:BA000007; PIDN:BA937456.1; PID:g13363506; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain R1MD 0509952

C:Genetics:

A:Gene: Ecs4033

Query Match 0.9%; Score 7; DB 2; Length 226;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 600 YNRVKG6 606

137 YNRVKG6 143

RESULT 84

D85978

hypothetical protein yrar [imported] - Escherichia coli (strain O157:H7, substrain EDL93)

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: D85978

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalante, E.; Potomousis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: D85978

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-226 <STO>

A:Cross-references: GB:AE005174; NID:g12517760; PIDN:AAG58288.1; GSPDB:GN00145; UMGF:Z45

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: yrar

Query Match 0.9%; Score 7; DB 2; Length 226;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 600 YNRVKG6 606

137 YNRVKG6 143

RESULT 85

G81894

probable integral membrane protein NMA1265 [imported] - Neisseria meningitidis (strain Z)

C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C:Accession: G81894

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; MUID:20222556; PMID:10761919

A:Accession: G81894

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-226 <PAR>

A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84520.1; PID:g737994

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA1265

Query Match 0.9%; Score 7; DB 2; Length 226;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 AEAFLSG 214
 |||||
 Db 189 AEAFLSG 195

RESULT 86
 D81125
 hypothetical protein NMB1066 [imported] - Neisseria meningitidis (strain MCS8 serogroup C)
 C/Species: Neisseria meningitidis
 C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C/Accession: D81125
 R/Retcelin, H.; Saunders, N.J.; Heidelberg, J.; Ueffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
 A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.; V. A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
 A/Reference number: AB1000; PMID:20175755; PMID:10710307
 A/Accession: D81125
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-226 <TET>
 A/Cross-references: GB:AE002457; GB:AE002098; NID:g7226304; PIDN:AAF41462.1; PID:g722630
 A/Experimental source: serogroup B, strain MCS8
 C/Genetics:
 A/Gene: NMB1066

Query Match 0.9%; Score 7; DB 2; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 AEAFLSG 214
 |||||
 Db 189 AEAFLSG 195

RESULT 87
 C83744
 two-component response regulator BH0755 [imported] - Bacillus halodurans (strain C-125)
 C/Species: Bacillus halodurans
 C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C/Accession: C83744
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
 A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A/Reference number: A83650; PMID:20512582; PMID:11058132
 A/Accession: C83744
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-232 <STO>
 A/Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04474.1; GSPDB:GN00
 A/Experimental source: strain C-125
 C/Genetics:
 A/Gene: BH0755
 C/Superfamily: cmpr protein; response regulator homology

Query Match 0.9%; Score 7; DB 2; Length 232;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 EVLLAKV 741
 |||||
 Db 106 EVLLAKV 112

RESULT 88
 G87286
 conserved hypothetical protein CC0304 [imported] - Caulobacter crescentus
 C/Species: Caulobacter crescentus
 C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C/Accession: G87286
 R/Nierman, W.C.; Feldbljum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; B.; Laub, M.T.; Debroy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A/Title: Complete Genome Sequence of Caulobacter crescentus.
 A/Reference number: A87249; PMID:21173698; PMID:1125647
 A/Accession: G87286
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-237 <STO>
 A/Cross-references: GB:AE005673; NID:g13421447; PIDN:AAK22291.1; GSPDB:GN00148
 C/Genetics:
 A/Gene: CC0304

Query Match 0.9%; Score 7; DB 2; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 GAVALLR 158
 |||||
 Db 152 GAVALLR 158

RESULT 89
 I67638
 proteasome activator rPA28 subunit beta - rat
 C/Species: Rattus sp. (rat)
 C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 24-Sep-1999
 C/Accession: I67638
 R/Joan Young, A.; Tanahashi, N.; Akiyama, K. FEBS-Lett. 366, 37-42, 1995
 A/Title: Primary structures of two homologous subunits of PA28, a gamma-interferon-induc A/Reference number: I53518; PMID:95309399; PMID:7789512
 A/Accession: I67638
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-238 <RES>
 A/Cross-references: GB:DA5250; NID:g1008931; PIDN:BA08207.1; PID:g1008932
 C/Superfamily: proteasome activator PA28 alpha chain

Query Match 0.9%; Score 7; DB 2; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 776 EKLLALL 782
 |||||
 Db 97 EKLLALL 103

RESULT 90
 D75203
 hypothetical protein PAB2251 - Pyrococcus abyssi (strain Orsay)
 C/Species: Pyrococcus abyssi
 C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C/Accession: D75203
 R/anonymous, Genoscope submitted to the EMBL Data Library, July 1999
 A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru A/Reference number: A75001
 A/Accession: D75203
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-240 <KAW>
 A/Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49075.1; PID:e151496
 A/Experimental source: strain Orsay
 C/Genetics:
 A/Gene: PAB2251

Query Match 0.9%; Score 7; DB 2; Length 240;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 LKEAEVL 737
 |||||
 Db 96 LKEAEVL 102

RESULT 91

C71725
amino-acid ABC transporter binding protein (ygiX) RP150 - *Rickettsia prowazekii*
C:Species: *Rickettsia prowazekii*
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C:Accession: C71725
R:Anderson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichertz-Fonten, T.; Alsmark, U.
Nature 396, 133-140, 1998
A:Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.
A:Reference number: A1630; MUID:99039499; PMID:9823893
A:Accession: C71725
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-241 <AND>
A:Cross-references: GB:AJ235270, GB:AJ235269, NID:g3860572, PIDN:CAA14618.1, PID:g386071
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: ygiX; RP150
C:Superfamily: lysine-arginine-ornithine-binding protein

Query Match 0.9%; Score 7; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 DALISEE 82
DB 173 DALISEE 179

RESULT 92

H97723
hypothetical protein ygiX [imported] - *Rickettsia conorii* (strain Malish 7)
C:Species: *Rickettsia conorii*
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 02-Nov-2001
C:Accession: H97723
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro-
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: H97723
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-241 <KID>
A:Cross-references: GB:AE006914; PIDN:AAL02730.1; PID:g15619241; GSPDB:GN00173
C:Genetics:
A:Gene: ygiX
C:Superfamily: lysine-arginine-ornithine-binding protein

Query Match 0.9%; Score 7; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 DALISEE 82
DB 173 DALISEE 179

RESULT 93

T03482
iron(III) dicitrate transporter ATP-binding protein - *Rhodobacter capsulatus*
C:Species: *Rhodobacter capsulatus*
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C:Accession: T03482
R:Vilek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fomstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A:Title: Sequence of a 189-kb segment of the chromosome of *Rhodobacter capsulatus* SB1003
A:Reference number: Z14955; MUID:97404404; PMID:9256491
A:Accession: T03482
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-255 <VLC>

A:Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AA016135.1; PID:g3128283
C:Genetics:
A:Gene: fecC
A:Map position: 1
C:Superfamily: inner membrane protein malK; ATP-binding cassette homology
C:Keywords: iron transport

Query Match 0.9%; Score 7; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 778 LVALKG 784
DB 181 LVALKG 187

RESULT 94

I38025
keratin-like protein - human (fragment)
C:Species: *Homo sapiens* (man)
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 13-Aug-1999
C:Accession: I38025; S60680
R:Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattei, M.G.; Chenard, M.P.; Lidereau, R...
Genomics 28, 367-376, 1995
A:Title: Identification of four novel human genes amplified and overexpressed in breast
A:Reference number: I37080; MUID:96039245; PMID:7490069
A:Accession: I38025
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-257 <RES>
A:Cross-references: EMBL:X80197; NID:g951271; PIDN:CAA56488.1; PID:g951272
C:Genetics:
A:Gene: MLN137
C:Superfamily: cytoskeletal keratin

Query Match 0.9%; Score 7; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 RTKEIN 133
DB 69 RTKEIN 75

RESULT 95

D86722
hypothetical protein accA [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
C:Species: *Lactococcus lactis* subsp. *lactis*
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002
C:Accession: D86722
R:Boiotin, A.; Winkler, P.; Mauger, S.; Jallou, O.; Malame, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: D86722
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <STO>
A:Cross-references: GB:AE005176; PID:g12723699; PIDN:AAK04878.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: accA
C:Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain

Query Match 0.9%; Score 7; DB 2; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 DALISEE 82
DB 222 DALISEE 228

RESULT 96
G70980
transcription initiation factor sigma F - Mycobacterium tuberculosis (strain H37RV)
N:Alternate names: SigF protein; sporulation sigma factor homolog; stress-response sigma
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: G70980; J06131
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltywell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
; Rajandream, M.A.; Rogers, J.; Ruter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
R:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70980
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-261 <COL>
A:Cross-references: GB:292771; GB:AL123456; NID:93242259; PIDN:CAB07069.1; PID:G1877341
A:Experimental source: strain H37RV
R:Demajo, J.; Zhang, Y.; Ko, C.; Young, D.B.; Bishai, W.R.
Proc. Natl. Acad. Sci. U.S.A. 93, 2790-2794, 1996
A:Title: A stationary-phase stress-response sigma factor from Mycobacterium tuberculosis
A:Reference number: J06131; MUID:96181544; PMID:8610119
A:Accession: J06131
A:Molecule type: DNA
A:Residues: 1-247, 'V', 249-261 <DEM>
A:Cross-references: GB:U41061; NID:91276888; PIDN:AA04103.1; PID:G1276889
C:Comment: This factor is a subunit of bacterial RNA polymerase and confer promoter spec
and persist during human infection.
C:Genetics:
A:Gene: sigF
A:Start codon: GTG
C:Superfamily: transcription sigma factor G; transcription initiation factor sigma katF
C:Keywords: DNA binding; sigma factor; transcription initiation
F:45-261/Domain: transcription initiation factor sigma katF homology <KTF>
Query Match 0.9%; Score 7; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 201 SASLEAA 207
Db 143 SASLEAA 149
RESULT 97
D71037
hypothetical protein PH1588 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C:Accession: D71037
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohikku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushiida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: D71037
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-264 <KAW>
A:Cross-references: GB:AP000006; NID:93236133; PIDN:BAA30700.1; PID:G3256017
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1588
C:Superfamily: heat-shock protein htpX
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 325 ERIARI 331

Db 245 ERIARI 251
RESULT 98
T32639
hypothetical protein F42G8.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32639
R:Gatung, S.; Holmes, A.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid F42G8.
A:Reference number: 221203
A:Accession: T32639
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-269 <GAT>
A:Cross-references: EMBL:AF038618; PIDN:AA92070.1; GSPDB:GN00022; CESP:F42G8.11
A:Experimental source: strain Bristol N2; clone F42G8
C:Genetics:
A:Gene: CESP:F42G8.11
A:Map position: 4
A:Introns: 40/1; 67/3; 107/2; 236/3
Query Match 0.9%; Score 7; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 606 EKRIPLV 612
Db 165 EKRIPLV 171
RESULT 99
EIRT2
pancreatic elastase II (EC 3.4.21.71) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Aug-1992 #sequence_revision 18-Aug-1992 #text_change 24-Sep-1999
C:Accession: A00961
R:Macdonald, R.J.; Swift, G.H.; Quinto, C.; Swain, W.; Pictet, R.L.; Nikovits, W.; Rutte
Biochemistry 21, 1453-1463, 1982
A:Title: Primary structure of two distinct rat pancreatic preproelastases determined by
A:Reference number: A00960; MUID:82182967; PMID:6918221
A:Accession: A00961
A:Molecule type: mRNA
A:Residues: 1-271 <MAC>
A:Cross-references: GB:L00124; GB:J00731; NID:9204019; PIDN:AAA98780.1; PID:G204021
C:Superfamily: trypsin; trypsin: homology
C:Keywords: hydrolase; pancreas; serine proteinase; zymogen
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-30/Domain: activation peptide #status predicted <APT>
F:31-271/Product: elastase II #status predicted <MP>
F:31-264/Domain: trypsin homology <TRY>
F:75,123,218/Active site: His, Asp, Ser #status predicted
Query Match 0.9%; Score 7; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 219 SNSRYR 225
Db 78 SNSRYR 84
RESULT 100
S62364
L-2-chloropropionic acid dehalogenase (EC 3.8.1.-) - Rhizobium sp.
N:Alternate names: L-2-haloalkanoate dehalogenase
C:Species: Rhizobium sp.
C>Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S62364
R:Cairns, S.S.; Cornish, A.; Cooper, R.A.

Eur. J. Biochem. 235, 744-749, 1996
A:Title: Cloning, sequencing and expression in Escherichia coli of two Rhizobium sp. gen
A:Reference number: S62363; MUID:96184554; PMID:8654424
A:Accession: S62364
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-279 <CAI>
A:Cross-references: EMBL:X93597; NID:G1103493; PID:CAA63794.1; PID:G1103495
C:Superfamily: Rhizobium L-2-chloropropionic acid dehalogenase
C:Keywords: hydrolase

Query Match 0.9%; Score 7; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 SSLKANA 750
|||
Db 243 SSLKANA 249

Search completed: November 14, 2003, 11:02:04
Job time : 56 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 10:44:30 ; Search time 24 Seconds
(without alignments)
1559.719 Million cell updates/sec

Title: US-09-765-271-56

Perfect score: 796
Sequence: 1 SYELGLYQARTVKNRVS.....KLIALIKGSPSPSVSKKIN 796

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 200 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	1.1	921	1 T2D3 DROME	P47825 drosophila
2	8	1.0	71	1 Y029_NPVAC	P41433 autographa
3	8	1.0	292	1 SC17_NEUCR	O9p645 neurospora
4	8	1.0	448	1 AAC2_DICDI	P14196 dictyostell
5	8	1.0	503	1 IRF7_HUMAN	O92985 homo sapien
6	8	1.0	795	1 LON_MYCPN	B78025 mycoplasma
7	8	1.0	861	1 Y240_ARATH	O22224 arabidopsis
8	8	1.0	1080	1 HDC_DROME	O9n2m8 drosophila
9	8	1.0	1205	1 SMC_MYCTU	O10970 mycobacteri
10	8	1.0	2033	1 EVPL_HUMAN	O92817 homo sapien
11	8	1.0	2035	1 EVPL_MOUSE	O9d952 mus musculu
12	7	0.9	70	1 Y872_PIRAB	O9v0b8 pyrococcus
13	7	0.9	99	1 CH10_MYCBO	P15020 mycobacteri
14	7	0.9	99	1 CH10_MYCBO	P09621 mycobacteri
15	7	0.9	101	1 GLR1_SCHPO	O36032 schizosacch
16	7	0.9	101	1 RS16_UREPA	O9p981 ureaplasma
17	7	0.9	106	1 Y0CC_HAEIN	O57152 haemophilus
18	7	0.9	115	1 RNPA_STRBP	O8cmu4 staphylococ
19	7	0.9	121	1 INSC_ECOLI	P19776 escherichia
20	7	0.9	121	1 INSC_SHIFL	P59444 shigella fl
21	7	0.9	124	1 RNP_ANTAM	P00668 antillocapra
22	7	0.9	143	1 Y082_RICPR	O92655 rickettsia
23	7	0.9	148	1 PTVA_ECOLI	P32155 escherichia
24	7	0.9	154	1 MUTT_STRAM	P32091 streptomyc
25	7	0.9	158	1 GREB_STRAM	O99etn9 staphylococ
26	7	0.9	158	1 Y052_ARCFU	O30184 archaeeoglob
27	7	0.9	166	1 GCSI_ARATH	O91q10 arabidopsis
28	7	0.9	174	1 HUNB_DROMU	O46250 drosophila
29	7	0.9	177	1 APT_CHUTE	O8kfm9 chlorobium
30	7	0.9	178	1 NUSG_NEIMA	O9j1d9 neisseria m
31	7	0.9	179	1 APT_HELPU	O9z1g9 helicobacte
32	7	0.9	185	1 VATE_DEIRA	O9rwh1 deinococcus
33	7	0.9	197	1 CYCL_METEX	P14774 methyllobact

34	7	0.9	201	1 RB1B_HUMAN	O9h0u4 homo sapien
35	7	0.9	201	1 RB1B_RAT	P10536 rattus norv
36	7	0.9	210	1 APS1_SCHPO	O09790 schizosacch
37	7	0.9	211	1 I4P_ARATH	O64628 arabidopsis
38	7	0.9	211	1 YRAE_ECOLI	P45469 escherichia
39	7	0.9	213	1 PCPE_SYNEL	P50038 synechococc
40	7	0.9	213	1 URE1_HELMU	P50044 helicobacte
41	7	0.9	238	1 PSE2_RAT	O63798 rattus norv
42	7	0.9	239	1 PSE2_MOUSE	P97372 mus musculu
43	7	0.9	271	1 EL2_RAT	P00774 rattus norv
44	7	0.9	280	1 FEG_OCEIH	O8ep66 oceanobacti
45	7	0.9	284	1 LICH_VIBCH	O07350 vibrio chol
46	7	0.9	284	1 TPM1_BIOGL	P42636 biophalari
47	7	0.9	284	1 TPM2_BIOGL	P34689 biophalari
48	7	0.9	284	1 TPMW_TRICO	P15846 trichostom
49	7	0.9	293	1 LECT_CICAU	O39528 clatrastis
50	7	0.9	316	1 TAL_BUCAP	O8ka27 buchnera ap
51	7	0.9	323	1 PTPA_RABIT	O28717 oryctolagus
52	7	0.9	327	1 FIP1_YEAST	P45976 saccharomyc
53	7	0.9	327	1 KAPR_DICDI	P05987 dictyostell
54	7	0.9	338	1 G3P2_AGAB1	P32636 agaricus bi
55	7	0.9	338	1 G3P_SCHMA	P20287 schistosoma
56	7	0.9	344	1 DCUP_AGRIS	O8ud16 agrobacteri
57	7	0.9	358	1 PTPA_HUMAN	O15257 homo sapien
58	7	0.9	386	1 PHEA_ECOLI	P07022 escherichia
59	7	0.9	387	1 YHFX_ECOLI	P45550 escherichia
60	7	0.9	394	1 PGK_THETN	O8r965 thermoaer
61	7	0.9	397	1 PGK_CHUTE	O8kae1 chlorobium
62	7	0.9	405	1 IF5_YEAST	P38431 saccharomyc
63	7	0.9	415	1 RPA3_YEAST	O1080 saccharomyc
64	7	0.9	416	1 HEM1_AERPE	O9y9j2 aeropyrum p
65	7	0.9	424	1 Y12A_ECOLI	P51026 escherichia
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68	7	0.9	446	1 TBG_SCHUP	O9y882 schizosacch
69	7	0.9	446	1 TBG_SCHPO	P25295 schizosacch
70	7	0.9	450	1 V50K_BYDVP	P09516 barley yell
71	7	0.9	451	1 TBG1_HUMAN	P23358 homo sapien
72	7	0.9	451	1 TBG1_MOUSE	O92310 mus musculu
73	7	0.9	451	1 TBG2_HUMAN	O9mth3 homo sapien
74	7	0.9	451	1 TBG2_MOUSE	O8vck3 mus musculu
75	7	0.9	451	1 TBG2_XENLA	P23330 xenopus lae
76	7	0.9	455	1 YXX5_CAEEL	O18179 caenorhabdi
77	7	0.9	460	1 SELA_PASWJ	O9c666 pasteurella
78	7	0.9	461	1 TBG1_EUPOC	P34786 euploies oc
79	7	0.9	461	1 TBG2_EUPOC	P90548 euploies oc
80	7	0.9	461	1 TBG2_NEUCR	P53377 neurospora
81	7	0.9	461	1 TRIB_HUMAN	P20403 euploies cr
82	7	0.9	462	1 TBG1_EUPCR	P54403 euploies cr
83	7	0.9	467	1 V51K_BMYVF	O99514 beet wester
84	7	0.9	471	1 V51K_BMYVG	P09515 beet wester
85	7	0.9	476	1 YHGF_NEIGO	O51062 neisseria g
86	7	0.9	479	1 YHGF_HSV2G	P03173 herpes simp
87	7	0.9	480	1 VGLC_HSV2J	P06475 herpes simp
88	7	0.9	480	1 VGLC_HSV2H	O89730 herpes simp
89	7	0.9	488	1 SUOX_HUMAN	P51687 homo sapien
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91	7	0.9	502	1 K2M3_SHEEP	P25691 ovis aries
92	7	0.9	508	1 V56K_PIRV1	P17525 potato leaf
93	7	0.9	508	1 V56K_PIRVW	P11426 potato leaf
94	7	0.9	509	1 GUAA_CLOPE	O8x146 clostridium
95	7	0.9	510	1 GUAA_CLOAB	O97748 clostridium
96	7	0.9	511	1 LYN_HUMAN	P07448 homo sapien
97	7	0.9	520	1 C84A_ARATH	O42600 arabidopsis
98	7	0.9	524	1 CP11_CANFA	P56590 canis fami1
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102	7	0.9	543	1 ZN08_HUMAN	P17098 homo sapien
103	7	0.9	570	1 PTI_BACSU	P08838 bacillus su
104	7	0.9	570	1 SYE_PYRAE	O8z833 pyrobaculum
105	7	0.9	580	1 GGT_ECOLI	P18956 escherichia
106	7	0.9	588	1 TAN_ASOPR	P78581 aspergillus

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P40439 saccharomyc
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Q92j36 rickettsia
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Q75925 homo sapien
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Q971c2 clostridium
P72a87 synchocyst
Q92a16 anabaena sp
Q05152 anabaena va
Q16281 homo sapien
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P53907 saccharomyc
Q9unp7 homo sapien
Q62538 drosophila
P57072 neisseria m
Q51152 neisseria m
P05084 drosophila
Q62541 drosophila
P40566 saccharomyc
Q62537 drosophila
P46837 escherichia
P08161 autographa
P13161 drosophila
P47250 mycoplasma
P80108 homo sapien
Q14460 schizosach
Q55733 schizosach
P11267 simian immu
P05884 simian immu
P05885 simian immu
Q92126 rickettsia
P41080 rickettsia
P57740 homo sapien
P52590 rattus norv
P49793 rattus norv
Q13753 homo sapien
Q9c8t5 mycobacteri
Q989g3 arabidopsis
P09547 saccharomyc
Q09847 schizosach
P77941 rickettsia
Q12680 saccharomyc
P10180 drosophila
Q93008 h probabile
P70398 m probabile
Q07017 streptomyc
P12255 bordetella
Q24742 drosophila
Q56715 vibrio proc
Q8kpp2 synchococc
Q8rth9 tubobacteri
P06392 marchantia
Q9yfer9 aeropyrum p
P21085 vaccinia vi
P19325 lymphocytic
Q44141 anabaena sp
Q9zced4 rickettsia
Q9zced4 conus pulic
Q97197 clostridium
Q24399 drosophila
Q24656 drosophila
Q24695 drosophila
Q24766 drosophila
P56509 mechanother
Q02232 halobacteri

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180 6 0.8 85 1 HKL6_MAIZE
181 6 0.8 85 1 HKL7_MAIZE
182 6 0.8 85 1 MLC1_DROSO
183 6 0.8 89 1 EAT1_ENTFA
184 6 0.8 89 1 EAT2_ENTFA
185 6 0.8 89 1 EATX_STREY
186 6 0.8 89 1 RS16_LACIA
187 6 0.8 90 1 YWJC_BACSU
188 6 0.8 93 1 CENA_BOVIN
189 6 0.8 93 1 L10K_RAT
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191 6 0.8 94 1 DEF2_RAT
192 6 0.8 95 1 DAF1_TRYCR
193 6 0.8 95 1 GRX_RICPR
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197 6 0.8 100 1 TH10_MYCGA
198 6 0.8 101 1 NULC_MAIZE
199 6 0.8 101 1 NULC_NEPOL
200 6 0.8 101 1 NULC_ORYSA

ALIGNMENTS
P56664 zea mays (m
P56665 zea mays (m
O44107 drosophila
O98101 enterococcu
O98119 enterococcu
O57231 streptococ
O95fb2 lactococcus
P45863 bacillus su
Q94449 bos taurus
O05310 rattus norv
Q62716 rattus norv
Q63731 rattus norv
Q26327 trypanosoma
Q92dwl rickettsia
Q9uzp1 pyrococcus
O74001 pyrococcus
P31606 escherichia
Q916p9 mycoplasma
P11646 zea mays (m
Q91kv2 nephrolelmi
P12128 oryza sativ

RESULT 1
T2D3_DROME
ID T2D3_DROME STANDARD; PRT; 921 AA.
AC P47825; P49845; Q879E0; Q9UVU7;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transcription initiation factor TFIID 110 Kda subunit (P110)
DE (TAF11-110) (110 Kda TSP-associated factor).
GN TAF4 OR TAF110 OR CG5444.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG), AND SEQUENCE OF 519-540; 597-616
RP AND 857-874.
RC TISSUE=Embryo;
RA Hoey T., Weinzierl R.O.J., Gill G., Chen J.-L., Dynlacht B.D.,
RA Tjian R.;
RT "Molecular cloning and functional analysis of Drosophila TAF110
RT reveal properties expected of coactivators.";
RL Cell 72:247-260(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG), AND SEQUENCE OF 398-406; 520-540
RP AND 860-877.
RC TISSUE=Embryo;
RA MEDLINE=9331591; PubMed=8327460;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.C., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abiri J.F., Agbayani A., An H.-J., Andrews-Piankovich C., Baldwin D.,
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

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RA Borkova D., Betchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Cener A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.D., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mikhina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wattaman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195 (2000).
RN [4]
RN SEQUENCE FROM N.A. (ISOFORM SHORT).
RP STRAIN=Berkley; TISSUE=embryo;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Campe M.,
RA George R.A., Guatin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celinker S.E.;
RT "A *Drosophila* full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.6 (2002).
CC -!- FUNCTION: TEIID IS A MULTIMERIC PROTEIN COMPLEX THAT PLAYS A
CC CENTRAL ROLE IN MEDIATING PROMOTER RESPONSES TO VARIOUS ACTIVATORS
CC AND REPRESSORS. MAY FUNCTION AS A COACTIVATOR BY SERVING AS A SITE
CC OF PROTEIN-PROTEIN CONTACT BETWEEN ACTIVATORS LIKE SPI (OR BTB)
CC AND TEIID COMPLEX.
CC -!- SUBUNIT: TEIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A
CC NUMBER OF TBP-ASSOCIATED FACTORS (TAFs).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P47825-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P47825-2; Sequence=VSP_004441;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: BELONGS TO THE TAF2C FAMILY.
CC
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CC
CC -----
CC EMBL, L06661; -, NOT ANNOTATED_CDS.
CC EMBL, S63550; AAB27433.1; -
CC EMBL, AE003528; AAF49536.1; -
CC EMBL, AY069807; AAL39952.1; -
CC PIR, A48184; A48184;
CC TRANSFAC, T02121, -
CC FLYBASE, FBgn010280; Taf4.
CC GO, GO:0005669; C:transcription factor TEIID complex; IPI.
CC GO, GO:0016251; I:general RNA polymerase II transcription fac. .; IPI.
CC GO, GO:0006355; P:regulation of transcription, DNA-dependent; IPI.

DR GO, GO:0006367; P:transcription initiation from Pol II promoter; IPI.
DR InterPro, IPR003894; TAF hom.
DR SMART, SM00549; TAFH; 1.
KW Transcription regulation; Nuclear protein; Alternative splicing.
FT DOMAIN 66 82 POLY-GLN.
FT DOMAIN 108 111 POLY-GLN.
FT DOMAIN 259 265 POLY-GLN.
FT VARSPLIC 138 207 Missing (in isoform Short).
FT FTID=VSP_004441.
FT V->M (IN REF. 4).
SQ CONFLICT 114 114
SQ SEQUENCE 921 AA; 99338 MW; 27B6852859872767 CRC64;
Query Match 1.1%; Score 9; DB 1; Length 921;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 249 TINTSNNSNT 257
DB 178 TINTSNNSNT 186
RESULT 2
Y029 NPVAC STANDARD; PRT; 71 AA.
AC P41433;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 8.6 kDa protein in IAP1-SOD intergenic region.
OS Autographa californica nuclear polyhedrosis virus (ACNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxId=46015;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=C6;
RX MEDLINE=94303173; PubMed=8030224;
RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
RT "The complete DNA sequence of Autographa californica nuclear
RT polyhedrosis virus.";
RL Virology 202:586-605 (1994).
CC -!- SIMILARITY: TO CORRESPONDING ORF IN OPNPV.
CC
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CC
CC -----
CC EMBL, L22858; AAA66659.1; -
CC DR PIR, E72853; E72853.
CC KW Hypothetical protein.
SQ SEQUENCE 71 AA; 8569 MW; ADF85AC68E16DD3 CRC64;
Query Match 1.0%; Score 8; DB 1; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 130 EIRNRQKQ 137
DB 20 EIRNRQKQ 27
RESULT 3
SC17 NEUCR STANDARD; PRT; 292 AA.
AC Q9P6A5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable vesicular-fusion protein sc17 homolog.

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GN B1D1.150.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A / FGSC 987;
RX PubMed=12655011;
RA Mannhaupt G., Monttrone C., Haase D., Mewes H.-W., Aign V.,
RA Honeitel J.D., Partmann B., Nyakatura G., Kempken F., Walter J.,
RA Schulte U.;
RT "What's in the genome of a filamentous fungus? Analysis of the
RT Neurospora genome sequence."
RL Nucleic Acids Res. 31:1944-1954 (2003).
CC -1- FUNCTION: REQUIRED FOR VESICULAR TRANSPORT BETWEEN THE ENDOPLASMIC
CC RETICULUM AND THE GOLGI APPARATUS (By similarity).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC PERIPHERAL MEMBRANE PROTEIN (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE SNAP FAMILY.
CC -----
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CC -----
CC EMBL; AL355927; CAB91264.1; -.
CC PIR; T49361; T49361.
CC InterPro; IPR000744; NSF_attach.
CC Pfam; PF02071; NSF_2.
CC PRINTS; PR00448; NSFATTCCHMNT.
CC TRANSPORT: Protein transport; Endoplasmic reticulum; Golgi stack.
CC SEQUENCE 292 AA; 32805 MW; C9BD75D8128E19E7 CRC64;

Query Match 1.0%; Score 8; DB 1; Length 292;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 NDGAVALA 157
Db 150 NDGAVALA 157

RESULT 4
AAC2_DICD1 STANDARD; PRT; 448 AA.
ID AAC2_DICD1
AC P14196;
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE AAC-rich mRNA clone AAC11 protein (Fragment).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90066348; PubMed=2511421;
RA Shaw D.R., Richter H., Giorda R., Ohmachi T., Ennis H.L.;
RT "Nucleotide sequences of Dictyostelium discoideum developmentally
RT regulated cDNAs rich in (AAC) imply proteins that contain clusters of
RT asparagine, glutamine, or threonine."
RL Mol. Genet. 218:453-459 (1989).
CC -1- DEVELOPMENTAL STAGE: THE CONCENTRATION OF AAC-RICH MNAS IS LOW
CC IN DOMANT SPORES AND GROWING CELLS, BUT INCREASES DURING
CC SPORE-GERMINATION AND MULTICELLULAR DEVELOPMENT.
CC -1- MISCELLANEOUS: SEVERAL PROTEINS DERIVE FROM AAC-RICH MRNA, WHICH,
CC DUE TO A FRAMESHIFT ALSO HAVE ACA AND CAA CODONS AND THUS ARE
CC ASN-, THR- OR GIN-RICH.
CC -1- SIMILARITY: Contains 4 A.T hook DNA-binding repeats.
CC -----

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CC -----
CC EMBL; X16522; CAA34529.1; -.
CC PIR; S05355; S05355.
CC DictyDB; DD05006; AT_hook.
CC InterPro; IPR000637; Highmobility_1Y.
CC InerPro; IPR000116; Highmobility_1Y.
CC Pfam; PF02178; AT_hook_4.
CC PRINTS; PR00929; ATHOOK.
CC PRODOM; PD005593; Highmobility_1Y; 1.
CC SMART; SM00384; AT_hook_4.
CC DNA-binding; Repeat.
CC FT NON TER 1
CC FT DOMAIN 5 25 GLN-RICH.
CC FT DOMAIN 115 144 ASN-RICH.
CC FT DOMAIN 268 384 ASN-RICH.
CC SEQUENCE 448 AA; 48636 MW; D8FD80D910D99817 CRC64;

Query Match 1.0%; Score 8; DB 1; Length 448;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 NTSNNSNT 257
Db 378 NTSNNSNT 385

RESULT 5
IRF7_HUMAN STANDARD; PRT; 503 AA.
ID IRF7_HUMAN
AC Q92985; O00331; O00332; O00333; O75924;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interferon regulatory factor 7 (IRF-7).
GN IRF7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Spleen;
RA Grossman A., Nicholl J., Antonio L., Luethy R., Suggs S.,
RA Sutherland G.R., Mak T.W.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
RX MEDLINE=97459673; PubMed=9315633;
RA Zhang L., Pagano J.S.;
RT "IRF-7, a new interferon regulatory factor associated with Epstein-
RT Barr virus latency."
RL Mol. Cell. Biol. 17:5748-5757 (1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM D).
RX MEDLINE=99003279; PubMed=9786932;
RA Au W.-C., Moore P.A., Lafleur D.W., Tombal B., Pitla P.M.;
RT "Characterization of the interferon regulatory factor-7 and its
RT potential role in the transcription activation of interferon A
RT genes."
RL J. Biol. Chem. 273:29210-29217 (1998).
CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INTERFERON-
CC STIMULATED RESPONSE ELEMENT (ISRE) IN IFN PROMOTERS AND IN THE Q
CC PROMOTER (QP) OF EBV NUCLEAR ANTIGEN-1 (EBNA1).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;

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CC      Name=A;
CC      IsoId=Q92985-1; Sequence=Displayed;
CC      Name=B; Synonyms=Beta;
CC      IsoId=Q92985-2; Sequence=VSP_002760;
CC      Name=C; Synonyms=Gamma;
CC      IsoId=Q92985-3; Sequence=VSP_002758, VSP_002759;
CC      Name=D; Synonyms=H;
CC      IsoId=Q92985-4; Sequence=VSP_002757;
CC      -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN SPLEEN, THYMUS, AND
CC      PERIPHERAL BLOOD LEUKOCYTES.
CC      -!- SIMILARITY: Belongs to the IRP family.
CC      -----
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CC      -----
DR      EMBL; U73036; AAB17190.1; -;
DR      EMBL; U53830; AAB80686.1; -;
DR      EMBL; U53831; AAB80688.1; -;
DR      EMBL; U53832; AAB80690.1; -;
DR      EMBL; AF076494; AAC70999.1; -;
DR      HSSP; P23906; 2IRF.
DR      TRANSFAC; T04674; -;
DR      Genew; HGNC:6122; IRF7.
DR      MIM; 605047; -;
DR      GO; GO:0005737; Cytoplasm; TAS.
DR      GO; GO:0005634; C:nucleus; TAS.
DR      GO; GO:0003704; F:specific RNA polymerase II transcription fa.; TAS.
DR      GO; GO:0000122; F:negative regulation of transcription from P.; TAS.
DR      GO; GO:0009615; P:response to viruses; TAS.
DR      InterPro; IPR001346; IRF.
DR      Pfam; PF00605; IRF.1.
DR      PRINTS; PR00267; INTERNEGCT.
DR      PRODOM; PD002355; IRF.1.
DR      SMART; SMO0348; IRF.1.
DR      PROSITE; PS00601; IRF.1.
KW      Transcription regulation; DNA-binding; Nuclear protein; Activator;
KW      Alternative splicing.
FT      DNA BIND 13 122
FT      VASPLIC 1 6
FT      TRYPROPIAN PENTAD REPEAT
FT      MALAF -> MEVPERPAGPSPPGTR (in isoform
FT      D).
FT      VASPLIC 152 164
FT      GGPPEPFLAHTHA -> AQSILGSGCTGQ (in
FT      isoform C).
FT      VASPLIC 165 503
FT      /FTId=VSP_002758.
FT      VASPLIC 228 256
FT      Missing (in isoform C).
FT      Missing (in isoform B).
FT      /FTId=VSP_002760.
FT      CONFLICT 179 179
FT      E -> K (in REF. 2).
FT      CONFLICT 412 412
FT      Q -> R (in REF. 3).
SQ      SEQUENCE 503 AA; 54278 MW; AAGAJ3E0E272727C CRC64;
Query Match 1.0%; Score 8; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 357 PSPGPQPA 364
|||
|||
Db 244 PSPGPQPA 251

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DE  ATP-dependent protease La (EC 3.4.21.53).
CN  LON OR MEM332 OR MP504.
OS  Mycoplasma pneumoniae.
OC  Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX  NCBI_TaxID=2104;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 29342 / M129;
RX  MEDLINE=97105885; PubMed=8948633;
RA  Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RT  Herrmann R.;
RL  "Complete sequence analysis of the genome of the bacterium Mycoplasma
   pneumoniae."
RL  Nucleic Acids Res. 24:4420-4449(1996).
CC  -1- FUNCTION: DEGRADES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS
CC  IN PRESENCE OF ATP. DEGRADES THE REGULATORY PROTEINS RCSA AND
CC  SULA. HYDROLYZES TWO ATPs FOR EACH PEPTIDE BOND CLEAVED IN THE
CC  PROTEIN SUBSTRATE (BY SIMILARITY).
CC  -1- CATALYTIC ACTIVITY: Hydrolysis of large proteins such as globin,
CC  casein and denaturated serum albumin, in presence of ATP.
CC  -1- SUBUNIT: Homotetramer (By similarity).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16.
CC  -----
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CC  -----
DR  EMBL; AE000050; AAB96152.1; -.
DR  PIR; S73830; S73830.
DR  MEROPS; S16.004; -.
DR  InterPro; IPR003593; AAA_ATPase.
DR  InterPro; IPR003959; AAA_ATPase_centre.
DR  InterPro; IPR003111; LON.
DR  InterPro; IPR001984; Lon_endopep.
DR  InterPro; IPR004815; Lon_fam.
DR  Pfam; PF00004; AAA; 1.
DR  Pfam; PF02190; LON; 1.
DR  Pfam; PF05362; Lon_C; 1.
DR  PRINTS; PR00830; ENDOLAPTASE.
DR  SMART; SM00382; AAA; 1.
DR  SMART; SM00464; LON; 1.
DR  TIGRFAMs; TIGR00763; lon; 1.
DR  PROSITE; PS01046; LON_SER; 1.
KW  Hydrolyase; Serine protease; ATP-binding; Complete proteome.
FT  DOMAIN 304 308
FT  NP_BIND 379 386
FT  ACT_SITE 702 702
FT  FT  BY SIMILARITY.
SQ  SEQUENCE 795 AA; 90203 MW; 7E7855082060C991 CRC64;
   Query Match 1.0%; Score 8; DB 1; Length 795;
   Best Local Similarity 100.0%; Pred. No. 15;
   Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 466 ALDKLRLR 473
Db 127 ALDKLRLR 134

RESULT 7
Y240 ARATH STANDARD; PRT; 861 AA.
AC 022224; O94CF2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein At2g41620.
DE AT2G41620 OR T32G6.14.
OS Arabidopsis thaliana (Mouse-ear cress).

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CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC Eucosida II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.C., Renning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Newman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.,
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:761-768 (1999).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/GEC).";
 RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
 RN
 RP IDENTIFICATION ON 2D-GELS.
 RC STRAIN=cv. Columbia;
 RA Sarazin B., Tonella L., Marques K., Paesano S., Chane-Favre L.,
 RA Heller M., Sanchez J.-C., Hochstrasser D.F., Thiellement H.;
 RL Unpublished observations (SEP-2000).
 CC
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 CC
 CC -----
 CC EMBL: AC002510; AAB84345.2; -;
 DR EMBL: AY034907; AAC59414.1; -;
 DR Pflam: PF04097; NIK: 1.
 SQ SEQUENCE 861 AA; 96615 MW; 9F53F0BF0D3D673 CRC64;
 Query Match 1.0%; Score 8; DB 1; Length 861;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 41 REGINAEO 48
 Db 69 REGINAEO 76
 RESULT 8
 HDC DROME STANDARD; PRT; 1080 AA.
 ID HDC DROME
 AC Q5NZM8; Q24480; Q9VAB4;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Headcase protein [Contains: Headcase short protein].
 GN HDC OR CG15532.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Empidoidea; Drosophilidae; Drosophila.
 CX NCBI_TaxID=7227;
 RN
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC TISSUE=Embryo;
 RX MEDLINE=96171720; PubMed=8575315;

RA Weaver T.A., White R.A.;
 RT "Headcase, an imaginal specific gene required for adult morphogenesis
 RT in Drosophila melanogaster.";
 RL Development 121:4149-4160 (1995).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Goeayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brindon R.C., Rogers Y.-H.C., Blazey R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mklos G.L.G.,
 RA Abril J.F., Agbayan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.T., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sidem-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 RN
 RP PARTIAL SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC TISSUE=Embryo;
 RX MEDLINE=98198453; PubMed=9531534;
 RA Steneberg P., Englund C., Kirohman J., Weaver T.A., Samkovlis C.;
 RT "Translational readthrough in the hdc mRNA generates a novel branching
 RT inhibitor in the drosophila trachea.";
 RL Genes Dev. 12:956-967 (1998).
 CC
 CC -!- FUNCTION: REQUIRED FOR IMAGINAL CELL DIFFERENTIATION. MAY BE
 CC INVOLVED IN HORMONAL RESPONSIVENESS DURING METAMORPHOSIS. INVOLVED
 CC IN AN INHIBITORY SIGNALING MECHANISM TO DETERMINE THE NUMBER OF
 CC CELLS THAT WILL FORM UNICELLULAR SPROUTS IN THE TRACHEA. REGULATED
 CC BY TRANSCRIPTION FACTOR E5G. THE LONGER HDC PROTEIN IS COMPLETELY
 CC FUNCTIONAL AND THE SHORTER PROTEIN CARRIES SOME FUNCTION.
 CC
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN A SUBSET OF TRACHEAL FUSION CELLS FROM
 CC STAGE 14 TO THE END OF EMBRYOGENESIS IN METAMERES 2-9, LATERAL
 CC TRUNK AND VENTRAL ANASTOMOSES.
 CC
 CC -!- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR UAA OCCURS BETWEEN
 CC CODONS FOR ALA-650 AND HIS-652. READTHROUGH IS NOT ALWAYS
 CC SUPPRESSED AS THE SHORTER PROTEIN IS MORE ABUNDANT.
 CC
 CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_Taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=keratinocytes;
 RX MEDLINE=96326676; PubMed=8707850;
 RA Ruhrberg C., Hajibagheri M.A.N., Simon M., Dooley T.P., Watt F.M.,
 RT "Envoplakin, a novel precursor of the cornified envelope that has
 RT homology to desmoplakin."
 RL J. Cell Biol. 134:715-729(1996).
 (2)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=99339988; PubMed=10409435;
 RA Risk J.M., Ruhrberg C., Hennies H.-C., Mills H.S., Di Colandrea T.,
 RA Evans K.E., Ellis A., Watt F.M., Bishop D.T., Spurr N.K.,
 RA Stevens H.P., Leigh I.M., Reis A., Kelsell D.P., Furd J.K.,
 RT "Envoplakin, a possible candidate gene for focal NEPK/esophageal
 RT cancer (TOC): the integration of genetic and physical maps of the TOC
 RT region on 17q25."
 RL Genomics 59:234-242(1999).
 CC -1- FUNCTION: COMPONENT OF THE CORNIFIED ENVELOPE OF KERATINOCYTES.
 CC MAY LINK THE CORNIFIED ENVELOPE TO DESMOSOMES AND INTERMEDIATE
 CC FILAMENTS.
 CC -1- SUBUNIT: MAY FORM A HOMODIMER OR A HETERODIMER WITH PPL.
 CC -1- SUBCELLULAR LOCATION: COLOCALIZED WITH DSP AT DESMOSOMES AND ALONG
 CC INTERMEDIATE FILAMENTS.
 CC -1- TISSUE SPECIFICITY: EXCLUSIVELY EXPRESSED IN STRATIFIED SQUAMOUS
 CC EPITHELIA.
 CC -1- INDUCTION: DURING DIFFERENTIATION OF EPIDERMAL KERATINOCYTES.
 CC -1- SIMILARITY: Contains 7 plectrin repeats.
 CC -1- SIMILARITY: Contains 1 spectrin repeat.
 CC -1- SIMILARITY: Belongs to the plakin or cytolinker family.
 CC -----
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 CC -----
 DR EMBL: U53786; AAC64662.1; -
 DR EMBL: U72849; AAD00186.1; -
 DR EMBL: U72843; AAD00186.1; JOINED.
 DR EMBL: U72845; AAD00186.1; JOINED.
 DR EMBL: U72846; AAD00186.1; JOINED.
 DR EMBL: U72847; AAD00186.1; JOINED.
 DR EMBL: U72848; AAD00186.1; JOINED.
 DR Genew: HGNC:3503; EVPL.
 DR MIM: 601590; -
 DR GO: GO:0009506; C:plasmodesma; TAS.
 DR GO: GO:0005198; F:structural molecule activity; TAS.
 DR GO: GO:0008544; P:epidermal differentiation; TAS.
 DR InterPro: IPR001101; Plectrin_repeat.
 DR Pfam: PF00681; Plectrin_3.
 DR SMART: SMO0250; Plectr_8.
 DR Keratinization; Repeat; Coiled coil; Cytoskeleton; Structural protein.
 FT DOMAIN 1 841 GLOBIULAR 1.
 FT DOMAIN 2 1673 CENTRAL FIBROUS ROD DOMAIN.
 FT DOMAIN 3 1674 GLOBIULAR 2.
 FT DOMAIN 4 1675 4 X 4 AA TANDEM REPEATS OF K-G-S-P.
 FT REPEAT 229 330 SPECTRIN.
 FT REPEAT 845 1135 COILED COIL (POTENTIAL).
 FT REPEAT 1185 1226 PLECTRIN 1.
 FT REPEAT 1678 1713 PLECTRIN 2.
 FT REPEAT 1818 1855 PLECTRIN 3.
 FT REPEAT 1856 1893 PLECTRIN 4.
 FT REPEAT 1894 1931 PLECTRIN 5.
 FT REPEAT 1932 1969 PLECTRIN 6.
 FT REPEAT 1970 2007 PLECTRIN 7.
 FT SEQUENCE 2033 AA; 231616 MW; B8DC6E2B52221938 CRC64;

Query Match 1.0%; Score 8; DB 1; Length 2033;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 731 LKAEVLL 738
 DB 87 LKAEVLL 94
 RESULT 11
 EVPL_MOUSE STANDARD; PRT; 2035 AA.
 ID EVPL_MOUSE
 AC Q9D952;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Envoplakin (p210) (210 kDa cornified envelope precursor).
 GN EVPL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_Taxid=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=20347896; PubMed=10747979;
 RA Maatta A., Ruhrberg C., Watt F.M.,
 RT "Structure and regulation of the envoplakin gene."
 RL J. Biol. Chem. 275:19857-19865(2000).
 (2)
 RP SEQUENCE OF 1860-2035 FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=pancreas;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arkawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,
 RA Kunitani L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli V., Mombearts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: COMPONENT OF THE CORNIFIED ENVELOPE OF KERATINOCYTES.
 CC MAY LINK THE CORNIFIED ENVELOPE TO DESMOSOMES AND INTERMEDIATE
 CC FILAMENTS.
 CC -1- SUBUNIT: MAY FORM A HOMODIMER OR A HETERODIMER WITH PPL.
 CC -1- SUBCELLULAR LOCATION: COLOCALIZED WITH DSP AT DESMOSOMES AND ALONG
 CC INTERMEDIATE FILAMENTS (BY SIMILARITY).
 CC -1- SIMILARITY: Contains 7 plectrin repeats.
 CC -1- SIMILARITY: Contains 1 spectrin repeat.
 CC -1- SIMILARITY: Belongs to the plakin or cytolinker family.
 CC -----
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 CC -----
 DR EMBL: AJ309317; CAC38864.2; -

DB 54 GEXRPL 60

RESULT 14

ID CH10 MYCTU STANDARD; PRT; 99 AA.

AC P09621;

DT 01-MAR-1989 (Rel. 10, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE 10 kDa chaperonin (Protein Cpn10) (groES protein) (BCG-A heat shock protein) (10 kDa antigen).

GN GROES OR GROES OR MOBP OR CPN10 OR RV3418C OR MT3527 OR MYCTY8.11.

OS Mycobacterium tuberculosis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OC NCBI_TaxID=1773;

OK [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H37RV;

RX MEDLINE=89016584; PubMed=2902558;

RA Baird P.N., Hall L.M., Coates A.R.M.;

RT "A major antigen from Mycobacterium tuberculosis which is homologous to the heat shock proteins groES from E. coli and the hspA gene product of *Coxiella burnetii*."

RL Nucleic Acids Res. 16:9047-9047 (1988).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=H37RV;

RX MEDLINE=90095443; PubMed=2480990;

RA Baird P.N., Hall L.M.C., Coates A.R.M.;

RT "Cloning and sequence analysis of the 10 kDa antigen gene of Mycobacterium tuberculosis."

RL J. Gen. Microbiol. 135:931-939 (1989).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Erdmann;

RX MEDLINE=89160258; PubMed=2564178;

RA Shinnick T.M., Plikaytis B.P., Hyche A.D., van Landingham R.M., Walker L.L.;

RT "The Mycobacterium tuberculosis BCG-a protein has homology with the *Escherichia coli* GroES protein."

RL Nucleic Acids Res. 17:1254-1254 (1989).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=Erdmann;

RX MEDLINE=93219332; PubMed=7681982;

RA Kong T.H., Coates A.R.M., Butcher P.D., Hickman C.J., Shinnick T.M.;

RT "Mycobacterium tuberculosis expresses two chaperonin-60 homologs."

RL Proc. Natl. Acad. Sci. U.S.A. 90:2608-2612 (1993).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=H37RV;

RX MEDLINE=98295987; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekela F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."

RL Nature 393:537-544 (1998).

RN [6]

RP SEQUENCE FROM N.A.

RC STRAIN=CDC 1551 / Oshkosh;

RX STRAIN=CDC 1551 / Oshkosh;

RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;

RT "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RN [7]

RP SEQUENCE OF 1-15.

RX MEDLINE=92176646; PubMed=1371791;

RA Barnes P.F., Mehra V., Riviere B., Fong S.J., Brennan P.J.;

RA Voegtline M.S., Minden P., Houghten R.A., Bloom B.R., Modlin R.L.;

RT "Immunoreactivity of a 10-kDa antigen of Mycobacterium tuberculosis."

RL J. Immunol. 148:1835-1840 (1992).

CC -1- FUNCTION: Binds to Cpn60 in the presence of Mg-ATP and suppresses the ATPase activity of the latter.

CC -1- SUBUNIT: Heptamer of 7 subunits arranged in a ring (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.

CC -----

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CC -----

DR EMBL; X60350; CAA42908.1; -;

DR EMBL; M25258; AAA25340.1; -;

DR EMBL; X13739; CAA32003.1; -;

DR EMBL; Z77165; CAB01005.1; -;

DR EMBL; AE007158; AAK47865.1; -;

DR PIR; S01381; BMYBBA.

DR PDB; 1HX5; 08-AUG-01.

DR PDB; 1JH2; 05-SEP-01.

DR TIGR; MJ3527; -;

DR Tuberculaet; RV3418c; -;

DR HAMAP; MF_00580; -; 1.

DR InterPro; IPR001476; Chaperin_Cpn10.

DR Pfam; PF00166; Cpn10; 1.

DR PRINTS; PR00297; CHAPERONIN10.

DR PRODOM; PD000566; Chaperin_Cpn10; 1.

DR PROSITE; PS00681; CHAPERONINS_CPN10; 1.

DR KEGG; Chaperone; Antigen; Heat shock; Complete proteome; 3D-structure.

FT INIT MET 0

FT INT MET 0

FT SEQUENCE 99 AA; 10673 MW; 1DD128B75CF19AF7 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 99;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 605 GEXRPL 611

DB 54 GEXRPL 60

RESULT 15

GLR1 SCHPO STANDARD; PRT; 101 AA.

ID O36032; Q9US58;

AC O36032; Q9US58;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Glutaredoxin 1.

GN GRX1 OR SPACAF10.20.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RA Kawamukai M.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RA SEQUENCE FROM N.A.
RA Kim H.-G., Cho Y.-W., Park E.-H., Lim C.-U.;
RT "Characterization of cDNA encoding thioltransferase (glutaredoxin)
RT from Schizosaccharomyces pombe.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RN Cho Y.-W., Kim H.-G., Lim C.-U.;
RT "Isolation and expression of the genomic DNA encoding thioltransferase
RT (glutaredoxin) from Schizosaccharomyces pombe.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RN STRAIN-972;
RX MEDLINE=21849401; PubMed=11859360;
RA Wood V., Gwilliam N., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouris J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jørgensen K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Noel S., Pearson K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pangall K., Murray D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares K., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voiclaert G., Aert R., Robben J., Grymoult B.,
RA Weltjens I., Vanterre E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzner E., Moestl D., Hilbert H.,
RA Borycz K., Langer I., Beck A., Lehnach R., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goifeau A., Cadet E., Dreano S., Gloux S., Lelaure V., Motlier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Fotsberg S.L.,
RA Cerrutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Unseery D., Bartell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: THE DISULFIDE BOND FUNCTIONS AS AN ELECTRON CARRIER IN
CC THE GLUTATHIONE-DEPENDENT SYNTHESIS OF DEOXYRIBONUCLEOTIDES BY THE
CC ENZYME RIBONUCLEOTIDE REDUCTASE. IN ADDITION, IT IS ALSO INVOLVED
CC IN REDUCING SOME DISULFIDES IN A COUPLED SYSTEM WITH GLUTATHIONE
CC REDUCTASE. THIOLESTERASE CATALYZES CELLULAR THIOLESTER-
CC TRANSFER REACTIONS. IT TRANSFERS REDUCING EQUIVALENTS
CC TO CYTOSOLIC PROTEIN AND NONPROTEIN DISULFIDES (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE GLUTAREDOXIN FAMILY.
CC -----
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DR EMBL; Z99880; CAB11722.1; -
DR EMBL; AB015167; BAA28750.1; -
DR EMBL; AF192764; AAF19628.1; -
DR EMBL; AF121275; AAD25391.1; -
DR PIR; T38824; T38824.
DR HSSP; P35754; 1JHB.
DR GenedB; SPombe; SPAC4F10.20; -
DR InterPro; IPR002109; Glutaredoxin.
DR InterPro; IPR006663; Thioresdox_dsm2.
DR Pfam; PF00462; Glutaredoxin; 1.
DR PRINTS; PS00160; GLUTAREDOXIN.
DR PROSITE; P00195; GLUTAREDOXIN; 1.
KW Redox-active center; Electron transport.
FT DISULFID 25 28 REDOX-ACTIVE (BY SIMILARITY).
FT CONFLICT 52 52 N -> D (IN REF. 3).

```

SQ  SEQUENCE 101 AA; 11261 MW; 30557E19BF33E9BB CRC64;
    Query Match 0.9%; Score 7; DB 1; Length 101;
    Best Local Similarity 100.0%; Pred. No. 26;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 461 NSDFQAL 467
    |||||
DB 82 NSDFQAL 88

RESULT 16
RS16_UREPA STANDARD; PRT; 101 AA.
AC Q9PPS1;
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE 30S ribosomal protein S16.
RSP OR RPS16 OR U0568.
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxId=134821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serovar 3;
RX MEDLINE=20500219; PubMed=11048724;
RA Glas J.J., Lefkowitz E.J., Glas J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
RT urealyticum."
RL Nature 407:757-762(2000).
--SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.
-----
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-----
DR EMBL; AE002155; AA930982.1; .
DR HSSP; P80379; IEMW.
DR HAMAP; MF_00385; -; 1.
DR InterPro; IPR000307; Ribosomal S16.
DR Pfam; PF00886; Ribosomal S16; 1.
DR ProDom; PD003791; Ribosomal_S16; 1.
DR TIGRfams; TIGR00002; S16; 1.
DR PROSITE; PS00732; RIBOSOMAL_S16; FALSE_NEG.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 101 AA; 11297 MW; FED91E1AB36CBF45 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 404 PSETVKN 410
    |||||
DB 66 PSETVKN 72

RESULT 17
YQCC_HAEIN STANDARD; PRT; 106 AA.
AC Q57152; Q05061;
DT 15-JUL-1998 (Rel. 36; Created)
DT 15-JUL-1998 (Rel. 36; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Hypothetical protein H11436.
GN H11436.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

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OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Rd / KM20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleisemann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Keilavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utechtback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RD Rd."
RL Science 269:496-512(1995).
CC -1- SIMILARITY: TO THE N-TERMINAL OF E.CAROTOVORA EXOENZYM REULATION
CC REGULON ORFL. THE C-TERMINAL PART IS COLINEAR WITH YOCB.
CC -1- SIMILARITY: STRONG, TO E.COLI YOCB.
CC -----
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CC -----
DR EMBL; U32822; AAC23085.1; -
DR PIR; I64171; I64171.
DR TIGR; H1436; -
DR Pfam; PF04287; DUF446; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 106 AA; 12273 MW; 0955920EBD63228C CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 106;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 207 AAEAFLS 213
DB 28 AAEAFLS 34

RESULT 18
RNPA_STAEP STANDARD; PRT; 115 AA.
AC O8CMN4;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribonuclease P protein component (EC 3.1.26.5) (RNase protein) (RNase
DE P protein) (Protein C5).
GN RNPA OR SE2418.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
RA Chen Z., Wen Y.;
RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: RNase catalyzes the removal of the 5'-leader sequence
CC from pre-tRNA to produce the mature 5' terminus. It can also cleave
CC other RNA substrates such as 4.5S RNA. The protein component plays
CC an auxiliary but essential role in vivo by binding to the 5'-
CC leader sequence and broadening the substrate specificity of the
CC ribozyme (By similarity).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-
CC extra-nucleotide from tRNA precursor.

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CC -1- SUBUNIT: Consists of a catalytic RNA component (M1 or rnpB) and a
CC protein subunit (By similarity).
CC -1- SIMILARITY: BELONGS TO THE RNPA FAMILY.
CC -----
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CC -----
DR EMBL; AE016752; AAC06061.1; -
DR HAMAP; MF 00227; -1.
DR Pfam; PF00625; Ribonuclease_P; 1.
DR Pfam; PF003629; Ribonuclease_P; 1.
DR TIGRFAMs; TIGR00188; rnpA; 1.
DR PROSITE; PS00648; RIBONUCLEASE_P; 1.
KW Hydrolyase; Nuclease; Endonuclease; tRNA processing; RNA-binding;
KW Complete proteome.
SQ SEQUENCE 115 AA; 13484 MW; 106B2592C8400F18 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 115;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 460 RNSDFQA 466
DB 9 RNSDFQA 15

RESULT 19
INSC_ECOLI STANDARD; PRT; 121 AA.
AC P19776; O07989; O08018; O08019; P76357; P77346;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transposase insc for insertion element IS2a/D/F/H/I/K.
GN (INSC1 OR B0160) AND (INSC2 OR B1403) AND (INSC3 OR B1997) AND
GN (INSC4 OR B2861) AND (INSC5 OR B3044) AND (INSC6 OR B4272).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RX MEDLINE=88137965; PubMed=2830172;
RA Ronecker H.J., Rak B.;
RT "Genetic organization of insertion element IS2 based on a revised
RT nucleotide sequence."
RL Gene 59:291-296(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=9534362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes."
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RL "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [4]

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RP SEQUENCE FROM N.A.
DT STRAIN=K12;
RC MEDLINE=97251357; PubMed=9097039;
RA Itoh T., Baba H., Fujita K., Hayashi K., Inada T., Isono K.,
RA Alha H., Kimura S., Kitagawa M., Makino K., Mori T.,
RA Kitagawa M., Makino K., Mori T., Mizouchi K., Mori H., Mori T.,
RA Motomura K., Nakade S., Nakamura Y., Nishio Y.,
RA Oshima T., Saito N., Sempel G., Seki Y., Sivasubram S.,
RA Yamaguchi H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
RA Yamamoto Y., Horuchi T.;
RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RA MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Baba H., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitagawa M., Makino K., Mori T.,
RA Mizouchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
RA Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horuchi T.;
RT "A 460-kb DNA sequence of the *Escherichia coli* K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
CC -!- FUNCTION: INVOLVED IN THE TRANSPOSITION OF THE INSERTION
SEQUENCE IS2.
CC -----
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CC -----
DR EMBL, V00279; CAA23542.1; ALT INIT.
DR EMBL, U14003; AAA97168.1; ALT INIT.
DR EMBL, U28377; AAA69212.1; ALT INIT.
DR EMBL, U28375; AAA83043.1; ALT INIT.
DR EMBL, AE000143; AAC73463.1; ALT INIT.
DR EMBL, AE000237; AAC74485.1; ALT INIT.
DR EMBL, AE000291; AAC75058.1; ALT INIT.
DR EMBL, AE000369; AAC75900.1; ALT INIT.
DR EMBL, AE000386; AAC76080.1; ALT INIT.
DR EMBL, AE000496; AAC77228.1; ALT INIT.
DR EMBL, D90778; BAA15013.1; ALT INIT.
DR EMBL, D90779; BAA15019.1; ALT INIT.
DR EMBL, D90838; BAA15822.1; ALT INIT.
DR EMBL, D90850; BAA16005.1; ALT INIT.
DR EMBL, D90851; BAA16013.1; ALT INIT.
DR EMBL, D90852; BAA16036.1; ALT INIT.
DR Ecogen; ECG40003; insC.
DR InterPro; IPR002514; Transposase_8.
DR Pfam; PF01527; Transposase_8; 1.
KW Transposable element; Transposition; DNA-binding; DNA recombination;
KW Complete proteome.
FT VARIANT 34 L -> F (IN B1997).
SQ SEQUENCE 121 AA; 13452 MW; 59431B5C452E067A CRC64;

Query Match 0.9%; Score 7; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 ASELAA 208
DB 70 ASELAA 76

RESULT 20
INSC_SHIFL STANDARD; PRT; 121 AA.
ID INSC_SHIFL

AC P59444;
DT 15-SEP-2003 (Rel. 42; Created)
DT 15-SEP-2003 (Rel. 42; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE Transposase insC for insertion element IS2.
GN (INSC1 OR SF0245) AND (INSC2 OR SF0879) AND (INSC3 OR SF0933) AND
GN (INSC4 OR SF0960) AND (INSC5 OR SF1054) AND (INSC6 OR SF1165) AND
GN (INSC7 OR SF1433) AND (INSC8 OR SF1463) AND (INSC9 OR SF1587) AND
GN (INSC10 OR SF2011) AND (INSC11 OR SF2615) AND
GN (INSC12 OR SF2694) AND (INSC13 OR SF2873) AND
GN (INSC14 OR SF2984) AND (INSC15 OR SF3431) AND
GN (INSC16 OR SF3512) AND (INSC17 OR SF3805) AND
GN (INSC18 OR SF3873) AND (INSC19 OR SF3988) AND
GN (INSC20 OR SF4097) AND (INSC21 OR SF4185).
OS *Shigella flexneri*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; *Shigella*.
OX NCBI_TaxID=623;
[1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Xu J.;
RT "Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity
RT through comparison with genomes of *Escherichia coli* K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
CC -!- FUNCTION: Involved in the transposition of the insertion
CC sequence IS2 (By similarity).
CC -----
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CC -----
DR EMBL, AE015060; AAM41906.1; ALT INIT.
DR EMBL, AE015116; AAM42511.1; ALT INIT.
DR EMBL, AE015123; AAM42562.1; ALT INIT.
DR EMBL, AE015125; AAM42588.1; ALT INIT.
DR EMBL, AE015133; AAM42676.1; ALT INIT.
DR EMBL, AE015143; AAM42781.1; ALT INIT.
DR EMBL, AE015160; AAM42947.1; ALT INIT.
DR EMBL, AE015170; AAM43060.1; ALT INIT.
DR EMBL, AE015180; AAM43173.1; ALT INIT.
DR EMBL, AE015218; AAM43556.1; ALT INIT.
DR EMBL, AE015277; AAM44112.1; ALT INIT.
DR EMBL, AE015284; AAM44187.1; ALT INIT.
DR EMBL, AE015301; AAM44359.1; ALT INIT.
DR EMBL, AE015311; AAM44465.1; ALT INIT.
DR EMBL, AE015351; AAM44892.1; ALT INIT.
DR EMBL, AE015359; AAM44970.1; ALT INIT.
DR EMBL, AE015387; AAM45245.1; ALT INIT.
DR EMBL, AE015394; AAM45310.1; ALT INIT.
DR EMBL, AE015405; AAM45422.1; ALT INIT.
DR EMBL, AE015418; AAM45522.1; ALT INIT.
DR EMBL, AE015427; AAM45606.1; ALT INIT.
KW Transposable element; Transposition; DNA-binding; DNA recombination.
SQ SEQUENCE 121 AA; 13452 MW; 59431B5C452E067A CRC64;

Query Match 0.9%; Score 7; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 ASELAA 208
DB 70 ASELAA 76


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RESULT 21
RNP_ANTAM STANDARD; PRT; 124 AA.
AC 200668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Antilocapra americana (Pronghorn).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Antilocapridae; Antilocapra.
OX NCBI_TaxID=9891;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=80075014; PubMed=513141;
RA Beintema J.J., Gaastera W., Munnikema J.;
RT "Primary structure of pronghorn pancreatic ribonuclease: close
relationship between giraffe and pronghorn.";
RL J. Mol. Evol. 13:305-316(1979).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphoglyconucleotides ending in C-P or U-P
with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Pancreas.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR: A00813; NRPXH.
DR HSSP; P00656; IRBG.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PP000535; RNaseA.1.
DR SMART; SM00092; RNase_PC.1.
DR PROSITE; PS00127; RNase_PANCREATIC.1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLCNAC... ) (PARTIAL).
SQ SEQUENCE 124 AA; 13711 MW; 9435EF532420F852 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 785 SNPSVS 791
DB 15 SNPSVS 21

RESULT 22
Y082_RICPR STANDARD; PRT; 143 AA.
AC Q92E65;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein RP082.
GN RP082.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Madrid E;

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RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichertitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naestlund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
mitochondria.";
RL Nature 396:133-140(1998).
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CC -----
DR EMBL; AJ235270; CAA14552.1; -
DR PIR; A71717; A71717.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 143 AA; 16939 MW; 57637C7A62FE9F10 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 143;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 133 NRKOEI 139
DB 106 NRKOEI 112

RESULT 23
P7VA_ECOLI STANDARD; PRT; 148 AA.
AC P3155; P76776;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE PTS system, fructose-1,6-bisphosphate (Phosphotransferase enzyme
II, A component) (EC 2.7.1.69).
GN PFVA OR B3900.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=93374854; PubMed=8396120;
RA Moralejo P., Egan S.M., Hidalgo B.F., Aguilar J.;
RT "Sequencing and characterization of a gene cluster encoding the
RT enzymes for L-rhamnose metabolism in Escherichia coli.";
RL J. Bacteriol. 175:5585-5594(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=93347969; PubMed=8346018;
RA Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
RT "Analysis of the Escherichia coli genome. III. DNA sequence of the
RT region from 87.2 to 89.2 minutes.";
RL Nucleic Acids Res. 21:3391-3398(1993).
RN [3]
RP REVISIONS TO 81 AND 104-108.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RP DISCUSSION OF SEQUENCE.
RX MEDLINE=94290319; PubMed=8019415;

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RA Reizer J., Michotey V., Reizer A., Saier M.H. Jr.;
 RT "Novel phosphotransferase system genes revealed by bacterial genome
 RT analysis: unique, putative fructose- and glucoside-specific
 RT systems."; Protein Sci. 3:440-450(1994)
 CC -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
 CC SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
 CC TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
 CC AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
 CC PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-PER; IIA TRANSFERS ITS
 CC PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
 CC THE SUGAR.
 CC -1- CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein
 CC histidine + sugar phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- SIMILARITY: Contains 1 PTS EIIA domain.
 CC -----
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 CC -----
 DR EMBL; X60472; CAA43004.1; -
 DR EMBL; L19201; AAB0303.2; -
 DR EMBL; AE000465; AAC76882.1; -
 DR PIR; D48649; D48649.
 DR EcoGene; EGI1864; ftyA.
 DR InterPro; IPR002178; PTS_EIIA_2.
 DR InterPro; IPR004715; PTSIIA_fnc.
 DR Pfam; PF00359; PTS_EIIA_2; 1.
 DR ProDom; PD001689; PTS_EIIA_2; 1.
 DR TIGRfam; TIGR00848; ftnA_1.
 DR PROSITE; PS00372; PTS_EIIA_2; 1.
 DR Phosphotransferase system; Sugar transport; Transferase;
 KW Phosphorylation; Complete proteome.
 FT MOD RES 64 64 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 81 81 A -> G (IN REF. 2).
 FT CONFLICT 104 107 QSGE -> KXZ (IN REF. 2).
 SQ SEQUENCE 148 AA; 16093 MW; 04AE87B9084BA1C6 CRC64;
 Query Match 0.9%; Score 7; DB 1; Length 148;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 303 GVAVPHG 309
 DB 59 GVAVPHG 65
 RESULT 24
 ID MUTT STRAM STANDARD; PRT; 154 AA.
 AC P32091;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mutt-like protein (ORF154).
 OS Streptomyces ambifaciens.
 OG Plasmid pSAM2.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 RX NCBI_TaxID=1889;
 RN [1]
 RP .SEQUENCE FROM N.A.
 RC STRAIN=ATCC 23877;
 RX MEDLINE=95020551; PubMed=7934842;
 RA Haggag J., Bernodet J.L., Friedmann A., Guerin M.;
 RT "Mode and origin of replication of pSAM2, a conjugative integrating
 RT element of Streptomyces ambifaciens."; Mol. Microbiol. 10:799-812(1993).

CC -1- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; Z19590; CAA79638.1; -
 DR PIR; S39873; S39873.
 DR HSSP; P08337; 1TUM.
 DR InterPro; IPR000086; NUDIX_hydrolase.
 DR Pfam; PF00293; NUDIX; 1.
 DR PRINTS; PR00502; NUDIXFAMILY.
 DR PROSITE; PS00893; NUDIX; 1.
 KW Plasmid; Hydrolase.
 FT DOMAIN 48 69 NUDIX BOX.
 SQ SEQUENCE 154 AA; 16689 MW; 8EC2EE99D272D656 CRC64;
 Query Match 0.9%; Score 7; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 33 LTPDEV 39
 DB 114 LTPDEV 120
 RESULT 25
 ID GREX STAM STANDARD; PRT; 158 AA.
 AC Q997N9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transcription elongation factor greA (Transcript cleavage factor
 DE greA).
 GN GREX OR SA11610 OR SA1438 OR MW1560.
 OS Staphylococcus aureus (strain N315) / ATCC 700699).
 OS Staphylococcus aureus (strain N315), and
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878, 158879, 196620;
 RN [1]
 RP .SEQUENCE FROM N.A.
 RC STRAIN=M350, and N315;
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus."; Lancet 357:1225-1240(2001).
 RL Lancet 357:1225-1240(2001).
 RT [2]
 RP .SEQUENCE FROM N.A.
 RC STRAIN=MW2;
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naim T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA."; Lancet 359:1819-1827(2002).
 RL Lancet 359:1819-1827(2002).
 CC -1- FUNCTION: Necessary for efficient RNA polymerase transcription
 CC elongation past template-encoded arresting sites. The arresting
 CC sites in DNA have the property of tripping a certain fraction of
 CC elongating RNA polymerases that pass through, resulting in locked

```

CC      ternary complexes. Cleavage of the nascent transcript by cleavage
CC      factors such as grea or greb allows the resumption of elongation
CC      from the new 3' terminus. Grea releases sequences of 2 to 3
CC      nucleotides (By similarity).
CC      -I- SIMILARITY: BELONGS TO THE GREB/GREB FAMILY.
CC      -----
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CC      -----
DR      EMBL; AP003362; BAB5772.1; -
DR      EMBL; AP003334; BAB42702.1; -
DR      EMBL; AP004827; BAB95425.1; -
DR      PIR; A89943; A89943.
DR      HSSP; P21346; IGRJ.
DR      HAMAP; MF_00105; -; 1.
DR      InterPro; IPR006359; Grea.
DR      InterPro; IPR001437; Grea_Greb.
DR      Pfam; PF01272; Grea_Greb; 1.
DR      Pfam; PF03449; Grea_Greb_N; 1.
DR      ProDom; PD004918; Grea_Greb; 1.
DR      TIGRFAMs; TIGR01462; grea; 1.
DR      PROSITE; PS00829; GREB_1; 1.
DR      PROSITE; PS00830; GREB_2; 1.
DR      PROSITE; PS00830; GREB_2; 1.
DR      Transcription regulation; DNA-binding; Coiled coil; Complete proteome.
DR      Transcription regulation; DNA-binding; Coiled coil (POTENTIAL).
DR      DOMAIN 4
DR      SEQUENCE 158 AA; 17743 MW; EC3B0F0E6238A107 CRC64;
SQ
Query Match          0.9%; Score 7; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      176 IIEDTGD 182
DB      77 IIEDTGD 83
-----
RESULT 26
Y052_ARCFU          STANDARD; PRT; 158 AA.
AC      C30184.
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical protein AF0052.
GN      AF0052.
OS      Archaeoglobus fulgidus.
OC      Archaeae; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC      Archaeoglobaceae; Archaeoglobus.
OX      NCBI_TaxID=2234;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX      MEDLINE=96049343; PubMed=9389475;
RA      Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA      Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA      Richardson D.L., Kesteven A.R., Graham D.E., Kyrgidis N.C.,
RA      Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA      Kitznes S.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA      Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA      Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,
RA      Cocton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
RA      Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA      Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA      Venter J.C.;
RT      "The complete genome sequence of the hyperthermophilic, sulphate-
RT      reducing archaeon Archaeoglobus fulgidus.";
RL      Nature 390:364-370 (1997).
CC      -----

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CC      -----
DR      EMBL; AE001102; AAB91174.1; -
DR      PIR; D69256; D69256.
DR      TIGR; AF0052; -
DR      Hypothetical protein; Complete proteome.
DR      Hypothetical protein; Complete proteome.
DR      SEQUENCE 158 AA; 17369 MW; 92DF7317D55ABFC CRC64;
SQ
Query Match          0.9%; Score 7; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      372 NSSLSVSQ 378
DB      36 NSSLSVSQ 42
-----
RESULT 27
GCSI_ARATH          STANDARD; PRT; 166 AA.
ID      GCSI_ARATH
AC      O91010.
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Probable glycine cleavage system H protein 2, mitochondrial precursor.
GN      ATIG32470 OR F5D14.25.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ecv. Columbia;
RX      MEDLINE=21016719; PubMed=11130712;
RA      Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA      White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
RA      Buehler E., Chan A., Chao Q., Chen H., Cheuk D.B., Chin C.W.,
RA      Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA      Dunn P., Egu P., Feldhym T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA      Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hutzar L.,
RA      Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA      Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA      Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA      Lin X., Liu S.X., Liu Z.A., Lueros J.S., Malti R., Marzilli A.,
RA      Miltschener J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA      Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA      Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA      Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA      Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA      Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT      "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT      thaliana.";
RL      Nature 408:816-820 (2000).
RC      -I- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYZES THE DEGRADATION OF
RC      GLYCINE. THE H PROTEIN SHUTTLES THE METHYLAMINE GROUP OF GLYCINE
RC      FROM THE P PROTEIN TO THE T PROTEIN (BY SIMILARITY).
CC      -I- CORAFCTOR: THE H CHAIN CONTAINS A COVALENTLY-BOUND LIPOYL COFACTOR
CC      (BY SIMILARITY).
CC      -I- SUBUNIT: The glycine cleavage system is composed of four proteins:
CC      P, T, L, and H (By similarity).
CC      -I- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC      -I- SIMILARITY: Contains 1 lipoyl-binding domain.
CC      -----
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DR EMBL: AC007767; AAF81345.1; -
DR PIR: A86450; A86450.
DR HSSP: P16048; IHTP.
DR InterPro: IPR002930; GCV_H.
DR InterPro: IPR003016; LipoyL.
DR Pfam: PF01597; GCV_H.1.
DR TIGRfam: TIGR00527; GCVH.1.
DR PROSITE: PS00189; LipoyL.1.
DR Mitochondrion; Transist peptide; LipoyL.
FT TRANSIT 1 35 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 36 166 PROBABLE GLYCINE CLEAVAGE SYSTEM H
FT BINDING 98 98 LipoYL (BY SIMILARITY).
FT SEQUENCE 166 AA; 17897 MW; C21658C0B9E75ADB CRC64;

Query Match 0.9%; Score 7; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 SSVSKEX 794
Db 83 SSVSKEX 89

RESULT 28
HUNB DROMU STANDARD; PRT; 174 AA.
AC 046250; 046251;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hunchback protein (Fragments).
OS HB.
GN Drosophila mulleri (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7231;
RN [1]
RP SEQUENCE FROM N.A.
RA Baker R.H., Desalle R.;
RT "Multiple sources of character information and the phylogeny of
RT Hawaiian Drosophilids.";
RL Syst. Biol. 46:654-673 (1997).
CC -1- FUNCTION: GAP CLASS SEGMENTATION PROTEIN THAT CONTROLS DEVELOPMENT
CC OF HEAD STRUCTURES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).
CC -1- SIMILARITY: BELONGS TO THE HUNCHBACK FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.
CC -----
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Query Match 0.9%; Score 7; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 PSPQPTP 355
Db 110 PSPQPTP 116

RESULT 29
APT CHLITE STANDARD; PRT; 177 AA.
AC 08KFM9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT).
GN APT OR C70293.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., Deboy R., Gwim M.L., Nelson W.C., Halt D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathavan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
CC -1- FUNCTION: Catalyzes a salvage reaction resulting in the formation
CC of AMP, that is energetically less costly than de novo synthesis.
CC -1- CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -1- PATHWAY: Purine salvage.
CC -1- SUBUNIT: Homodimer (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.

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DR EMBL: AE012808; AAM71539.1; -
DR TIGR: C70293; -
DR HAMAP: MF_00004; -; 1.
DR InterPro: IPR005764; Ade_phospho_trans.
DR InterPro: IPR002375; Pr/PY rp transf.
DR InterPro: IPR000836; PRTtransferase.
DR Pfam: PF00156; Pribosyltran; 1.
DR TIGRfam: TIGR01090; apt; 1.
DR PROSITE: PS00103; PUR_PYR_TRANSER; 1.
DR Transferrase; Glycosyltransferase; Purine salvage; Complete proteome.
SQ SEQUENCE 177 AA; 19319 MW; A060DD2DD9C242B41 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 484 LVDDLLA 490
|||||||

Db 118 LVDDL1A 124

RESULT 30

NUSG_NEIMA STANDARD; PRT; 178 AA.

ID NUSG_NEIMA

AC Q9JRD9;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Transcription antitermination protein nusG.

GN NUSG OR NMA0147 OR NMB0126.

OS Neisseria meningitidis (serogroup A), and

OC Neisseria meningitidis (serogroup B).

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OX NCBI_TaxID=65699, 491;

SEQUENCE FROM N.A.

RC STRAIN=Z2491 / Serotype 4A;

RX MEDLINE=20222556; PubMed=10761919;

RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Mottell G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagers K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrall B.G.;

RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491."

RL Nature 404:502-506(2000).

[2]

SEQUENCE FROM N.A.

RP STRAIN=MC58 / Serogroup B;

RX MEDLINE=20175751; PubMed=10710307;

RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B., Cotton M.D., Ullrich T.R., Khouiri H., Qin H., Vamathevan J., Gill J., Scarlato V., Maignan V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappunli R., Venter J.C.;

RA "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58."

RT Science 287:1809-1815(2000).

RL

CC -!- FUNCTION: INFLUENCES TRANSCRIPTION TERMINATION AND ANTERMINATION. ACTS AS A COMPONENT OF THE TRANSCRIPTION COMPLEX, AND INTERACTS WITH THE TERMINATION FACTOR RHO AND RNA POLYMERASE (BY SIMILARITY).

CC -!- SIMILARITY: Belongs to the nusG family.

CC -----

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CC -----

CC EMBL; AL162752; CAB83462.1; -

CC EMBL; AE002371; AAP40585.1; -

CC PIR; C81235; C81235.

CC TIGR; NMB0126; -

CC InterPro; IPR005824; K0M.

CC InterPro; IPR006646; K0M_sub.

CC InterPro; IPR006645; NGN.

CC InterPro; IPR001062; NUSG.

CC Pfam; PF00467; K0M; 1.

CC Pfam; PF02357; NUSG; 1.

CC PRINTS; PR00338; NUSG; 1.

CC SMART; SM00739; K0M; 1.

CC SMART; SM00738; NGN; 1.

CC TIGRfams; TIGR00922; nusG; 1.

DR PROSITE; PS01014; NUSG; 1.

KW Transcription termination; Complete proteome.

SC SEQUENCE 178 AA; 20550 MW; 3171FDC957FECB3 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 178;

Best local similarity 100.0%; Pred. No. 44;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 323 LEER1AR 329

Db 22 LEER1AR 28

RESULT 31

APT_HELPJ STANDARD; PRT; 179 AA.

ID APT_HELPJ

AC Q9ZLQ9;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT).

GN APT OR JHP0519.

OS Helicobacter pylori J99 (Campylobacter pylori J99).

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;

OC Helicobacteraceae; Helicobacter.

OX NCBI_TaxID=85963;

SEQUENCE FROM N.A.

RP MEDLINE=99120557; PubMed=9923682;

RX Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tunmino P.J., Carnuso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., Trust T.J.;

RT "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori."

RL Nature 397:176-180(1999).

CC -!- FUNCTION: Catalyzes a salvage reaction resulting in the formation of AMP, that is energetically less costly than de novo synthesis.

CC -!- CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5-phospho-alpha-D-ribose 1-diphosphate.

CC -!- PATHWAY: Purine salvage.

CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: BELONGS TO THE PURINE/PRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.

CC -----

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CC -----

CC EMBL; AE001485; AAD06100.1; -

CC PIR; H71920; H71920.

CC HAVAP; MF_00004; -; 1.

CC InterPro; IPR005764; Ade_phospho_trans.

CC InterPro; IPR002375; Pr/py_rp_transf.

CC InterPro; IPR000836; PRTtransferase.

CC Pfam; PF00156; Pribosyltran; 1.

CC TIGRfams; TIGR01090; apt; 1.

CC PROSITE; PS00103; PUR_PYR_PR_TRANSFERR; 1.

CC TRANSFERASE; Glycosyltransferase; Purine salvage; Complete proteome.

SC SEQUENCE 179 AA; 19846 MW; F287FDAA23CB57C9 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 179;

Best local similarity 100.0%; Pred. No. 44;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 LVDDL1A 490

|||||||

Db 124 LVDDLLA 130

RESULT 32

VATE DEIRA STANDARD; PRT; 185 AA.

AC Q9RWH1; 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE V-type ATP synthase subunit E (EC 3.6.3.14) (V-type ATPase subunit E).

GN ATP8 OR DR0697.

OS Deinococcus radiodurans.

OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;

OC Deinococcaceae; Deinococcus.

OX NCBI_Taxid=1299;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;

RX MEDLINE=20036896; PubMed=10567266;

RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwin M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.U., Lam P., McDonald L., Utterback T., Zaleski C., Makarewicz K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Fraser C.M.;

RA "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";

RT Science 286:1571-1577(1999).

RL CC -1- FUNCTION: Produces ATP from ADP in the presence of a proton gradient across the membrane.

CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate + H(+) (Out)

CC -1- SIMILARITY: Belongs to the V-ATPase E subunit family.

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CC CC -----

DR EMBL; AE001926; AAF10275.1; -

DR PIR; F75487; F75487.

DR TIGR; DR0697; -

DR HAMAP; MF_00311; -; 1.

DR InterPro; IPR002842; ATPsyn Esub.

DR Pfam; PF01991; VATP-synt E; 1.

KW Hydrolase; ATP synthetase; Hydrogen ion transport;

KW Complete proteome.

SQ SEQUENCE 185 AA; 20140 MW; CFAF2F8987C3CF2 CRC64;

QY 466 ALDKLIE 472

Db 2 ALDKLIE 8

Query Match 0.9%; Score 7; DB 1; Length 185;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Methyllobacteriaceae; Methyllobacterium.

OX NCBI_Taxid=408;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AM1 / NCIMB 9133;

RX MEDLINE=88319960; PubMed=2842733;

RA Nunn D.N., Anthony C.;

RT "The nucleotide sequence and deduced amino acid sequence of the genes for cytochrome c1 and a hypothetical second subunit of the methanol dehydrogenase of Methyllobacterium AM1.";

RT Nucleic Acids Res. 16:7722-7722(1988).

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN=AM1 / NCIMB 9133;

RX MEDLINE=89134152; PubMed=2851998;

RA Nunn D.N., Anthony C.;

RT "The nucleotide sequence and deduced amino acid sequence of the cytochrome c1 gene of Methyllobacterium extorquens AM1, a novel class of c-type cytochrome.";

RT Biochem. J. 256:673-676(1988).

RN [3]

RP SEQUENCE OF 1-8 FROM N.A.

RC STRAIN=AM1 / NCIMB 9133;

RA Anderson D.J., Morris C.J., Nunn D.N., Anthony C., Lidstrom M.E.;

RL Submitted (JAN-1990) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: ELECTRON ACCEPTOR FOR MDH. ACTS IN METHANOL OXIDATION.

CC THIS CYTOCHROME HAS A REDOX POTENTIAL OF ABOUT +256 MV.

CC -1- SUBCELLULAR LOCATION: Periplasmic (Potential).

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CC CC -----

DR EMBL; X07856; CAA30704.1; -

DR EMBL; M31108; AAA25382.1; -

DR HSSP; P29899; 2MTA.

DR InterPro; IPR003088; Cyt C1.

DR InterPro; IPR000345; Cytochrome c1.

DR Pfam; PF00034; Cytochrome c1.

DR PROSITE; PS00190; CYTOCHROME C1.

KW Electron transport; Heme; Signal; Methanol utilization; Periplasmic.

FT SIGNAL 1 25

FT CHAIN 26 197

FT BINDING 90 90

FT BINDING 93 93

FT METAL 94 94

FT METAL ? ?

SQ SEQUENCE 197 AA; 21226 MW; 58F22BACB90258CE CRC64;

QY 31 ENLTPDE 37

Db 139 ENLTPDE 145

Query Match 0.9%; Score 7; DB 1; Length 197;

Best Local Similarity 100.0%; Pred. No. 48;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 33

CYCL METEX STANDARD; PRT; 197 AA.

AC P14774; 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Cytochrome c-L precursor.

MOXG.

GN Methyllobacterium extorquens.

OS

RESULT 34

RB1B HUMAN STANDARD; PRT; 201 AA.

AC Q9H0T4; 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ras-related protein Rab-1B.

RAB1B.

GN Homo sapiens (Human).

OS

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Anorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koshier K., Strack N.,
RA Mewes H.-W., Oltenswaelder B., Oetemaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RA "Towards a catalog of human genes and proteins: sequencing and
RT genome Res. 11:422-435(2001).
RL Genomes Res. 11:422-435(2001).
CC -!- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
CC TRAFFIC (BY SIMILARITY).
CC -!- MISCELLANEOUS: RAB-1B BINDS GTP AND GDP AND POSSESS INTRINSIC
CC GTPASE ACTIVITY (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAB FAMILY.
CC -----
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CC -----
DR EMBL; AL136635; CAB66570.1; -.
DR Genew; HGNC:18370; RAB1B.
DR HSSP; P05713; 3RAB.
DR InterPro; IPR001806; GTPase_Rab.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTRNSFRNG.
DR SMART; SM00175; RAB; 1.
DR TIGRfams; TIGR00231; small GTP; 1.
KW GTP-binding; Lipoprotein; Prenylation; Protein transport.
FT NP_BIND 15 22 GTP (BY SIMILARITY).
FT NP_BIND 63 67 GTP (BY SIMILARITY).
FT NP_BIND 121 124 GTP (BY SIMILARITY).
FT DOMAIN 37 45 EFFECTOR REGION (BY SIMILARITY).
FT LIPID 200 200 GERANYL-GERANYL (BY SIMILARITY).
FT LIPID 201 201 GERANYL-GERANYL (BY SIMILARITY).
SQ SEQUENCE 201 AA; 22171 MW; 9812F4DAC34B2B CRC64;

Query Match 0.9%; Score 7; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 PNLKIDS 371
DB 184 PNLKIDS 190

RESULT 35
RIB_RAT STANDARD; PRT; 201 AA.
AC P10536;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ras-related protein Rab-1B.
GN RAB1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RX SEQUENCE FROM N.A.
RP MEDLINE=89160341; PubMed=2493636;

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RA Zahraoui A., Touchot N., Chardin P., Tavittian A.;
RT "Nucleotide sequence of a rat cDNA: rab1b, encoding a rab1-YPT
RT related protein.";
RL Nucleic Acids Res. 17:1770-1770(1989).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=9003316; PubMed=2509243;
RA Touchot N., Zahraoui A., Viel E., Tavittian A.;
RT "Biochemical properties of the YPT-related rab1b protein. Comparison
RT with rab1a.";
RL FEBS Lett. 256:79-84(1989).
RN [3]
RP ISOPRENOID.
RX MEDLINE=91296801; PubMed=1648736;
RA Khosravi-Far R., Lutz R.J., Cox A.D., Conroy L., Bourne J.R.,
RA Sienkney M., Balch W.E., Buss J.E., Der C.J.;
RT "Isoprenoid modification of rab proteins terminating in CC or CXC
RT motifs.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:6264-6268(1991).
CC -!- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
CC TRAFFIC (BY SIMILARITY).
CC -!- MISCELLANEOUS: RAB-1B BINDS GTP AND GDP AND POSSESS INTRINSIC
CC GTPASE ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAB FAMILY.
CC -----
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CC -----
DR EMBL; X13905; CAA32105.1; -.
DR PIR; S06147; S06147.
DR HSSP; P05713; 3RAB.
DR InterPro; IPR003579; GTPase_Rab.
DR InterPro; IPR001806; Ras trnsfrmg.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTRNSFRNG.
DR SMART; SM00175; RAB; 1.
DR TIGRfams; TIGR00231; small GTP; 1.
KW GTP-binding; Lipoprotein; Prenylation; Protein transport.
FT NP_BIND 15 22 GTP (BY SIMILARITY).
FT NP_BIND 63 67 GTP (BY SIMILARITY).
FT NP_BIND 121 124 GTP (BY SIMILARITY).
FT DOMAIN 37 45 EFFECTOR REGION (BY SIMILARITY).
FT LIPID 200 200 GERANYL-GERANYL.
FT LIPID 201 201 GERANYL-GERANYL.
FT MUTAGEN 21 21 K->M; ABOLISHES GTP-BINDING.
SQ SEQUENCE 201 AA; 22163 MW; 8D3EDC2AF42F CRC64;

Query Match 0.9%; Score 7; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 PNLKIDS 371
DB 184 PNLKIDS 190

RESULT 36
APSI_SCHPO STANDARD; PRT; 210 AA.
AC Q09790;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Diadenosine 5',5'-P1,P6-hexaphosphate hydrolase (EC 3.6.1.-)
DE (Ap6A hydrolase).
GN APS1 OR SPAC13G6.14 OR SPAC24B11.03.
OS Schizosaccharomyces pombe (Fission yeast).

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OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=972;
 RC MEDLINE=99192402; PubMed=10090752;
 RT Ingram S.W., Stratemann S.A., Barnes L.D.;
 RT "Schizosaccharomycetes pombe Apsl, a didenotone 5',5''-p1, P6-
 RT hexaphosphate hydrolase that is a member of the nudix (MUT) family of
 RT hydrolases: cloning of the gene and characterization of the purified
 RT enzyme";
 RT Biochemistry 38:3649-3655(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RC MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham S., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grynolprez B.,
 RA Wolfens I., Vansteelt G., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
 RA Gottfau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shporkovskii G.V., Ussery D., Barrett B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomycetes pombe";
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF DINUCLEOSIDE
 CC OLIGOPHOSPHATES, WITH APE6 AND APE8 BEING THE PREFERRED
 CC SUBSTRATES. THE MAJOR REACTION PRODUCTS ARE ADP AND P4A FROM APE6
 CC AND ADP AND ATP FROM APE8.
 CC -1- COFACTOR: REQUIRES MAGNESIUM (BY SIMILARITY).
 CC -1- SUBUNIT: Monomer.
 CC -1- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY.
 CC -----
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 CC -----
 CC EMBL, AF125215; AAD20015.1; -;
 DR EMBL, Z54308; CAA91107.1; -;
 DR EMBL, Z67757; CAA91768.1; -;
 DR PIR, S62443; S62443.
 DR GeneDB, SPombe, SPAC136.14; -;
 DR InterPro, IPR000086; NUDIX_hydrolase.
 DR Pfam, PF00293; NUDIX, 1.
 DR PROSITE, PS00893; NUDIX, 1.
 DR HydroLase, Magnesium.
 FT DOMAIN 74 95 NUDIX BOX.
 SQ SEQUENCE 210 AA; 23724 MW; 492F7BF9563A1C98 CRC64;

Query Match

0.9%; Score 7; DB 1; Length 210;

Best Local Similarity 100.0%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 773 AEAEXKL 779
 DB 143 AEAEXKL 149
 RESULT 37
 14P ARATH
 ID 14P ARATH STANDARD; PRT; 211 AA.
 AC 064628;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein At2g18990
 GN AT2G18990 OR F19P24.19.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RC MEDLINE=20083487; PubMed=10617197;
 RX Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldlyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Renning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Niernman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana";
 RL Nature 402:761-768(1999).
 CC -1- SIMILARITY: BELONGS TO THE UPF0071 FAMILY. SOME SIMILARITY TO THE
 CC THIOREDOXIN FAMILY.
 CC -----
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 CC -----
 CC EMBL, AC003673; AAM14890.1; -;
 DR PIR, T01627; T01627.
 DR InterPro, IPR006663; Thioredox_dom2.
 SQ SEQUENCE 211 AA; 24451 MW; 43B26F01CF7F6D14 CRC64;
 Query Match 0.9%; Score 7; DB 1; Length 211;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 323 LERRAR 329
 DB 169 LERRAR 175
 RESULT 38
 YRAR ECOLI
 ID YRAR ECOLI STANDARD; PRT; 211 AA.
 AC P45469;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein yrar.
 GN YRAR OR B3152.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;


```

OC Enterobacteriaceae; Escherichia.
RX NCBI_TaxId=562;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474 (1997).
CC -1- SIMILARITY: TO YEAST YER004W.
CC -----
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CC -----
DR EMBL; U18997; AA57955.1; ALT_INIT.
DR EMBL; AE000396; AAC76186.1; ALT_INIT.
DR EcoGene; EG12783; YEA8.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 211 AA; 23198 MW; 5E3793BBADC891FF CRC64;

Query Match 0.9%; Score 7; DB 1; Length 213;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 YNRVKG 606
Db 122 YNRVKG 128

RESULT 39
CPCF_SYNEL STANDARD; PRT; 213 AA.
ID CPCF_SYNEL
AC P50038;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-EB-2003 (Rel. 41, Last annotation update)
DE Phycocyanobilin lyase beta subunit (Ec 4.1.1.1) (Phycocyanin operon
DE protein cpcF).
GN CPCF OR TLR1962.
OS Synecococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxId=32046;
RN [1]
RP SEQUENCE FROM N.A.
RA Shimazu T., Soga M., Hirano M., Katoh S.;
RT "Cloning and sequencing of the phycocyanin operon from the
RT thermophilic cyanobacterium Synecococcus elongatus."
RL Submitted (SEP-1992) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=BP-1;
RC MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriuchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1."
RL DNA Res. 9:123-130 (2002).
CC -1- FUNCTION: REQUIRED FOR THE CHROMOPHYLLATION OF THE CP26 GENE
CC PRODUCT (BY SIMILARITY).
CC -1- SUBUNIT: CPCF AND CPCF ASSOCIATES TO FORM A LYASE.
CC -1- SIMILARITY: BELONGS TO THE CPCF/RPCF/BECP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D13173; BAA02460.1; -.
DR EMBL; AP005375; BAC09514.1; -.
DR InterPro; IPR004155; PBS_Lyase_HEAT.
DR Pfam; PF03130; HEAT_PBS; 3.
KW Phycobillosome; Lyase; Complete proteome.
SQ SEQUENCE 213 AA; 22654 MW; 45D99720985F2683 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 213;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 EAQJKA 734
Db 135 EAQJKA 141

RESULT 40
URE1_HELMU STANDARD; PRT; 213 AA.
ID URE1_HELMU
AC P50044;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase) (Fragment).
GN UREA.
OS Helicobacter mustelae.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteriaceae; Helicobacter.
OX NCBI_TaxId=217;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCCTC 12032;
RX MEDLINE=95369940; PubMed=7642313;
RA Solnick J.V., Josephans C., Tompkins L.S., Labigne A.;
RT "Construction and characterization of an isogenic urease-negative
RT mutant of Helicobacter mustelae."
RL Infect. Immun. 63:3718-3721 (1995).
CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -1- SUBUNIT: CONSIST OF TWO SUBUNITS (ALPHA AND BETA).
CC -1- CAUTION: IN HELICOBACTER THE ALPHA SUBUNIT IS WHAT IS KNOWN, IN
CC OTHER BACTERIA AS THE BETA SUBUNIT.
CC -----
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CC -----
DR EMBL; L33462; AAC1483.1; -.
DR HSSP; P41022; IUBP.
DR InterPro; IPR002019; Urease_beta.
DR InterPro; IPR002026; Urease_gamma.
DR Pfam; PF00699; Urease_beta; 1.
DR Pfam; PF00547; Urease_gamma; 1.
DR PIRSF; PIRSF01225; Urease_gammabeta; 1.
DR ProDom; PD002319; Urease_beta; 1.
DR ProDom; PD002319; Urease_gamma; 1.
DR TIGRFAMs; TIGR00192; Urease_beta; 1.
DR TIGRFAMs; TIGR00193; Urease_gamma; 1.
KW Hydrolase.
FT NON_TER 1
SQ SEQUENCE 213 AA; 23794 MW; B97A6A3FD2CB2F40 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 213;

```


Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 92 LKEDIV 98
Db 101 LKEDIV 107

RESULT 41

PSE2_RAT ID_PSE2_RAT STANDARD; PRT; 238 AA.

AC Q63798; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Proteasome activator complex subunit 2 (proteasome activator 28-beta subunit) (PA28beta) (PA28b) (Activator of multicatalytic protease subunit 2) (11S regulator complex beta subunit) (REG-beta).
DE subunit 2) (11S regulator complex beta subunit) (REG-beta).
GN PSME2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_Taxid=10116;
RN SEQUENCE FROM N.A.
RX MEDLINE=95309399; PubMed=7789512;
RA Ahn J.Y., Tanahashi N., Akiyama K., Hisamatsu H., Noda C., Tanaka K., Chung C.H., Shimbara N., Willy P.J., Mott J.D., Slaughter C.A., Demetrio G.N.;

RT "Primary structures of two homologous subunits of PA28, a gamma-interferon-inducible protein activator of the 20S proteasome.";
RL FEBS Lett. 366:37-42(1995).
CC -!- FUNCTION: Implicated in immunoproteasome assembly and required for efficient antigen processing. The PA28 activator complex enhances the generation of class I binding peptides by altering the cleavage pattern of the proteasome.
CC -!- SUBUNIT: HETERODIMER OF PSME1 AND PSME2, WHICH FORMS A HEXADIMERIC RING.
CC -!- INDUCTION: BY interferon gamma.
CC -!- SIMILARITY: BELONGS TO THE PA28 FAMILY.

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CC -----
DR EMBL: D45250; BAA08207.1; -
DR HSSP: Q06323; LAVO.
DR InterPro: IPR003185; PA28_alpha.
DR InterPro: IPR003186; PA28_beta.
DR Pfam: PF02251; PA28_alpha; 1.
DR Pfam: PF02252; PA28_beta; 1.
KW Proteasome; Interferon induction.
SQ SEQUENCE 238 AA; 26857 MW; AFA0F013CECE1CD3 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 238;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 776 EXTLALL 782
Db 97 EXTLALL 103

RESULT 42

PSE2_MOUSE ID_PSE2_MOUSE STANDARD; PRT; 239 AA.

AC P97372; O35562; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Proteasome activator complex subunit 2 (proteasome activator 28-beta subunit) (PA28beta) (PA28b) (Activator of multicatalytic protease subunit 2) (11S regulator complex beta subunit) (REG-beta).
DE subunit 2) (11S regulator complex beta subunit) (REG-beta).
GN (PSME2 OR PA28B1) AND (PSME2B OR PA28B2).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6; TISSUE=Spleen;
RC MEDLINE=97364691; PubMed=9218537;
RA Kandil E., Kohda K., Ishibashi T., Tanaka K., Kasahara M.;
RT "PA28 subunits of the mouse proteasome: primary structures and chromosomal localization of the genes.";
RL Immunogenetics 46:337-344(1997).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=B10.
RC MEDLINE=97306277; PubMed=9162094;
RA Jiang H., Monaco J.U.;

RT "Sequence and expression of mouse proteasome activator PA28 and the related autoantigen Ki.";
RL Immunogenetics 46:93-98(1997).
RN [3]
RP SEQUENCE FROM N.A.
RP STRAIN=129/SvJ;
RC MEDLINE=98250122; PubMed=9590240;
RA Kohda K., Ishibashi T., Shimbara N., Tanaka K., Matsuda Y., Kasahara M.;
RT "Characterization of the mouse PA28 activator complex gene family: complete organizations of the three member genes and a physical map of the approximately 150-kb region containing the alpha- and beta-subunit genes.";
RL J. Immunol. 160:4923-4935(1998).
RN [4]
RP SEQUENCE FROM N.A. (PSME2 AND PSME2B).
RP STRAIN=129.
RC MEDLINE=99115499; PubMed=9914329;
RA Li Y., Chambers J., Pang J., Ngo K., Peterson P.A., Leung W.P., Yang Y.;

RT "Characterization of the mouse proteasome regulator PA28b gene.";
RL Immunogenetics 49:149-157(1999).
RN [5]
RP SEQUENCE FROM N.A. (PSME2B).
RP STRAIN=129/SvJ;
RC MEDLINE=99241037; PubMed=10222192;
RA Zaiss D.M., Klotzel P.M.;
RT "A second gene encoding the mouse proteasome activator PA28beta subunit is part of a LINE1 element and is driven by a LINE1 promoter.";
RL J. Mol. Biol. 287:829-835(1999).
RN [6]
RP SEQUENCE FROM N.A.
RP STRAIN=129/SvJ;
RC MEDLINE=21243724; PubMed=11345588;
RA Yawata M., Murata S., Tanaka K., Ishigatsubo Y., Kasahara M.;

RT "Nucleotide sequence analysis of the ~35-kb segment containing interferon-gamma-inducible mouse proteasome activator genes.";
RL Immunogenetics 53:119-129(2001).
RN [7]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Embryo;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I., Saio T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner W., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Glass C., King B., Kochiwa H., Kuehl P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,

FT ACT_SITE 75 75 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 123 123 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 218 218 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 60 76 BY SIMILARITY.
 FT DISULFID 157 224 BY SIMILARITY.
 FT DISULFID 188 204 BY SIMILARITY.
 FT DISULFID 214 245 BY SIMILARITY.
 SQ SEQUENCE 271 AA; 28885 MW; 125C783B857B71E3 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 271;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 219 SNSRTYR 225
 |||||
 Db 78 SNSRTYR 84

RESULT 44
 FPG_OCEIH STANDARD; PRT; 280 AA.
 AC 08EP6;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DE Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23) (Fapy-DNA glycosylase).
 GN MUTM OR FPG OR OB2162.
 OS Oceanobacillus iheyensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
 OX NCBI_TaxID=18210;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
 RX MEDLINE=22220767; PubMed=12235376;
 RA Takami H., Takaki Y., Uchiyama I.;
 RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
 RT Rides and its unexpected adaptive capabilities to extreme
 RT environments";
 RL Nucleic Acids Res. 30:3927-3935(2002).
 CC -1- FUNCTION: This enzyme may play a significant role in processes
 CC leading to recovery from mutagenesis and/or cell death by
 CC alkylating agents (By similarity).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of DNA containing ring-opened N(7)-
 CC methylguanine residues, releasing 2,6-diamino-4-hydroxy-5-(N-
 CC methyl)formamidopyrimidine.
 CC -1- Cofactor: Binds 1 zinc ion (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE FPG FAMILY.
 CC -----
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 CC -----
 CC EMBL: AP004600; BAC14118.1; -.
 DR HAMAP: MF_00103; -; 1.
 DR Pfam: PF01149; Fapy_DNA_glyco; 1.
 DR ProDom: PD003680; Fapy_DNA_glyco; 1.
 DR TIGRFAMs: TIGR00577; fpg; 1.
 DR PROSITE: PS01242; FPG_1
 KM DNA repair; Hydrolyase; Glycosidase; Zinc; Zinc-finger;
 KM Complete proteome.
 FT ZN FING 249 272 POTENTIAL.
 SQ SEQUENCE 280 AA; 32235 MW; 8E83A26CB786C286 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 280;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 413 SKLSKOE 419

Db 193 SKLSKOE 199
 |||||

RESULT 45
 LICH_VIBCH STANDARD; PRT; 284 AA.
 ID LICH_VIBCH 007350;
 AC 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lipase chaperone (Lipase foldase) (Lipase helper protein)
 DE (Lipase activator protein) (Lipase modulator).
 GN LIPB OR VCA0222.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor O17 / Serotype O1;
 RA Manning P.A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Ginn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
 RA McDonald L., Ueberback T., Fleischmann R.D., Niemann W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae";
 RL Nature 406:477-483(2000).
 CC -1- FUNCTION: SEEMS TO BE ACTING IN THE FOLDING OF THE EXTRACELLULAR
 CC LIPASE DURING ITS PASSAGE THROUGH THE PERIPLASM (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Inner membrane-anchored (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE LIPASE CHAPERONE FAMILY.
 CC -----
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 CC -----
 CC EMBL: Y00557; CAA68635.1; -.
 DR EMBL: AE004362; AAF96134.1; -.
 DR PIR: D82486; D82486.
 DR TIGR: VCA0222; -.
 DR InterPro: IPR004961; Lipase_chap.
 DR Pfam: PF03280; Lipase_chap.1
 KM Lipid degradation; Chaperone; Transmembrane; Periplasmic;
 KM Inner membrane; Complete proteome.
 FT TRASNEM 4 24 POTENTIAL.
 SQ SEQUENCE 284 AA; 32561 MW; B0064285C85C0BC7 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 284;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 NELSASE 204
 |||||
 Db 246 NELSASE 252

RESULT 46
 TPML_BIOGL STANDARD; PRT; 284 AA.
 ID TPML_BIOGL

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AC 242636;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tropomyosin 1 (TMI) (BG39).
OS Biomphalaria glabrata (Bloodfluke planorb).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Biomphalaria.
OX NCBI_TaxID=6526;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91218806; PubMed=2090946;
RA Dissous C., Torpier G., Duvaux-Miret O., Capron A.;
RT "Structural homology of tropomyosins from the human trematode
RT Schistosoma mansoni and its intermediate host Biomphalaria
RT glabrata."
RL Mol. Biochem. Parasitol. 43:245-255(1990).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE
CC EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.
CC -1- SIMILARITY: BELONGS TO THE TROPOMYOSIN FAMILY.
CC -----
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CC -----
CC EMBL; M85199; AAA27817.1; -.
CC PIR; A33085; A33085.
CC InterPro; IPR002017; Spectrin.
CC InterPro; IPR000533; Tropomyosin.
CC Pfam; PF00261; Tropomyosin.1.
CC PRINTS; PR00194; TROPOMYOSIN.
CC Coiled coil; Repeat; Multigene family.
CC SEQUENCE 284 AA; 32716 MW; 13735417CE49A8 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 728 EAOLKEA 734
DB 145 EAOLKEA 151

RESULT 47
TPM2 BIOGL STANDARD; PRT; 284 AA.
AC P43689;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tropomyosin 2 (TMI).
OS Biomphalaria glabrata (Bloodfluke planorb).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Biomphalaria.
OX NCBI_TaxID=6526;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Brazilian;
RA MEDLINE=93292622; PubMed=7685709;
RA Weston D.S., Kemp W.M.;
RT "Schistosoma mansoni: comparison of cloned tropomyosin antigens
RT shared between adult parasites and Biomphalaria glabrata."
RL Exp. Parasitol. 76:358-370(1993).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE
CC EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.
CC -1- SIMILARITY: BELONGS TO THE TROPOMYOSIN FAMILY.
CC -----

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CC -----
CC EMBL; M97554; AAA27816.1; -.
CC InterPro; IPR002017; Spectrin.
CC InterPro; IPR000533; Tropomyosin.
CC Pfam; PF00261; Tropomyosin.1.
CC PRINTS; PR00194; TROPOMYOSIN.
CC Coiled coil; Repeat; Multigene family.
CC SEQUENCE 284 AA; 32683 MW; 2E6103712D9B4C3 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 728 EAOLKEA 734
DB 145 EAOLKEA 151

RESULT 48
TPM2 TRICO STANDARD; PRT; 284 AA.
AC P15846;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tropomyosin, muscle.
OS Trichostrongylus colubriformis (Black scour worm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdida; Strongylida;
OC Trichostrongylidae; Trichostrongylinae;
OC Trichostrongylus.
OX NCBI_TaxID=6319;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90114326; PubMed=2514356;
RX Frenkel M.J., Savin K.W., Bakker R.E., Ward C.W.;
RA "Characterization of cDNA clones coding for muscle tropomyosin of the
RT nematode Trichostrongylus colubriformis."
RL Mol. Biochem. Parasitol. 37:191-200(1989).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=89339870; PubMed=2759773;
RX O'Donnell I.J., Dineen J.K., Wagland B., Letho S., Werkmeister J.A.,
RA Ward C.W.;
RT "A novel host-protective antigen from Trichostrongylus
RT colubriformis."
RL Int. J. Parasitol. 19:327-335(1989).
CC -1- FUNCTION: TROPOMYOSIN, IN ASSOCIATION WITH THE TROPONIN COMPLEX,
CC PLAYS A CENTRAL ROLE IN THE CALCIUM DEPENDENT REGULATION OF
CC STRIATED MUSCLE CONTRACTION.
CC -1- SUBUNIT: Homodimer.
CC -1- DEVELOPMENTAL STAGE: PRESENT IN L3 (THIRD STAGE), L4 AND ADULT
CC WORKS.
CC -1- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE
CC EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.
CC -1- SIMILARITY: BELONGS TO THE TROPOMYOSIN FAMILY.
CC -----
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CC -----
CC EMBL; J04669; AAA30103.1; -.
CC InterPro; IPR000533; Tropomyosin.

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DR Pfam, PF00261, Tropomyosin, 1.
 DR PRINTS, PR00194, TROPOMYOSIN.
 DR PROSITE, PS00326, TROPOMYOSIN, 1.
 KW Muscle protein; Coiled coil; Repeat.
 FT DOMAIN 1 284 T -> R (IN REF. 2).
 FT CONFLICT 277 277 COILED COIL.
 SQ SEQUENCE 284 AA, 33050 MW, 230573B1EE2449C1 CRC64;
 Query Match 0.9%; Score 7; DB 1; Length 284;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 728 EAQKKEA 734
 Db 145 EAQKKEA 151
 RESULT 49
 ID LECT1 CLALU STANDARD; PRT; 293 AA.
 AC 039528;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Agglutinin I precursor (ClAI) (LecClAI).
 OS Cladastis lutea (Yellow wood).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosid 1; Fabales; Fabaceae; Papilionoideae; Sophoreae; Cladastis.
 NCBI_TaxID=38412;
 RN (1)
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 36-55 AND 162-181.
 RX MEDLINE=66123235; PubMed=8534854;
 RA TISSUE-Bark;
 RA van Damme E.J.M., Barre A., Bemer V., Van Leuven F.,
 RA Peumans W.J.;
 RA "A lectin and a lectin-related protein are the two most prominent
 RT proteins in the bark of yellow wood (Cladastis lutea).";
 RL Plant Mol. Biol. 29:579-598(1995).
 CC -1- FUNCTION: N-MANNAN/GALACTOSE BINDING BARK LECTIN.
 CC -1- FUNCTION: BARK LECTINS ARE STORAGE PROTEIN THAT PROBABLY MAINTAINS
 CC STOCKS OF NITROGEN DURING DORMANT PERIOD. SELF-AGGREGATABLE
 CC MOLECULES THAT CAN BIND THEIR OWN CARBOHYDRATE SIDE CHAINS. THEY
 CC COULD ALSO PLAY A ROLE IN THE PLANT'S DEFENCE AGAINST PHYTOPHAGOUS
 CC INVERTEBRATES OR HERBIVOROUS HIGHER ANIMALS.
 CC -1- SUBUNIT: HOMOTETRAMER OF FOUR 32 KDa MONOMERS WHICH ARE POST-
 CC TRANSLATIONALLY CLEAVED INTO A TWO SUBUNITS: A AND B.
 CC -1- MISCELLANEOUS: BINDS ONE MANGANESE (OR OTHER TRANSITION METAL) ION
 CC AND ONE CALCIUM ION. THE METAL IONS ARE ESSENTIAL FOR THE
 CC SACCHARIDE-BINDING AND CELL-AGGLUTININATING ACTIVITIES (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: TO OTHER LEGUMINOUS LECTINS.
 CC -----
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 CC -----
 CC EMBL, U21958; AAC49136.1; -
 CC PIR, S66356; S66356.
 CC HSSP, P19588; ILUL.
 DR InterPro, IPR000985; Lectin_legA.
 DR InterPro, IPR001220; Lectin_legB.
 DR Pfam, PF00138; lectin_legA; 1.
 DR Pfam, PF00139; lectin_legB; 1.
 DR ProDom, PD000671; Lectin_legA; 1.
 DR ProDom, PD000711; Lectin_legB; 1.
 DR ProSITE, PS00307; LECTIN_LEGME_BETA; 1.
 DR PROSITE, PS00308; LECTIN_LEGME_ALPHA; 1.
 KW Lectin; Calcium; Manganese; Glycoprotein; Signal; Mannose-Binding.

FT SIGNAL 1 35
 FT CHAIN 36 161
 FT CHAIN 162 293
 FT METAL 171 171
 FT METAL 173 173
 FT METAL 175 175
 FT METAL 177 177
 FT METAL 181 181
 FT METAL 186 186
 FT CARBOHYD 64 64
 FT CARBOHYD 152 152
 FT CARBOHYD 162 162
 FT CONFLICT 47 47
 FT CONFLICT 162 162
 SQ SEQUENCE 293 AA; 32128 MW; EDBBD3FF5FA3C6C CRC64;
 Query Match 0.9%; Score 7; DB 1; Length 293;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 424 TITAKKE 430
 Db 279 TITAKKE 285
 RESULT 50
 ID TAL_BUCAP STANDARD; PRT; 316 AA.
 AC 08KA27;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transaldolase (EC 2.2.1.2).
 DE TAL OR BUSG085.
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 NCBI_TaxID=98794;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22084549; PubMed=12089438;
 RA Tamas I., Klasson L., Canhaeck B., Naeslund A.K., Eriksson A.-S.,
 RA Werngren J.J., Sandstrom J.P., Moran N.A., Anderson S.G.E.;
 RT "50 million years of genomic stasis in endosymbiotic bacteria.";
 RL Science 296:2376-2379(2002).
 CC -1- FUNCTION: Transaldolase is important for the balance of
 CC metabolites in the pentose-phosphate pathway (By similarity).
 CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glucose 6-phosphate
 CC 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
 CC -1- PATHWAY: Pentose phosphate pathway; nonoxidative part.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.
 CC -----
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 CC -----
 CC EMBL, AE014084; AAM67655.1; -
 CC HAMAP, MF_00492; -1.
 DR InterPro, IPR001585; Transaldolase.
 DR InterPro, IPR004730; Transaldolase_AB.
 DR Pfam, PF00923; Transaldolase; 1.
 DR TIGRfam, TIGR00874; talAB; 1.
 DR PROSITE, PS01054; TRANSALDOLASE_1; 1.
 DR PROSITE, PS00958; TRANSALDOLASE_2; FALSE_NEG.
 KW Transferrase; Pentose shunt; Complete proteome.
 FT ACT SITE 131 131
 FT ACT SITE 131 131
 SQ SEQUENCE 316 AA; 35825 MW; 2BF7A4E4AC3425B0 CRC64;

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Query Match          0.9%; Score 7; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      390 EEKGSR 396
      |||||
Db      119 EEKGSR 125

RESULT 51
PTPA_RABIT STANDARD; PRT; 323 AA.
ID PTPA_RABIT
AC Q28717;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein phosphatase 2A, regulatory subunit B' (PP2A, subunit B', PR53
DE isoform) (phosphotyrosyl phosphatase activator) (PTPA).
GN PPP2R4 OR PTPA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skletal muscle;
RX MEDLINE=94253154; PubMed=8195217;
RA Cayla X., Van Hoof C., Bosch W., Waalkens E., Peeters B.,
RA Merlevede W., Goris J.;
RT "Molecular cloning, expression, and characterization of PTPA, a
RT protein that activates the tyrosyl phosphatase activity of protein
RT phosphatase 2A."
RT J. Biol. Chem. 269:15668-15675(1994).
RU
CC - FUNCTION: REVERSIBLY STIMULATES THE VARIABLE PHOSPHOTYRSL
CC PHOSPHATASE ACTIVITY OF PP2A CORE HETERODIMER IN PRESENCE OF ATP
CC AND MG(2+) (IN VITRO).
CC - SUBUNIT: ASSOCIATES WITH PP2A HETERODIMERIC CORE ENZYME, COMPOSED
CC OF A 36 KDA CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 KDA CONSTANT
CC REGULATORY SUBUNIT (PR53 OR SUBUNIT A).
CC - TISSUE SPECIFICITY: Widely expressed.
CC -----
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CC -----
DR EMBL: X73479; CAA51874.1; -.
DR PIR: B54021; B54021.
DR InterPro: IPR004327; PhosTyR_phatase.ac.
DR Pfam: PF03095; PTPA; 1.
SQ SEQUENCE 323 AA; 36587 MW; 808F404934F3D85 CRC64;

Query Match          0.9%; Score 7; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      776 EKLALL 782
      |||||
Db      75 EKLALL 81

RESULT 52
FIP1_YEAST STANDARD; PRT; 327 AA.
ID FIP1_YEAST
AC P45976;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE FIP1 protein.
GN FIP1 OR YJR093C OR J1911.

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OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95254648; PubMed=7736590;
RA Preker P.J., Lingner J., Manvielle-Sebastia L., Keller W.;
RT "The FIP1 gene encodes a component of a yeast pre-mRNA
RT polyadenylation factor that directly interacts with poly(A)
RT polymerase."
RT Cell 81:379-389(1995).
RU
CC [2]
CC SEQUENCE FROM N.A.
CC Ramezani Rad M., Kirchbach L., Hollenberg C.P.;
CC Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: PRE-MRNA POLYADENYLATION FACTOR THAT DIRECTLY INTERACTS
CC WITH POLY(A) POLYMERASE. SEEMS TO TETHER PAPI TO THE CLEAVAGE
CC FACTOR I. INTERACTS WITH RNA14.
CC - SUBCELLULAR LOCATION: Nuclear.
CC - SIMILARITY: TO S. POMBE SPAC2267.10.
CC -----
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CC -----
DR EMBL: X83796; CAA58727.1; -.
DR EMBL: Z49593; CAA89621.1; -.
DR PIR: A56545; A56545.
DR SCD: S0003853; FIP1.
DR GO: GO:0006379; P:RNA cleavage; IDA.
DR GO: GO:0006378; P:RNA polyadenylation; IDA.
DR Pfam: PF05182; Fip1; 1.
KW mRNA processing; Nuclear protein.
FT DOMAIN 61 80 ASP-RICH (ACIDIC).
FT DOMAIN 284 318 PRO-RICH.
FT DOMAIN 258 266 POLY-ASN.
SQ SEQUENCE 327 AA; 35777 MW; 471CA2B0CDF99D0A CRC64;

Query Match          0.9%; Score 7; DB 1; Length 327;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      709 PVEETPA 715
      |||||
Db      51 PVEETPA 57

RESULT 53
KAPR_DICDI STANDARD; PRT; 327 AA.
ID KAPR_DICDI
AC P05987;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CAMP-dependent protein kinase regulatory chain.
DE PKAR.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87092396; PubMed=3467359;
RA Mutzel R., Lacombe M.-E., Simon M.-N., de Gunzburg J., Veron M.;
RT "Cloning and cDNA sequence of the regulatory subunit of CAMP-dependent
RT protein kinase from Dictyostelium discoideum."
RT Proc. Natl. Acad. Sci. U.S.A. 84:6-10(1987).
RU [2]
RN MUTANT RDEC.

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RX MEDLINE-92186968; PubMed1312226;
RA Simon M.-N., Pellegrini O., Veron M., Kay R.R.;
RT "Mutation of protein kinase A causes heterochronic development of
RL Dictyostelium.";
RL Nature 356:171-172 (1992).
CC -1- SUBUNIT: IN DICTYOSTELIUM THE HOLOENZYME IS A DIMER COMPOSED OF
CC A REGULATORY (R) AND A CATALYTIC (C) SUBUNIT. IN THE PRESENCE OF
CC CAMP IT DISSOCIATES INTO THE ACTIVE C SUBUNIT AND AN R MONOMER.
CC (IN OTHER EUKARYOTES THE HOLOENZYME IS A TETRAMER COMPOSED OF 2
CC REGULATORY (R) & 2 CATALYTIC (C) SUBUNITS. IN THE PRESENCE OF CAMP
CC IT DISSOCIATES INTO ACTIVE MONOMERIC C SUBUNITS AND AN R DIMER).
CC -1- DOMAIN: LACKS THE N-TERMINAL DOMAIN REQUIRED FOR THE ASSOCIATION
CC OF REGULATORY SUBUNIT INTO DIMERS IN OTHER EUKARYOTES.
CC -1- PTM: THE PSEUDOPHOSPHORYLATION SITE BINDS TO THE SUBSTRATE-
CC BINDING REGION OF THE CATALYTIC CHAIN BUT IS NOT PHOSPHORYLATED.
CC THE PHYSIOLOGICAL SIGNIFICANCE OF PHOSPHORYLATIONS BY OTHER
CC KINASES IS UNCLEAR.
CC -1- MISCELLANEOUS: IN DICTYOSTELIUM EACH R SUBUNIT CARRIES ONLY 1
CC HIGH-AFFINITY CAMP BINDING SITE (2 IN OTHER EUKARYOTES).
CC -1- MISCELLANEOUS: IN REBC MUTANTS AGGREGATION IS FOLLOWED ABRUPTLY BY
CC THE MATURATION OF SPORE AND STALK CELLS. THIS IS A DUE TO
CC MUTATION(S) IN THE R SUBUNIT. THE MUTANT R SUBUNIT BINDS CAMP BUT
CC INHIBITS POORLY THE ENZYMATIC ACTIVITY OF THE C SUBUNIT.
CC -1- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CAMP-DEPENDENT KINASE REGULATORY CHAIN
CC FAMILY.
CC -----
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CC -----
CC EMBL: M15081; AAA3236.1; -.
CC PIR: A29076; OKDRC.
CC DR HSSP: P00514; IAPK.
CC DR DICTYDB: D02006; PKAR.
CC DR InterPro: IPR002373; CAMP_kin.
CC DR Pfam: PF00027; cAMP_binding; 2.
CC DR PRINTS: PR00103; CAMPKINASE.
CC DR SMART: SMO0100; cAMP; 2.
CC DR PROSITE: PS00888; cAMP_BINDING_1; 2.
CC DR PROSITE: PS00889; cAMP_BINDING_2; 2.
CC DR PROSITE: PS00889; cAMP_BINDING_3; 2.
CC DR PROSITE: PS00442; cAMP_BINDING; 2.
CC KW CAMP-binding; Phosphorylation; Repeat.
CC FT DOMAIN 1 65 DIMERIZATION AND PHOSPHORYLATION.
CC FT SITE 27 31 PSEUDOPHOSPHORYLATION MOTIF.
CC FT NP_BIND 66 188 CAMP (HIGH AFFINITY).
CC FT NP_BIND 189 327 CAMP (LOW AFFINITY).
CC FT REPEAT 66 188 1.
CC FT REPEAT 189 327 2.
CC FT MOD_RES 32 32 PHOSPHORYLATION (BY SIMILARITY).
CC FT BINDING 136 136 CAMP.
CC FT BINDING 145 145 CAMP.
CC FT BINDING 262 262 CAMP.
CC FT BINDING 271 271 CAMP.
CC FT VARIANT 30 30 A -> T (IN REBC MUTANT).
CC FT VARIANT 327 AA; 36836 MW; D76BF40E3FE22CA1 CRC64;
CC SQ SEQUENCE

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Query Match 0.9%; Score 7; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 TEKVEAQ 730
 |||||
 DB 12 TEKVEAQ 18

RESULT 54
 G3P2_AGABI

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ID G3P2_AGABI STANDARD; PRT; 338 AA.
AC P32636;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase 2 (EC 1.2.1.12) (GAPDH 2).
GN GPD2.
OS Agaricus bisporus (Common mushroom).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Agaricaceae; Agaricus.
OX NCBI_Taxid=5341;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Hors U3;
RX MEDLINE-93113715; PubMed1473176;
RA Harnsen M.C., Schuren F.H.J., Mouska S.M., van Zuijen C.M., Punt P.J.,
RA Wessels J.G.H.;
RT "Sequence analysis of the glyceraldehyde-3-phosphate dehydrogenase
RT genes from the basidiomycetes Schizophyllum commune, Phanerochaete
RT chrysosporium and Agaricus bisporus.";
RL Curr. Genet. 22:447-454(1992).
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC -1- PATHWAY: Second phase of glycolysis; first step.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
CC dehydrogenase family.
CC -----
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CC -----
CC EMBL: M81728; AAA32634.1; -.
CC PIR: S26976; S26976.
CC DR HSSP: P00357; 4GPD.
CC DR InterPro: IPR000173; GAP_dhndrogenase.
CC DR Pfam: PF00044; gpdh; 1.
CC DR Pfam: PF02800; gpdh_C; 1.
CC DR PRINTS: PR00078; G3PDHRCGNASE.
CC DR TIGRfams: TIGR01534; GAPDH-1; 1.
CC DR PROSITE: PS00071; GAPDH; 1.
CC KW Glycolysis; Oxidoreductase; NAD; Multigene family.
CC FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
CC FT ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
CC SQ SEQUENCE 338 AA; 36570 MW; 3381DBBF73B84469 CRC64;

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Query Match 0.9%; Score 7; DB 1; Length 338;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 621 TVEVNGK 627
 |||||
 DB 57 TVEVNGK 63

RESULT 55
 G3P_SCHMA
 ID G3P_SCHMA STANDARD; PRT; 338 AA.
 AC P20287;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH) (Major
 DE larval surface antigen) (P-37).
 OS Schistosoma mansoni (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.


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OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Puerto Rican;
RX MEDLINE=90063470; PubMed=2584935;
RA Gondot-Crozal V., Gallot D., Djabali M., Dessein A.J.;
RT "The major parasite surface antigen associated with human resistance
  to schistosomiasis is a 37-kD glyceraldehyde-3P-dehydrogenase.";
RL J. Exp. Med. 170:2065-2080(1989)
CC - FUNCTION: THIS ANTIGEN IS ASSOCIATED WITH HUMAN RESISTANCE TO
  SCHISTOSOMIASIS.
CC - CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
  NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC - PATHWAY: Second phase of glycolysis; first step.
CC - SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
  dehydrogenase family.
CC PIR: JLO121; JLO121.
DR HSSP; P56649; IDS.
DR InterPro; IPR000173; GAPDH-1.
DR Pfam; PF00044; gpdh; 1.
DR Pfam; PF02800; gpdh; 1.
DR PRINTS; PR00078; G3PDHGRNASE.
DR TIGRFPMS; TIGR01534; GAPDH-1; 1.
DR PROSITE; PS00071; GAPDH; 1.
KW Glycolysis; Oxidoreductase; NAD; Antigen.
FT BINDING 153 153
FT ACT_SITE 180 180
FT SEQUENCE 338 AA; 36377 MW; 3DAC70E93C1E24BE CRC64;
SQ
Query Match 0.9%; Score 7; DB 1; Length 338;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 509 EYTEDV 515
Db 276 EYTEDV 282

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RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Oucello B., Goldman B.S., Cao Y., Akenazi M., Halling C., Mullin L.,
RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
  Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
CC - CATALYTIC ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen + 4
  CO(2).
CC - PATHWAY: Porphyrin biosynthesis.
CC - SUBCELLULAR LOCATION: Cytoplasmic (probable).
CC - SIMILARITY: BELONGS TO THE UROPORPHYRINOGEN DECARBOXYLASE FAMILY.
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CC -----
DR EMBL; AE009230; AAU43816.1; -
DR EMBL; AE008196; AAK8546.1; -
DR PIR; A97699; A97699.
DR PIR; AB2925; AB2925.
DR HAMAP; MF_00218; -; 1.
DR InterPro; IPR006361; Heme.
DR InterPro; IPR000257; Uro. decarboxyls.
DR Pfam; PF01208; URO-D; 1.
DR ProDom; PD003225; Uro. decarboxyls; 1.
DR TIGRFPMS; TIGR01464; Heme; 1.
DR PROSITE; PS00906; UROD_1; 1.
DR PROSITE; PS00907; UROD_2; 1.
DR Lysase; Decarboxylase; Porphyrin biosynthesis; Complete proteome.
KW SEQUENCE 344 AA; 37173 MW; 96351DE3393ECB46 CRC64;
SQ
Query Match 0.9%; Score 7; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 776 EKLALL 782
Db 174 EKLALL 180

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RESULT 56
DCUP_AGRS STANDARD; PRT; 344 AA.
AC Q8UBJ6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).
GN HEME OR ATU2835 OR AGR C 5140.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Secubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen Y., Wood G.E., Almeida N.F., Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Boyee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavina T., Levy R., Li M.-J., McClelland E., Palmeri A.,
RA Raymond C., Rouse G., Senghinmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Petry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
  C58.";
RL Science 294:2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;

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RA PTTPA HUMAN STANDARD; PRT; 358 AA.
AC Q15257; Q15258; Q9BUK1; Q9NNZ7; Q9NNZ8; Q9NNZ9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein phosphatase 2A, regulatory subunit B' (PP2A, subunit B', PR53
  isoform) (Phosphotyrosyl phosphatase activator) (PTPA).
GN PP2R4 OR PTPA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metazoa; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE (ISOFORM 1).
RC TISSUE=Heart;
RX MEDLINE=94253154; PubMed=8195217;
RA Cayla X., Van Hoof C., Bosch M., Waelkens E., Peeters B.,
RA Merlevede W., Goris J.;
RT "Molecular cloning, expression, and characterization of PTPA, a
  protein that activates the tyrosyl phosphatase activity of protein
  phosphatase 2A.";
RL J. Biol. Chem. 269:15668-15675 (1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).

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RC TISSUE=Blood;
 RX MEDLINE=96015056; PubMed=8530035;
 RA Van Hoof C., Aly M., Garcia A., Cayla X., Cassiman J., Merlevede W.,
 RA Goris J.;
 RT "Structure and chromosomal localization of the human gene of the
 RT phosphotyrosyl phosphatase activator (PTPA) of protein phosphatase
 RT 2A.";
 RL Genomics 28:261-272(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4).
 RX MEDLINE=20341117; PubMed=10880964;
 RA Janssens V., van Hoof C., Martens E., de Baere I., Merlevede W.,
 RA Goris J.;
 RT "Identification and characterization of alternative splice products
 RT encoded by the human phosphotyrosyl phosphatase activator gene.";
 RL Eur. J. Biochem. 267:4406-4413(2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
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 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -I- FUNCTION: REVERSIBLY STIMULATES THE VARIABLE PHOSPHOTYROSYL
 CC PHOSPHATASE ACTIVITY OF PP2A CORE HETERODIMER IN PRESENCE OF ATP
 CC AND MG(2+) (IN VITRO).
 CC -I- SUBUNIT: ASSOCIATES WITH PP2A HETERODIMERIC CORE ENZYME, COMPOSED
 CC OF A 36 KDA CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 KDA CONSTANT
 CC REGULATORY SUBUNIT (PR65 OR SUBUNIT A).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=2; Synonyms=Beta;
 CC IsoId=Q15257-1; Sequence=Displayed;
 CC Name=1; Synonyms=Alpha;
 CC IsoId=Q15257-2; Sequence=VSP_005123;
 CC Name=3; Synonyms=Delta;
 CC IsoId=Q15257-3; Sequence=VSP_005122;
 CC Name=4; Synonyms=Epsilon;
 CC IsoId=Q15257-4; Sequence=VSP_005124;
 CC -I- TISSUE SPECIFICITY: Widely expressed.
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 DR EMBL; X86431; CAA60163.1; JOINED.
 DR EMBL; X86432; CAA60163.1; JOINED.
 DR EMBL; X86433; CAA60163.1; JOINED.
 DR EMBL; X86434; CAA60163.1; JOINED.
 DR EMBL; X86435; CAA60163.1; JOINED.
 DR EMBL; X86436; CAA60163.1; JOINED.
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 DR EMBL; X86428; CAA60163.1; JOINED.
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 DR EMBL; X86433; CAA60163.1; JOINED.
 DR EMBL; X86434; CAA60163.1; JOINED.
 DR EMBL; X86435; CAA60163.1; JOINED.
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 DR EMBL; X86437; CAA60163.1; JOINED.
 DR EMBL; X86438; CAA60163.1; JOINED.
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 DR EMBL; X86435; CAA60163.1; JOINED.
 DR EMBL; X86436; CAA60163.1; JOINED.
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 DR EMBL; X86428; CAA60163.1; JOINED.
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 DR EMBL; X86433; CAA60163.1; JOINED.
 DR EMBL; X86434; CAA60163.1; JOINED.
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 DR EMBL; X86437; CAA60163.1; JOINED.
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 DR EMBL; X86439; CAA60163.1; JOINED.
 DR EMBL; X86428; CAA60163.1; JOINED.
 DR EMBL; X86429; CAA60163.1; JOINED.
 DR EMBL; X86430; CAA60163.1; JOINED.
 DR EMBL; X86431; CAA60163.1; JOINED.
 DR EMBL; X86432; CAA60163.1; JOINED.
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 DR EMBL; X86435; CAA60163.1; JOINED.
 DR EMBL; X86436; CAA60163.1; JOINED.
 DR EMBL; X86437; CAA60163.1; JOINED.
 DR EMBL; X86438; CAA60163.1; JOINED.
 DR EMBL; X86439; CAA60163.1; JOINED.
 DR EMBL; X86428; CAA60163

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DE dehydratase (EC 4.2.1.51) (PDT)].
GN pHEA OR B2599 OR Z3891 OR EC53462 OR SF2659.
OS Escherichia coli.
OC Escherichia coli O157:H7, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxId=562, 83334, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=85134883; PubMed=6396419;
RA Hudson G.S., Davidson B.E.;
RT "Nucleotide sequence and transcription of the phenylalanine and
RL tyrosine operons of Escherichia coli K12.";
RN J. Mol. Biol. 180:1023-1051(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Coliado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubraman S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT -K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Morita T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kunara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [6]
RP SEQUENCE OF 1-50 FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=91072346; PubMed=2254312;
RA Gavini N., Davidson B.E.;
RT "pneao mutants of Escherichia coli have a defective pheA attenuator.";
RN J. Biol. Chem. 265:21532-21535(1990).
RN [7]
RP SEQUENCE OF 1-9 FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=79033820; PubMed=3602214;
RA Zurawski G.R., Brown K., Killingly D., Yanofsky C.;
RT "Nucleotide sequence of the leader region of the phenylalanine operon
RT of Escherichia coli";
RL Proc. Natl. Acad. Sci. U.S.A. 75:4271-4275(1978).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1-109.
RN SPECIES=E.coli;
RA Lee A.Y., Karplus P.A., Ganem B., Clardy J.;
RT "Atomic structure of the buried catalytic pocket of Escherichia coli
RT chorismate mutase.";
RL J. Am. Chem. Soc. 117:3627-3628(1995).
RN [10]
RP DOMAIN.
RC SPECIES=E.coli;
RX MEDLINE=96165805; PubMed=9497350;
RA Zhang S., Pohnert G., Kongsaree P., Wilson D.B., Clardy J.,
RA Ganem B.;
RT "Chorismate mutase-prephenate dehydratase from Escherichia coli: Study
RT of catalytic and regulatory domains using genetically engineered
RL proteins";
RN J. Biol. Chem. 273:6248-6253(1998).
RN [11]
RP -1- CATALYTIC ACTIVITY: Chorismate = prephenate.
RN -1- CATALYTIC ACTIVITY: Prephenate = phenylpyruvate + H(2)O + CO(2).
RN -1- PATHWAY: L-phenylalanine biosynthesis.
RN -1- SUBCELLULAR LOCATION: Cytoplasmic.
RN -1- SIMILARITY: TO OTHER PDT ENZYMES OR DOMAINS.
CC -----
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CC -----
DR EMBL: M10431; AAA2430.1; -
DR EMBL: AE000346; AAC75648.1; -
DR EMBL: D90887; BAA16482.1; -
DR EMBL: D90888; BAA16484.1; -
DR EMBL: AE005490; AAG57710.1; -
DR EMBL: AP002562; BAB36885.1; -
DR EMBL: M58024; AAA62784.1; -
DR EMBL: V00314; CAA23601.1; -
DR EMBL: AE015281; AAN44155.1; -
DR PIR: A30261; KMECPW.
DR PIR: F91061; F91061.
DR PDB: 1ECM; 01-DEC-95.
DR EcoGene: EG10707; pheA.
DR InterPro: IPR002701; Chorismate mut.
DR InterPro: IPR001086; Preph. dehydratase.
DR Pfam: PF01817; Chorismate_mut; 1.
DR Pfam: PF00800; PDT; 1.
DR PIRSF: PIRSF001500; Chor_mut_pdt_Ppr; 1.
DR PROSITE: PS00857; PREPHENATE DEHYDR 1; 1.
DR PROSITE: PS00858; PREPHENATE DEHYDR 2; 1.
KM Phenylalanine biosynthesis; Isomerase; Lyase; Multifunctional enzyme;
KM 3D-structure; Complete proteome.
FT DOMAIN 1 109 CHORISMATE MUTASE.
FT DOMAIN 110 285 PREPHENATE DEHYDRATASE.
FT DOMAIN 286 386 REGULATORY (PHE-BINDING).

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FT ACT_SITE 278 278 ESSENTIAL FOR PREPHENATE DEHYDRATASE
FT HELIX 7 42 ACTIVITY (POTENTIAL).
FT TURN 43 43
FT HELIX 49 65
FT TURN 66 67
FT HELIX 70 99
SQ SEQUENCE 386 AA; 43111 MW; 4B0960854C75A4F1 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 386;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 776 EKLALL 782
Db 19 EKLALL 25

RESULT 59
YHFX_ECOLI STANDARD; PRT; 387 AA.
AC P45550:
DT 01-NOV-1995 (rel. 32, Created)
DT 01-NOV-1995 (rel. 32, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Hypothetical protein yHfx.
GN YHFX OR B3381.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxId=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MC1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; U18997; AAA58178.1; -
CC DR EMBL; AE000413; AAC76406.1; -
CC DR PIR; H65132; H65132.
CC DR Ecocyc; E012919; yHfx.
CC DR Pfam; PF01168; Ala racemase N; 1.
CC KW Hypothetical protein; Complete proteome.
CC SQ SEQUENCE 387 AA; 42294 MW; EEF7881339ED5971 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 387;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 775 AEKLAL 781
Db 70 AEKLAL 76

RESULT 60
PGK_THETN STANDARD; PRT; 394 AA.
AC Q8R965;
DT 28-FEB-2003 (rel. 41, Created)
DT 28-FEB-2003 (rel. 41, Last sequence update)

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DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Phosphoglycerate kinase (EC 2.7.2.3).
GN PGK OR TTE1761.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxId=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
CC -1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-
CC phospho-D-glyceroyl phosphate.
CC -1- PATHWAY: Second phase of glycolysis; second step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the phosphoglycerate kinase family.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; AE013129; AAM24955.1; -
CC DR HAMAP; MF_00145; -
CC DR InterPro; IPR001576; PGK.
CC DR Pfam; PF00162; PGK; 1.
CC DR ProSITE; PS00111; PGK; 1.
CC KW Transferrase; Kinase; Glycolysis; Complete proteome.
CC SQ SEQUENCE 394 AA; 42816 MW; 983EA95959C240A32 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 394;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 593 GDSAAI 599
Db 351 GDSAAI 357

RESULT 61
PGK_CHLITE STANDARD; PRT; 397 AA.
AC Q8KAE1;
DT 15-SEP-2003 (rel. 42, Created)
DT 15-SEP-2003 (rel. 42, Last sequence update)
DT 15-SEP-2003 (rel. 42, Last annotation update)
DE Phosphoglycerate kinase (EC 2.7.2.3).
GN PGK OR CT2222.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxId=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TUS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., Deboy R., Gwin M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nierman W.C., Feldblum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TUS, a

```

RT photosynthetic, anaerobic, green-sulfur bacterium";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
 CC -1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glycerol phosphate.
 CC -1- PATHWAY: Second phase of glycolysis; second step.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- SIMILARITY: Belongs to the phosphoglycerate kinase family.
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 CC -----
 CC EMBL: AE012967; AAM73438.1; -.
 CC TIGR: CT2222; -.
 CC HAMAP: MF_00145; -; 1.
 CC InterPro: IPR001576; PGK.
 CC Pfam: PF00162; PGK; 1.
 CC PRINTS: PR00477; PHGLYCKINASE.
 CC PROSITE: PS00111; PGLYCERATE_KINASE; 1.
 CC KMW: Transferase; Kinase; Glycolysis; Complete proteome.
 SQ SEQUENCE 397 AA; 42289 MW; 375A08041F0224A7 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 397;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 593 GDSAAAI 599
 |||||
 Db 355 GDSAAAI 361

RESULT 62
 IF5_YEAST STANDARD; PRT; 405 AA.
 AC P38F31;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Eukaryotic translation initiation factor 5 (eIF-5).
 GN TIF5 OR YPR041W OR YP1085.05.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 19-30; 326-340 AND 363-377.
 RC STRAIN=X2180 / ATCC 26109;
 RX MEDLINE=93252941; PubMed=8486705;
 RA Chakravarti D., Maitra U.;
 RT "Eukaryotic translation initiation factor 5 from Saccharomyces cerevisiae. Cloning, characterization, and expression of the gene encoding the 45346-Da protein.";
 RL J. Biol. Chem. 268:10524-10533(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL125-2B;
 RX MEDLINE=98398050; PubMed=9730282;
 RA Maciejewicz-Staniszewska B., Skala J., Jasinski M., Grenson M.,
 RA Goffeau A., Ulaszewska S.;
 RT "Functional analysis of three adjacent open reading frames from the right arm of yeast chromosome XVI.";
 RL Yeast 14:1027-1039(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX MEDLINE=9731371; PubMed=9169875;
 RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansoorge W.,
 RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

RA Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
 RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
 RA Dietrich F.S., Dilius H., Dipolo T., Dubois E., Duesterhoeft A.,
 RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
 RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
 RA Huntje-Smith S., Hyman R., Johnston M., Kaiman S., Kleine K.,
 RA Komp C., Kurdi O., Laskhary D., Lew H., Lin A., Lin D., Louis E.J.,
 RA Marathe R., Messing R.F., Mewes H.-W., Mirzaiati S., Moestl D.,
 RA Mueller-Auer S., Namath A., Newlich U., Oefner P., Pearson D.,
 RA Petel F.X., Pohl T.M., Purnelle D., Schaefer M., Scharfe M.,
 RA Scherens B., Schramm S., Schroeder M., Scluz A.M., Tettelin H.,
 RA Uristarsazu L.A., Ushinsky S., Viereckels F., Vissers S., Voss H.,
 RA Walsh S.V., Wambut R., Wang Y., Wedler E., Wedler H., Winnett E.,
 RA Zhong W.W., Zollner A., Vo D.H., Hani J.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
 RL Nature 387:103-105(1997).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF GTP BOUND TO THE 40S RIBOSOMAL INITIATION COMPLEX (40S.MRNA.MET-TRNA[Met].EIF-2.GTP) WITH THE SUBSEQUENT JOINING OF A 60S RIBOSOMAL SUBUNIT RESULTING IN THE RELEASE OF EIF-2 AND THE GUANINE NUCLEOTIDE. THE SUBSEQUENT JOINING OF A 60S RIBOSOMAL SUBUNIT RESULTS IN THE FORMATION OF A FUNCTIONAL 80S INITIATION COMPLEX (80S.MRNA.MET-TRNA[Met]). EIF-5 IS ESSENTIAL FOR CELL VIABILITY.
 CC -1- SUBUNIT: Monomer.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative initiation;
 CC Comment=2 isoforms, long (shown here) and short, are produced by alternative initiation.
 CC -1- SIMILARITY: BELONGS TO THE EIF-2-BETA / EIF-5 FAMILY.
 CC -----
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 CC -----
 CC EMBL: L10840; -; NOT ANNOTATED_CDS.
 CC EMBL: Z71255; CA949489.1; -.
 CC EMBL: Z68111; CA92145.1; -.
 CC EMBL: Z73616; CA97991.1; -.
 CC PIR: A46699; A46699.
 CC SCD: S006245; TIF5.
 CC GO: GO:0005843; C:cytosolic small ribosomal subunit (sensu Eu. . .; IPI.
 CC GO: GO:0005096; F:GTPase activator activity; IPI.
 CC GO: GO:0042256; P:mature ribosome assembly; IMP.
 CC GO: GO:006446; P:regulation of translational initiation; IMP.
 CC InterPro: IPR002735; eIF5_eIF2B.
 CC InterPro: IPR003307; eIF5C.
 CC Pfam: PF01873; eIF5_eIF2B; 1.
 CC Pfam: PF02020; W2; 1.
 CC ProDom: PD004078; eIF5_eIF2B; 1.
 CC SMART: SMO0653; eIF2B_5; 1.
 CC SMART: SMO0515; eIF5C; 1.
 CC KMW: Initiation factor; Protein biosynthesis; Alternative initiation;
 KW GTP-binding.
 FT CHAIN 1 405
 FT
 FT CHAIN 18 405
 FT
 FT INIT MET 18 18
 FT DOMAIN 152 156
 FT NP_BIND 27 34
 FT DOMAIN 396 405
 FT SEQUENCE 405 AA; 45261 MW; 1A1DA5634ED1B1F CRC64;

Query Match 0.9%; Score 7; DB 1; Length 405;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 94 DEDIVNE 100
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Db 297 DEDIVNE 303

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RESULT 63
RPA3_YEAST STANDARD; PRT; 415 AA.
ID_RPA3_YEAST
AC 001080;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE DNA-directed RNA polymerase I 49 kDa polypeptide (EC 2.7.7.6) (A49).
GN RPA49 OR RNRI3 OR YNLI248C OR N0880.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMY214;
RC MEDLINE=93028452; PubMed=1409638;
RA Liljelund P., Mariotte S., Buhler J.-M., Sentenac A.;
RT "Characterization and mutagenesis of the gene encoding the A49
RT subunit of RNA polymerase I in Saccharomyces cerevisiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:9302-9305 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / FY1679;
RC MEDLINE=97377992; PubMed=9234673;
RA Sen-Gupta M., Gueldeher U., Beinhauer J.D., Fiedler T.A.,
RA Hegemann J.H.;
RT "Sequence analysis of the 33 kb long region between ORC5 and SU11
RT from the left arm of chromosome XIV from Saccharomyces cerevisiae.";
RL Yeast 13:849-860 (1997).
CC -I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES. RNA POLYMERASE A IS ESSENTIALLY USED TO TRANSCRIBE
CC RIBOSOMAL DNA UNITS.
CC -I- FUNCTION: A49 IS EASILY DISSOCIATED FROM THE REST OF POL A,
CC PRODUCING THE FORM A', WHICH SHOWS IMPAIRED TRANSCRIPTIONAL
CC ACTIVITY AND INCREASED SENSITIVITY TO ALPHA-AMANTIN. THE FUNCTION
CC OF A49 MIGHT BE LINKED TO THE RNASE H ACTIVITY THAT WAS FOUND
CC ASSOCIATED WITH THIS SUBUNIT.
CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -I- SUBUNIT: RNA POLYMERASE I CONSISTS OF 14 DIFFERENT SUBUNITS.
CC -I- SUBCELLULAR LOCATION: Nuclear.
CC -I- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
CC PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
CC III FOR 5S AND TRNA GENES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M96600; AAA34380.1; -
CC EMBL; X96722; CAA65496.1; -
CC EMBL; Z71524; CAA96155.1; -
CC PIR; S63221; S63221
CC SGD; S0005192; RPA49.
KW Transferase; DNA-directed RNA polymerase; Transcription;
KW Nuclear protein.
FT CONFLICT 66 T -> P (IN REF. 1).
FT CONFLICT 157 S -> C (IN REF. 1).
FT CONFLICT 157 S -> C (IN REF. 1).
SQ SEQUENCE 415 AA; 46650 MW; 3DBP05440D26021 CRC64;

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Query Match 0.9%; Score 7; DB 1; Length 415;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 469 KILLERLN 475
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| | | | |
282 KILLERLN 288

RESULT 64
HEM1_AERPE STANDARD; PRT; 416 AA.
ID_HEM1_AERPE
AC 093372;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamyl-tRNA reductase (EC 1.2.1.-) (GLUTR).
GN HEMA OR APE2296.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KI;
RC MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix KI.";
RL DNA Res. 6:83-101 (1999).
CC -I- CATALYTIC ACTIVITY: Glutamyl-tRNA(Glu) + NADPH = glutamate-1-
CC semialdehyde + NADP(4+) + tRNA(Glu).
CC -I- PATHWAY: Porpyrin biosynthesis by the C5 pathway; first step.
CC -I- SIMILARITY: Belongs to the glutamyl-tRNA reductase family.
CC -----
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CC -----
CC EMBL; AP000064; BAA81308.1; -
CC PIR; D72456; D72456.
CC HAMAP; MF_00087; -; 1.
CC InterPro; IPR000343; GLUTR.
CC Pfam; PF00745; GLUTR_dimer; 1.
CC Pfam; PF05201; GLUTR_N; 1.
CC Pfam; PF05200; GLUTR_NAD_bind; 1.
CC TIGRPFAM; TIGR01035; hema; 1.
CC PROSITE; PS00747; GLUTR; 1.
KW Porpyrin biosynthesis; Oxidoreductase; NADP; Complete proteome.
FT ACT_SITE 47 47 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 87 87 BASE (BY SIMILARITY).
SQ SEQUENCE 416 AA; 45244 MW; 6E087B36FC6853D CRC64;

Query Match 0.9%; Score 7; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 753 TLGLRN 759
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346 TLGLRN 352

RESULT 65
Y12A_ECOLI STANDARD; PRT; 424 AA.
ID_Y12A_ECOLI
AC P51026; Q47535;
DT 01-OCT-1996 (Rel. 34, Created)

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DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Insertion element IS2A hypothetical 48.2 kda protein.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Nishimoto H., Saito N.;
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TRANSPOSASE FAMILY 8.
 CC -----
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 CC -----
 CC EMBL: D85613; BAA12836.1; -
 DR PIR: S78610; S78610.
 DR InterPro: IPR001584; Rve.
 DR InterPro: IPR002514; Transposase_8.
 DR Pfam: PF00665; rve; 1.
 DR Pfam: PF01527; Transposase_8; 1.
 DR Transposable element: Hypothetical protein.
 KW SEQUENCE 424 AA; 48153 MW; A791CE858D05A329 CRC64;
 SQ

Query Match 0.9%; Score 7; DB 1; Length 424;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 ASELAAA 208
 DB 85 ASELAAA 91

RESULT 66
 TRPB_HALN1 STANDARD; PRT; 430 AA.
 AC G9HSC0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tryptophan synthase beta chain (EC 4.2.1.20).
 GN TRPB OR VNG0307G.
 OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
 OC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welte R., Goo Y.A.,
 RA Leitbauer B., Keiler K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angewine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlischer M., Spidich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
 RT "Genome sequence of Halobacterium species NRC-1."
 CC -1- Genome sequence of Halobacterium species NRC-1."
 CC -1- FUNCTION: The beta subunit is responsible for the synthesis of L-
 CC tryptophan from indole and L-serine.
 CC -1- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
 CC = L-tryptophan + glyceraldehyde 3-phosphate.
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- PATHWAY: Tryptophan biosynthesis; fifth (last) step.
 CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (By

CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE TRPB FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE004991; AAC8887.1; -
 DR PIR: C84190; C84190.
 DR HSSP: P00933; 2MSY.
 DR HAMAP: MF_00133; -; 1.
 DR InterPro: IPR001926; B6_enzyme_beta.
 DR InterPro: IPR006653; TYP_synth_beta.
 DR InterPro: IPR006654; TYP_synth_beta.
 DR Pfam: PF00291; PALP; 1.
 DR TIGRFAMs: TIGR00263; trpb; 1.
 DR PROSITE: PS00168; TRP SYNTHASE_BETA; 1.
 DR Tryptophan biosynthesis; Pyridoxal phosphate; lyase;
 KW Complete proteome.
 KM BINDING 95
 SQ SEQUENCE 430 AA; 45451 MW; B1B56DAC9AD0BCDC CRC64;
 FT

Query Match 0.9%; Score 7; DB 1; Length 430;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AIISEEL 83
 DB 214 AIISEEL 220

RESULT 67
 GSA_AERPE STANDARD; PRT; 432 AA.
 ID G9Y3I9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) (GSA)
 DE (Glutamate-1-semialdehyde aminotransferase) (GSA-AT).
 GN HEM1 OR APE2299.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 OC Desulfurococcaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anai A., Kosugi H.,
 RA Hoshino A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki Y., Kusuda N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1."
 RL DNA Res. 6:83-101 (1999).
 CC -1- CATALYTIC ACTIVITY: (S)-4-amino-5-oxopentanoate = 5-
 CC aminovalinate.
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- PATHWAY: Porphyrin biosynthesis by the C5 pathway; second step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
 CC -1- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
 CC aminotransferases.
 CC -----
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CC EMBL: AB000064; BAA81311.1; -
 DR PIR: G72456; G72456.
 DR HSSP: P24630; 2GSA.
 DR HAMAP: MF_00375; -; 1.
 DR InterPro: IPR005814; AminoTrans_3.
 DR Pfam: PF02022; aminotran_3; 1.
 DR TIGRPFAM: TIGR00713; hemL; 1.
 DR PROSITE: PS00600; AA_TRANSF_R CLASS 3; 1.
 DR Porphyryn biosynthesis; Isomerase; Pyridoxal phosphate;
 KW Complete proteome.
 FT BINDING 269 269 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 432 AA; 46281 MW; A8FC01657A163BD2 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 432;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 733 EAEVLLA 739
 DB 94 EAEVLLA 100

RESULT 68
 TBG_SCHUP STANDARD; PRT; 446 AA.

AC 09Y882;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tubulin gamma chain (Gamma tubulin).
 GN TUG1 OR GTB1.
 OS Schizosaccharomyces japonicus.
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4897;
 RP SEQUENCE FROM N.A.
 RA Horio T., Shimizu M., Akashi T., Tanaka K.;
 RT "Isolation and characterization of gamma-tubulin gene from
 Schizosaccharomyces japonicus."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.
 CC GAMMA TUBULIN IS FOUND AT MICROTUBULE ORGANIZING CENTERS (MTOC)
 CC SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT
 CC IS INVOLVED IN THE MINUS-END NUCLEATION OF MICROTUBULE ASSEMBLY.
 CC -!- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.

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CC EMBL: AF159163; AAD41900.1; -
 DR InterPro: IPR000217; Tubulin.
 DR InterPro: IPR003008; Tubulin_FtsZ.
 DR Pfam: PF00901; tubulin_1.
 DR Pfam: PF03953; tubulin_C; 1.
 DR PRINTS: PRO1161; TUBULIN.
 DR PROSITE: PS00227; TUBULIN; 1.
 KW Microtubules; GTP-binding.
 FT NP_BIND 142 148 GTP (POTENTIAL).
 SQ SEQUENCE 446 AA; 50158 MW; B86BBE95A94A2C CRC64;

Query Match 0.9%; Score 7; DB 1; Length 446;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 470 LIERLND 476
 DB 153 LIERLND 159

RESULT 69
 TBG_SCHPO STANDARD; PRT; 446 AA.

AC P25295;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tubulin gamma chain (Gamma tubulin).
 GN TUG1 OR GTB1 OR SPBC32F12.04.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91249389; PubMed=1840506;
 RA Stearns T., Evans L., Kirschner M.;
 RT "Gamma-tubulin is a highly conserved component of the centrosome."
 RL Cell 65:825-836(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=972;
 RX MEDLINE=92121241; PubMed=1770000;
 RT Horio T., Uzawa S., Jung M.K., Oakley B.R., Tanaka K., Yanagida M.;
 RT "The fission yeast gamma-tubulin is essential for mitosis and is
 RT localized at microtubule organizing centers."
 RL J. Cell Sci. 99:693-700(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA STRAIN=972;
 RX MEDLINE=21849401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgourou J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
 RA Rutherford K., Rutter S., Saunders J., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grynpres B.,
 RA Welteens I., Vanstreels E., Rieger M., Schaefer M., Meller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Meestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wandut R., Purrelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Useery D., Barrett B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).

CC -!- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.
 CC GAMMA TUBULIN IS FOUND AT MICROTUBULE ORGANIZING CENTERS (MTOC)
 CC SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT
 CC IS INVOLVED IN THE MINUS-END NUCLEATION OF MICROTUBULE ASSEMBLY.
 CC -!- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.

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 CC -----
 CC EMBL: M63447; AAA35305.1; -
 CC EMBL: X62031; CAA3976.1; -
 CC EMBL: AL023796; CAA19365.1; -
 CC PIR: B39528; UBZPG.
 CC GeneDB: SPombe; SPBC32F12.04; -
 CC InterPro: IPR000217; Tubulin.
 CC InterPro: IPR003008; Tubulin_FtsZ.
 CC Pfam: PF00091; tubulin.1.
 CC Pfam: PF03953; tubulin.C.1.
 CC PRINTS: PR01161; TUBULIN.
 CC PROSITE: PS00227; TUBULIN; 1.
 CC Microtubules: GTP-binding.
 CC NP BIND 142 148 GTP (POTENTIAL).
 CC FT SEQUENCE 446 AA; 49965 MW; 8A48833EAB3BD469 CRC64;
 CC
 CC Query Match 0.9%; Score 7; DB 1; Length 446;
 CC Best Local Similarity 100.0%; Pred. No. 99;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Oy 470 LIERAND 476
 CC |||||
 CC Db 153 LIERAND 159
 CC
 CC RESULT 70
 CC V50K_BYDVP STANDARD; PRT; 450 AA.
 CC ID V50K_BYDVP STANDARD; PRT; 450 AA.
 CC AC P09516;
 CC DT 01-MAR-1989 (Rel. 10; Created)
 CC DT 28-FEB-2003 (Rel. 41; Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41; Last annotation update)
 CC DE 50 kDa protein (ORF 4).
 CC OS Bartley yellow dwarf virus (isolate PAV) (BYDV).
 CC OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
 CC OC Luteovirus.
 CC OC NCBI_TaxID=12040;
 CC [1]
 CC RN SEQUENCE FROM N.A.
 CC RX MEDLINE=88289355; PubMed=3399386;
 CC RA Miller W.A., Waterhouse P.M., Gerlach W.L.;
 CC RT "Sequence and organization of Bartley yellow dwarf virus genomic RNA";
 CC RL Nucleic Acids Res. 16:6097-6111(1988).
 CC CC -1- SIMILARITY: TO ORF 6 OF BEET WESTERN YELLOW VIRUS. ORF6 OF
 CC POTATO LEAFROLL VIRUS AND OF 54K PROTEIN OF BEET NECROTIC
 CC YELLOW VEIN VIRUS.
 CC -----
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 CC -----
 CC EMBL: X07653; CAA30495.2; -
 CC InterPro: IPR002929; PLRV_ORFS.
 CC Pfam: PF01690; PLRV_ORFS; 1.
 CC SEQUENCE 450 AA; 49765 MW; 3960B2663D45331D CRC64;
 CC
 CC Query Match 0.9%; Score 7; DB 1; Length 450;
 CC Best Local Similarity 100.0%; Pred. No. 99;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Oy 351 PPTPEP 357
 CC |||||

Db 24 PPTPEP 30
 CC
 CC RESULT 71
 CC TBGI_HUMAN STANDARD; PRT; 451 AA.
 CC ID TBGI_HUMAN STANDARD; PRT; 451 AA.
 CC AC P23258; Q9BM59;
 CC DT 01-NOV-1991 (Rel. 20; Created)
 CC DT 28-FEB-2003 (Rel. 41; Last sequence update)
 CC DT 15-SEP-2003 (Rel. 42; Last annotation update)
 CC DE Tubulin gamma-1 chain (Gamma-1 tubulin) (Gamma-tubulin complex
 CC component 1) (GCP-1).
 CC GN TBGI OR TUBG.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 CC [1]
 CC RN SEQUENCE FROM N.A.
 CC RX MEDLINE=91249388; PubMed=1904010;
 CC RA Zheng Y., Jung M.K., Oakley B.R.;
 CC RT "Gamma-tubulin is present in Drosophila melanogaster and Homo sapiens
 CC and is associated with the centrosome";
 CC RL Cell 65:817-823(1991).
 CC [2]
 CC RN SEQUENCE FROM N.A.
 CC RP TISSUE=Skin;
 CC RX MEDLINE=22388257; PubMed=12477932;
 CC RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 CC RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 CC RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 CC RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 CC RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 CC RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 CC RA Brownstein M.J., Usdin T.B., Toshimiyu S., Carninci P., Prange C.,
 CC RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 CC RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 CC RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 CC RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 CC RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 CC RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
 CC RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 CC RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 CC RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 CC RA Schercher A., Schein J.E., Jones S.J.M., Matra M.A.;
 CC RT "Generation and initial analysis of more than 15,000 full-length
 CC human and mouse cDNA sequences";
 CC RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC [3]
 CC RN MASS SPECTROMETRY.
 CC RP TISSUE=Breast cancer;
 CC RX MEDLINE=21829512; PubMed=11840567;
 CC RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herach A.,
 CC RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
 CC RA Zvelebil M.J.;
 CC RT "Cluster analysis of an extensive human breast cancer cell line
 CC protein expression map database";
 CC RL Proteomics 2:212-223(2002).
 CC [4]
 CC RN SUBCELLULAR LOCATION.
 CC RP MEDLINE=98234404; PubMed=9566969;
 CC RA Tassin A.-M., Celati C., Moudjou M., Bornens M.;
 CC RT "Characterization of the human homologue of the yeast spc98p and its
 CC association with gamma-tubulin";
 CC RL J. Cell Biol. 141:689-701(1998).
 CC CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.
 CC GAMMA TUBULIN IS FOUND AT MICROTUBULE ORGANIZING CENTERS (MTOC)
 CC SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT
 CC IS INVOLVED IN THE MINUS-END NUCLEATION OF MICROTUBULE ASSEMBLY.
 CC CC -1- SUBUNIT: Interacts with GCP2 and GCP3.
 CC CC -1- SUBCELLULAR LOCATION: Centrosome.
 CC CC -1- MASS SPECTROMETRY: MW=51197.98; METHOD=MALDI.
 CC CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.


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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M61764; AAA52620.1; -
DR EMBL; BC000619; AAH00619.1; -
DR PIR; A39527; UBHUG.
DR Genew; HGNC:12417; TUBG1.
DR MIM; 191135; -
DR GO; GO:0005813; C:centrosome; TAS.
DR GO; GO:0005874; C:microtubule; TAS.
DR GO; GO:0005816; C:spindle pole body; TAS.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; TAS.
DR GO; GO:0000226; P:microtubule cytoskeleton organization and b.; TAS.
DR InterPro; IPR000217; Tubulin.
DR InterPro; IPR003008; Tubulin_Fcsz.
DR Pfam; PF00091; tubulin_1.
DR Pfam; PF03953; tubulin_C; 1.
DR PRINTS; PR01161; TUBULIN.
DR PROSITE; PS00227; TUBULIN; 1.
DR Microtubules; GTP-binding.
DR NP BIND 142 148 GTP (POTENTIAL).
FT CONFLICT 35 35 G -> A (IN REF. 1).
FT CONFLICT 202 202 V -> L (IN REF. 1).
SQ SEQUENCE 451 AA; 51170 MW; E2A4C0179ED0CFE8 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 451;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 LIERLAND 476
Db 153 LIERLAND 159

RESULT 72
TBG1 MOUSE STANDARD; PRT; 451 AA.
ID TBG1 MOUSE
AC 092310;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tubulin gamma-1 chain (Gamma-1 tubulin) (Gamma-tubulin complex
component 1) (GCP-1).
GN TUBG1 OR TUBG.
OS Mus musculus (Mouse). and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCB1_TaxID=10090, 10116;
[1]
RP SEQUENCE FROM N.A.
RC SPECTES=Mouse;
RX MEDLINE=2238257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodegriem E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECTES=Cat;
RX MEDLINE=99397453; PubMed=10470852;
RA Nakada T., Okada N., Makino Y., Tamura T.;
RT "Structure of rat gamma-tubulin and its binding to Hp33.";
RL DNA Res. 6:207-209(1999).
CC -1- FUNCTION: Tubulin is the major constituent of microtubules. Gamma
CC tubulin is found at microtubule organizing centers (MTOC) such as
CC the spindle poles or the centrosome, suggesting that it is
CC involved in the minus-end nucleation of microtubule assembly (By
CC similarity).
CC -1- SUBUNIT: Interacts with GCP2 and GCP3 (By similarity).
CC -1- SUBCELLULAR LOCATION: Centrosome (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; BC006581; AAH06581.1; -
DR EMBL; AB015946; BAA36504.1; -
DR MGD; MGI:101834; Tubb.
DR InterPro; IPR000217; Tubulin.
DR InterPro; IPR003008; Tubulin_Fcsz.
DR Pfam; PF00091; tubulin_1.
DR Pfam; PF03953; tubulin_C; 1.
DR PRINTS; PR01161; TUBULIN.
DR PROSITE; PS00227; TUBULIN; 1.
DR Microtubules; GTP-binding.
DR NP BIND 142 148 GTP (POTENTIAL).
FT CONFLICT 142 148 AEF1068D12DOC88A CRC64;
SQ SEQUENCE 451 AA; 51100 MW; A8F1068D12DOC88A CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 451;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 LIERLAND 476
Db 153 LIERLAND 159

RESULT 73
TBG2 HUMAN STANDARD; PRT; 451 AA.
ID TBG2 HUMAN
AC 09NR33;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tubulin gamma-2 chain (Gamma-2 tubulin).
GN TUBG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCB1_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20366133; PubMed=10903841;
RA Wise D.O., Krahe R., Oakley B.R.;
RT "The gamma-tubulin gene family in humans.";
RL Genomics 67:164-170(2000).
RN [2]
RP SEQUENCE FROM N.A.

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RC TISSUE=Mammary gland;
 RA Isocai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H.,
 RA Watanabe S., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishi S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
 RA Niimiya K., Iwayanagi T.,
 RT "NEDO human cDNA sequencing project";
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Tubulin is the major constituent of microtubules. Gamma
 tubulin is found at microtubule organizing centers (MTOC) such as
 the spindle poles or the centrosome, suggesting that it is
 involved in the minus-end nucleation of microtubule assembly.
 CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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 or send an email to license@isb-sib.ch).
 CC EMBL; AF225971; AAF34188.1; -
 CC EMBL; AK022324; BAB14012.1; -
 CC EMBL; BC009670; AAH09670.1; -
 CC GeneW; HGNC:12419; TUBG2.
 DR MIM; 605785; -
 DR GO; GO:0005198; F:structural molecule activity; TMS.
 DR InterPro; IPR000217; Tubulin.
 DR InterPro; IPR003008; Tubulin_FtsZ.
 DR Pfam; PF00091; tubulin_1.
 DR Pfam; PF03953; tubulin_C; 1.
 DR PRINTS; PR01161; TUBULIN.
 DR PROSITE; PS00227; TUBULIN; 1.
 KW Microtubules; GTP-binding.
 FT NP BIND 142 148
 FT SEQUENCE 451 AA; 51091 MW; FDE2CB5A33D92691 CRC64;
 SQ
 Query Match 0.9%; Score 7; DB 1; Length 451;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 470 LLERLND 476
 Db 153 LLERLND 159

RESULT 74
 TBG2 MOUSE STANDARD; PRT: 451 AA.
 ID TBG2 MOUSE
 AC O8VCK3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tubulin gamma-2 chain (Gamma-2 tubulin).
 GN TUBG2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.
 CC GAMMA TUBULIN IS FOUND AT MICROTUBULE ORGANIZING CENTERS (MTOC)
 SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT
 IS INVOLVED IN THE MINUS-END NUCLEATION OF MICROTUBULE ASSEMBLY.
 CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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 or send an email to license@isb-sib.ch).
 CC EMBL; BC019652; AAH19652.1; -
 CC InterPro; IPR000217; Tubulin.
 CC InterPro; IPR003008; Tubulin_FtsZ.
 CC Pfam; PF00091; tubulin_1.
 CC Pfam; PF03953; tubulin_C; 1.
 CC PRINTS; PR01161; TUBULIN.
 CC PROSITE; PS00227; TUBULIN; 1.
 KW Microtubules; GTP-binding.
 FT NP BIND 142 148
 FT SEQUENCE 451 AA; 51121 MW; 1FC0CF1E04839A CRC64;
 SQ
 Query Match 0.9%; Score 7; DB 1; Length 451;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 470 LLERLND 476
 Db 153 LLERLND 159
 RESULT 75
 TBG_XENLA

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ID TBG_XENLA STANDARD; PRT; 451 AA.
AC P23330;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tubulin gamma chain (gamma tubulin).
GN XGAM.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91249389; PubMed=1840506;
RA Stearns T., Evans L., Kirschner M.;
RT "Gamma-tubulin is a highly conserved component of the centrosome";
RL Cell 65:825-836(1991).
CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.
CC GAMMA TUBULIN IS FOUND AT MICROTUBULE ORGANIZING CENTERS (MTOC)
CC SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT
CC IS INVOLVED IN THE MINUS-END NUCLEATION OF MICROTUBULE ASSEMBLY.
CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M63446; AAA49720.1; -
DR PIR; A39528; UBXLG.
DR InterPro; IPR000217; Tubulin.
DR InterPro; IPR003008; Tubulin_fte2.
DR Pfam; PF00091; tubulin_1.
DR Pfam; PF03953; tubulin_C_1.
DR PRINTS; PR01161; TUBULIN.
DR PROSITE; PS00227; TUBULIN; 1.
DR Microtubules; GTP-binding.
KW NP BIND 142 148 GTP (POTENTIAL).
FT SEQUENCE 451 AA; 51167 MW; 52195DA5921EF246 CRC64;
SQ
Query Match 0.9%; Score 7; DB 1; Length 451;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 470 LLERLND 476
DB 153 LLERLND 159

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CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U41028; AAA82357.1; -
DR PIR; T15622; T15622.
DR WormPep; C25G6.5; CE04086.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_RHOOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 66 1 (POTENTIAL).
FT DOMAIN 67 86 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 87 107 2 (POTENTIAL).
FT DOMAIN 108 120 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 121 135 3 (POTENTIAL).
FT DOMAIN 136 152 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 153 173 4 (POTENTIAL).
FT DOMAIN 174 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 231 5 (POTENTIAL).
FT DOMAIN 232 272 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 273 293 6 (POTENTIAL).
FT DOMAIN 294 307 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 308 328 7 (POTENTIAL).
FT DOMAIN 329 455 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 455 AA; 52187 MW; CID33C3C2E26C6F5 CRC64;
Query Match 0.9%; Score 7; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 TTNNTNS 252
DB 250 TTNNTNS 256

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RESULT 76
ID YXXS CAEEL STANDARD; PRT; 455 AA.
AC 018179;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative neuropeptide Y receptor (NPY-R).
GN C25G6.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RA Martin U.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COULD BE A RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

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RESULT 77
ID SELA PASMU STANDARD; PRT; 460 AA.
AC Q9CK66;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-seryl-tRNA(Sec) selenium transferase (EC 2.9.1.1) (Cysteiny]-
DE tRNA(Sec) selenium transferase) (Selenocysteine synthase)
DE (Selenocysteinyl-CRNA (Sec) synthase).
GN SELA OR PM1768.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21145666; PubMed=11248100;
RX STRAIN=Pm70;
RA May B.J., Zhang O., Li L.L., Paustian M.L., Whitlam T.S., Kapur V.;
RT Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- FUNCTION: Converts seryl-tRNA(Sec) to selenocysteinyl-tRNA(Sec
CC UCA) during selenoprotein biosynthesis (By similarity).
CC -1- CATALYTIC ACTIVITY: L-seryl-tRNA(Sec) + selenophosphate = L-
CC selenocysteinyl-tRNA(Sec) + H(2)O + phosphate.

```

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CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SELA FAMILY.
CC -----
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CC -----
DR EMBL; AE006214; AK03852.1; -
DR HAMAP; MF_00423; -; 1.
DR InterPro; IPR004534; Sela.
DR Pfam; PF03841; Sela; 1.
DR TIGRfam; TIGR00474; Sela; 1.
DR TrEMBL; TIGR00474; Sela; 1.
DR TRANSFAM; Pyridoxal phosphate; Selenium; Complete proteome.
KW BINDING 293 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT SEQUENCE 460 AA; 50667 MW; FP96AB86A0BCD7 CRC64;
SQ
Query Match 0.9%; Score 7; DB 1; Length 460;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 266 DIDSLLK 272
Db 449 DIDSLLK 455

RESULT 78
TBG1_EUPOC STANDARD; PRT; 461 AA.
ID TBG1_EUPOC
AC P34786.
DT 01-FEB-1994 (Rel. 28. Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tubulin gamma-1 chain (Gamma-1 tubulin).
OS Euplores octocarinatus.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotida; Euplotidae; Euplores.
OC NCBI_TaxID=5937;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3(58) -IX;
RX MEDLINE=94124022; PubMed=8294024;
RA Liang A.; Heckmann K.;
RT "The macronuclear gamma-tubulin-encoding gene of Euplores
RT octocarinatus contains two introns and an in-frame TGA.";
RL Gene 136:319-322(1993).
RN [2]
RP REVISIONS.
RA Liang A.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.
CC GAMMA TUBULIN IS FOUND AT MICROTUBULE ORGANIZING CENTERS (MTOC)
CC SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT
CC IS INVOLVED IN THE MINUS-END NUCLEATION OF MICROTUBULE ASSEMBLY.
CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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CC -----
DR EMBL; X71353; CA50488.1; -
DR EMBL; Y09552; CAA70743.1; -
DR EMBL; Y09554; CAA70745.1; -
DR InterPro; IPR000217; Tubulin.
DR InterPro; IPR003008; Tubulin_Ftsz.

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DR Pfam; PF00091; tubulin; 1.
DR Pfam; PF03953; tubulin C; 1.
DR PRINTS; PR01161; TUBULIN.
DR PROSITE; PS00227; TUBULIN; 1.
KW Microtubules; GTP-binding.
FT NP BIND 142 148
SQ SEQUENCE 461 AA; 51992 MW; 2E029859BB9C96 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 461;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 470 LLERLND 476
Db 153 LLERLND 159

RESULT 79
TBG2_EUPOC STANDARD; PRT; 461 AA.
ID TBG2_EUPOC
AC P90548.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tubulin gamma-2 chain (Gamma-2 tubulin).
OS Euplores octocarinatus.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotida; Euplotidae; Euplores.
OC NCBI_TaxID=5937;
RN [1]
RP SEQUENCE FROM N.A.
RA Tan M.; Liang A.; Heckmann K.;
RT "The two gamma tubulin genes of Euplores octocarinatus code for a
RT slightly different protein.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.
CC GAMMA TUBULIN IS FOUND AT MICROTUBULE ORGANIZING CENTERS (MTOC)
CC SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT
CC IS INVOLVED IN THE MINUS-END NUCLEATION OF MICROTUBULE ASSEMBLY.
CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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CC -----
DR EMBL; Y09553; CAA70744.1; -
DR EMBL; Y17254; CAA76714.1; -
DR InterPro; IPR000217; Tubulin.
DR InterPro; IPR003008; Tubulin_Ftsz.
DR Pfam; PF00091; tubulin; 1.
DR Pfam; PF03953; tubulin C; 1.
DR PRINTS; PR01161; TUBULIN.
DR PROSITE; PS00227; TUBULIN; 1.
KW Microtubules; GTP-binding.
FT NP BIND 142 148
SQ SEQUENCE 461 AA; 51952 MW; DBED624C4B824A46 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 461;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 470 LLERLND 476
Db 153 LLERLND 159

RESULT 80
TBG_NEUCR STANDARD; PRT; 461 AA.
ID TBG_NEUCR

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AC P53377;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tubulin gamma chain (Gamma tubulin).
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98019102; PubMed=9358070;
 RA Heckmann S., Schliwa M., Kube-Grandgerath E.;
 RT "Primary structure of Neurospora crassa gamma-tubulin.";
 RL Gene 199:303-309(1997).
 CC - FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.
 CC - SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT
 CC IS INVOLVED IN THE MINUS-END NUCLEATION OF MICROTUBULE ASSEMBLY.
 CC - SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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 CC -----
 CC DR EMBL; X97753; CAA66348.1;
 CC DR InterPro; IPR000217; Tubulin.
 CC DR InterPro; IPR003008; Tubulin_Fte2.
 CC DR Pfam; PF00091; tubulin; 1.
 CC DR Pfam; PF03953; tubulin; C. 1.
 CC DR PRINTS; PR01161; TUBULIN.
 CC DR PROSITE; PS00227; TUBULIN; 1.
 CC KW Microtubules; GTP-binding.
 CC FT NP BIND 142 148 GTP (POTENTIAL).
 CC SQ SEQUENCE 461 AA; 51598 MW; 70DCCBEA224B6343 CRC64;
 QY Query Match 0.9%; Score 7; DB 1; Length 461;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 470 LITERLND 476
 153 LITERLND 159
 RESULT 81
 TR1B_HUMAN STANDARD; PRT; 461 AA.
 AC P20333; Q16042; Q9U1H1;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
 DE necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Etanercept)
 DE [Contains: Tumor necrosis factor binding protein 2 (TNFR2)].
 GN TNFRSF1B OR TNFR2 OR TNFR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90260639; PubMed=2160731;
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
 RA Dower S.K., Cosman D., Goodwin R.G.;
 RT "A receptor for tumor necrosis factor defines an unusual family of
 RT cellular and viral proteins.";
 RL Science 248:1019-1023(1990).
 RN [2]

RP SEQUENCE FROM N.A., AND VARIANT ARG-196.
 RX MEDLINE=9104591; PubMed=2172983;
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
 RT "A second tumor necrosis factor receptor gene product can shed a
 RT naturally occurring tumor necrosis factor inhibitor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9629745; PubMed=8661109;
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
 RA Lepailier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;
 RA Brodeur G.M.;
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";
 RL Genomics 35:94-100(1996).
 RN [4]
 RP SEQUENCE OF 37-461 FROM N.A.
 RX MEDLINE=91370690; PubMed=1966549;
 RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
 RA Brockhaus M., Lesslauer W.;
 RT "Two human TNF receptors have similar extracellular, but distinct
 RT intracellular, domain sequences.";
 RL Cytokine 2:231-237(1990).
 RN [5]
 RP SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.
 RX MEDLINE=90349572; PubMed=2166946;
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
 RA Ringold G.M.;
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor
 RT and demonstration of a shed form of the receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
 RN [6]
 RP SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
 RX MEDLINE=21069356; PubMed=1197692;
 RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
 RT "New single nucleotide polymorphisms in the coding region of human
 RT TNFR2: association with systemic lupus erythematosus.";
 RL Genes Immun. 1:501-503(2000).
 RN [7]
 RP SEQUENCE OF 27-31.
 RX MEDLINE=90110215; PubMed=2153136;
 RA Engelmann H., Novick D., Wallach D.;
 RT "Two tumor necrosis factor-binding proteins purified from human
 RT urine. Evidence for immunological cross-reactivity with cell surface
 RT tumor necrosis factor receptors.";
 RL U. Biol. Chem. 265:1531-1536(1990).
 RN [8]
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
 RX MEDLINE=91056048; PubMed=2173696;
 RA Loetscher H., Schlaepper E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
 RA Brockhaus M.;
 RT "Purification and partial amino acid sequence analysis of two
 RT distinct tumor necrosis factor receptors from HL60 cells.";
 RL J. Biol. Chem. 265:20131-20138(1990).
 RN [9]
 RP CHARACTERIZATION.
 RX MEDLINE=93016040; PubMed=1328224;
 RA Penhica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.;
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 RT Characterization of ligand binding, internalization, and receptor
 RT phosphorylation.";
 RL U. Biol. Chem. 267:21172-21178(1992).
 RN [10]
 RP INTERACTION WITH TRAF2.
 RX MEDLINE=94349371; PubMed=8069916;
 RA Rothe M., Mong S.C., Henzel W.J., Goeddel D.V.;
 RT "A novel family of putative signal transducers associated with the
 RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
 RL Cell 78:681-692(1994).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
 RP TRAF2.

```

RX MEDLINE=99221490; PubMed=10206649;
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Mu H.;
RT "Structural basis for self-association and receptor recognition of
RL human TRAF2."
CC Nature 398:533-538 (1999).
CC -1- FUNCTION: Receptor with high affinity for TNFalpha and
CC approximately 5-fold lower affinity for homotrimeric
CC TNFalpha/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the
CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2.
CC -1- SUBUNIT: Binds to TRAF2.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC -1- PTM: Phosphorylated; mainly on serine residues and with a very low
CC level on threonine residues.
CC -1- PTM: A soluble form (tumor necrosis factor binding protein 2) is
CC produced from the membrane form by proteolytic processing.
CC -1- PHARMACEUTICAL: Available under the name Embrel (Immunex and
CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid
CC arthritis (RA). Embrel consist of the extracellular ligand-binding
CC portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to
CC TNF-alpha and blocks its interactions with receptors.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
CC -1- DATABASE: NAME=Embrel; NOTE=Clinical information on Embrel;
CC WWW="http://www.embrel.com/".
CC -----
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CC -----
DR EMBL; M32315; AAA59929.1; -
DR EMBL; U52165; AAC50622.1; JOINED.
DR EMBL; U52157; AAC50622.1; JOINED.
DR EMBL; U52158; AAC50622.1; JOINED.
DR EMBL; U52159; AAC50622.1; JOINED.
DR EMBL; U52160; AAC50622.1; JOINED.
DR EMBL; U52161; AAC50622.1; JOINED.
DR EMBL; U52162; AAC50622.1; JOINED.
DR EMBL; U52163; AAC50622.1; JOINED.
DR EMBL; U52164; AAC50622.1; JOINED.
DR EMBL; M53994; AAA36755.1; -
DR EMBL; S63368; AAA19824.2; -
DR EMBL; M35857; AAA63262.1; -
DR EMBL; AB030950; BAA89053.1; -
DR PIR; A35356; A35356.
DR PDB; 1CA9; 12-APR-99.
DR Gene; HGNC:11917; TNFRSF1B.
DR MIM; 191191; -
DR GO; GO:0005031; F: tumor necrosis factor receptor activity; TAS.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
KW Phosphorylation; Pharmaceutical; Polymorphism; 3D-structure.
FT SIGNAL 1 22
FT CHAIN 23 461
FT CHAIN 27 461
FT CHAIN 27 461
FT DOMAIN 23 257
FT TRANSMEM 258 287
FT DOMAIN 288 461
FT REPEAT 37 76
FT REPEAT 77 118
FT REPEAT 119 162
FT REPEAT 163 201
FT DISULFID 40 53
FT BY SIMILARITY.

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FT DISULFID 54 67
FT DISULFID 57 75
FT DISULFID 78 93
FT DISULFID 96 110
FT DISULFID 100 116
FT DISULFID 120 128
FT DISULFID 134 143
FT DISULFID 137 161
FT DISULFID 164 179
FT CARBOHYD 171 171
FT CARBOHYD 193 193
FT VARIANT 196 196
FT VARIANT 232 232
FT VARIANT 363 363
FT CONFLICT 141 141
FT CONFLICT 363 363
FT SEQUENCE 461 AA; 48291 MW; 603D0AE1CD69ACBF CRC64;

Query Match 0.9%; Score 7; DB 1; Length 461;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 352 QPREPS 358
Db 228 QPREPS 234

RESULT 82
TBGI_EUPCR STANDARD; PRT; 462 AA.
AC P54403;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tubulin gamma-1 chain (Gamma-1 tubulin).
OS Euplocea crassus.
OC Euploidea; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euploidea; Euploceidae; Moneuploceae.
OX NCBI_TaxID=5936;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98192540; PubMed=9524221;
RA Tan M., Heckmann K.;
RT "The two gamma-tubulin-encoding genes of the ciliate Euplocea crassus
RT differ in their sequences, codon usage, transcription initiation
RT sites and poly(A) addition sites."
RL Gene 210:53-60 (1998).
CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.
CC GAMMA TUBULIN IS FOUND AT MICROTUBULE ORGANIZING CENTERS (MTOC)
CC SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT
CC IS INVOLVED IN THE MINDS-END NUCLEATION OF MICROTUBULE ASSEMBLY.
CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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CC -----
DR EMBL; X85234; CAAS9489.1; -
DR EMBL; Y09550; CAA70741.1; -
DR PIR; S53084; S53084.
DR InterPro; IPR000217; Tubulin.
DR InterPro; IPR003008; Tubulin_Fts2.
DR Pfam; PF00091; tubulin_1.
DR Pfam; PF03953; tubulin_C_1.
DR PRINTS; PR01161; TUBULIN.
DR PROSITE; PS00227; TUBULIN; 1.
DR Microtubules; GTP-binding; Multigene family.
KW NP_BIND 142 148
FT GTP (POTENTIAL).

```

SQ SEQUENCE 462 AA; 51959 MW; 773A5DE37DF53AF6 CRC64;
 Query Match 0.9%; Score 7; DB 1; Length 462;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 LIERLAND 476
 DB 153 LIERLAND 159

RESULT 83
 VS1K_BMYVF STANDARD; PRT; 467 AA.
 ID VS1K_BMYVF
 AC P09514;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DE 51 kDa protein (ORF 6).
 OS Beet western yellows virus (isolate FL-1) (BMYV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
 OC Polerovirus.
 CC NCBI_TaxID=12043;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89057523; PubMed=3194229;
 RA Veidt I., Lot H., Leister M., Scheidecker D., Guillely H., Richards K.,
 RA Jonard G.;
 RT "Nucleotide sequence of beet western yellows virus RNA."
 RL Nucleic Acids Res. 16:9917-9932(1988).
 CC -1- SIMILARITY: TO ORF 4 OF BARLEY YELLOW DWARF VIRUS AND ORF6 OF
 POTATO LEAFROLL VIRUS.

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CC EMBL; X13063; CAA31467.1; -
 DR PIR; S01943; S01943.
 DR InterPro; IPR001517; Luteo coat.
 DR InterPro; IPR000893; Luteo_ORF6.
 DR InterPro; IPR002929; PLRV_ORF5.
 DR Pfam; PF01690; PLRV_ORF5; 1.
 DR PRINTS; PR00910; LVIRUSORF6.
 SQ SEQUENCE 467 AA; 51386 MW; 418C4E85FC23783 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 PSPQPTP 355
 DB 13 PSPQPTP 19

RESULT 84
 VS1K_BMYVG STANDARD; PRT; 471 AA.
 ID VS1K_BMYVG
 AC P09515;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-OCT-1989 (Rel. 12, Last annotation update)
 DE 51 kDa protein (ORF 6).
 OS Beet western yellows virus (isolate GBI) (BMYV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
 OC Polerovirus.
 CC NCBI_TaxID=12044;
 RN (1)
 RP SEQUENCE FROM N.A.

RX MEDLINE=89057523; PubMed=3194229;
 RA Veidt I., Lot H., Leister M., Scheidecker D., Guillely H., Richards K.,
 RA Jonard G.;
 RT "Nucleotide sequence of beet western yellows virus RNA."
 RL Nucleic Acids Res. 16:9917-9932(1988).
 CC -1- SIMILARITY: TO ORF 4 OF BARLEY YELLOW DWARF VIRUS AND ORF6 OF
 POTATO LEAFROLL VIRUS.

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 or send an email to license@isb-sib.ch).

CC EMBL; X13062; CAA31461.1; -
 DR PIR; S01937; S01937.
 DR InterPro; IPR000893; Luteo ORF6.
 DR InterPro; IPR002929; PLRV_ORF5.
 DR Pfam; PF01690; PLRV_ORF5; 1.
 DR PRINTS; PR00910; LVIRUSORF6.
 SQ SEQUENCE 471 AA; 52108 MW; D8B7E48070597EB8 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 471;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 PSPQPTP 355
 DB 13 PSPQPTP 19

RESULT 85
 YHGF_NEIGO STANDARD; PRT; 476 AA.
 ID YHGF_NEIGO
 AC O51062;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein in region E (Fragment).
 OS Neisseria gonorrhoeae.
 CC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 CC Neisseriaceae; Neisseria.
 CC NCBI_TaxID=485;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11-E1;
 RX MEDLINE=96236055; PubMed=8655518;
 RA Petering H., Hammerschmidt S., Froesch M., van Putten J.P.M.,
 RA Ison C.A., Robertson B.D.;
 RT "Genes associated with meningococcal capsule complex are also found
 in Neisseria gonorrhoeae."
 RL J. Bacteriol. 178:3342-3345(1996).
 CC -1- SIMILARITY: Contains 1 SI motif domain.

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 or send an email to license@isb-sib.ch).

CC EMBL; Z21508; CAA79717.1; -
 DR InterPro; IPR006411; YggFc.
 DR SMART; SM00732; YggFc; 1.
 KW Hypothetical protein; RNA-binding.
 FT NON_TER 476 476
 SQ SEQUENCE 476 AA; 52830 MW; 389E22AC91B8E065 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 476;
 Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 SASELAA 207
DB 413 SASELAA 419

RESULT 86
VGLC_HSV2G STANDARD; PRT; 479 AA.

ID_VGLC_HSV2G
AC P03173;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Glycoprotein C precursor (Glycoprotein F).
GN GC OR UL44.
OS Herpes simplex virus (type 2 / strain G).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxId=10314;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85009847; PubMed=6090692;
RA Dombenko D.J., Lasky L.A.;
RT "Extensive homology between the herpes simplex virus type 2 glycoprotein F gene and the herpes simplex virus type 1 glycoprotein C gene";
RL J. Virol. 52:154-163(1984).
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND 2: GH, GB, GC, GD, GI, AND GE.
CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN C FAMILY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC EMBL; X01456; CAA25687.1; -.
DR PIR; A03734; VGBEF2.
DR InterPro: IPR001038; Gp13_EHV.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR001654; Marek_A.
DR Pfam; PF02124; Marek_A; 1.
DR PRINTS; PR00668; GLYCOPROTEINC.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 27
FT CHAIN 28 479
FT DOMAIN 225 327
FT CARBOHYD 40 40
FT CARBOHYD 51 51
FT CARBOHYD 116 116
FT CARBOHYD 149 149
FT CARBOHYD 165 165
FT CARBOHYD 330 330
SQ SEQUENCE 479 AA; 51667 MW; 9EDF4075108A933 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 VFDPQOI 296
DB 276 VFDPQOI 282

RESULT 87
VGLC_HSV23 STANDARD; PRT; 480 AA.

ID_VGLC_HSV23

AC P06475;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Glycoprotein C precursor.
GN GC OR UL44.
OS Herpes simplex virus (type 2 / strain 333).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxId=10313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85108149; PubMed=2982036;
RA Swain M.A., Peet R.W., Galloway D.A.;
RT "Characterization of the gene encoding herpes simplex virus type 2 glycoprotein C and comparison with the type 1 counterpart";
RL J. Virol. 53:561-569(1985).
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND 2: GH, GB, GC, GD, GI, AND GE.
CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN C FAMILY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC EMBL; U12178; AAA20532.1; -.
DR EMBL; X01996; CAA26025.1; -.
DR EMBL; M10053; AAA66442.1; -.
DR InterPro: IPR001038; Gp13_EHV.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR001654; Marek_A.
DR Pfam; PF02124; Marek_A; 1.
DR PRINTS; PR00668; GLYCOPROTEINC.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 27
FT CHAIN 28 480
FT DOMAIN 236 328
FT CARBOHYD 40 40
FT CARBOHYD 52 52
FT CARBOHYD 117 117
FT CARBOHYD 150 150
FT CARBOHYD 166 166
FT CARBOHYD 331 331
SQ SEQUENCE 480 AA; 51611 MW; CBB0F5BFE42A85 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 VFDPQOI 296
DB 277 VFDPQOI 283

RESULT 88
VGLC_HSV2H STANDARD; PRT; 480 AA.

ID_VGLC_HSV2H
AC Q89730; O12512;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Glycoprotein C precursor.
GN GC OR UL44.
OS Herpes simplex virus (type 2 / strain HG52).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxId=10315;

RN [1]
 RA SEQUENCE FROM N.A.
 RA Dolan A.;
 RN Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RC STRAIN=WTW1A;
 RA Terhune S.S.; Spear P.G.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
 CC 2: GH, GB, GC, GG, GP, GI, AND GE.
 CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN C FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
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 CC -----
 DR EMBL; Z86099; CAB06730.1; -;
 DR EMBL; U12179; AAB60551.1; -;
 DR EMBL; U12177; AAB60550.1; -;
 DR InterPro; IPR001038; GP13_EHV.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR001654; Marek_A.
 DR Pfam; PF02124; Marek_A.1.
 DR PRINTS; PR00668; GLYCOPROTEIN_C.
 DR PROSITE; PS50835; IG_LIKE.1.
 KM Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 480
 FT DOMAIN 236 328
 FT CARBOHYD 40 40
 FT CARBOHYD 52 52
 FT CARBOHYD 117 117
 FT CARBOHYD 150 150
 FT CARBOHYD 166 166
 FT CARBOHYD 331 331
 FT CARBOHYD 480 AA; 51671 MW; C145H4EPEF582B63 CRC64;
 SQ SEQUENCE 480 AA; 51671 MW; C145H4EPEF582B63 CRC64;
 Query Match 0.9%; Score 7; DB 1; Length 480;
 Best Local Similarity 100.0%; Pred No.1.le+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE FROM N.A.
 RA Coyne K.E.; Johnson J.L.; Rajagopalan K.V.;
 RT "Genomic DNA sequence of human sulfite oxidase SUOX";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RP VARIANTS GLN-160; ASP-208; TYR-370 AND ASP-473.
 RX MEDLINE=98088796; PubMed=9428520;
 RA Kisker C.; Schindelin H.; Pacheco A.; Wehli W.A.; Garrett R.M.;
 RA Rajagopalan K.V.; Enemark J.H.; Rees D.C.;
 RT "Molecular basis of sulfite oxidase deficiency from the structure of
 RT sulfite oxidase";
 RL Cell 91:973-983(1997).
 RN [4]
 RP VARIANT GLN-160.
 RX MEDLINE=98263367; PubMed=9600976;
 RA Garrett R.M.; Johnson J.L.; Graf T.N.; Feigenbaum A.;
 RA Rajagopalan K.V.;
 RT "Human sulfite oxidase R160Q: identification of the mutation in a
 RT sulfite oxidase-deficient patient and expression and characterization
 RT of the mutant enzyme";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6394-6398(1998).
 CC -1- CATALYTIC ACTIVITY: Sulfite + O(2) + H(2)O = sulfate + H(2)O(2).
 CC -1- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN) AND ONE PROTHIEME GROUP.
 CC -1- PATHWAY: TERMINAL REACTION IN THE OXIDATIVE DEGRADATION OF SULFUR-
 CC CONTAINING AMINO ACIDS. IT USES CYTOCHROME C AS AN ELECTRON
 CC ACCEPTOR.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial intermembrane space.
 CC -1- DISEASE: DEFECTS IN SUOX ARE A CAUSE OF SULFITE OXIDASE
 CC DEFICIENCY, CHARACTERIZED BY NEUROLOGICAL ABNORMALITIES. OFTEN
 CC LEADS TO DEATH AT AN EARLY AGE.
 CC -1- SIMILARITY: WITH CYTOCHROME B5 AND NITRATE REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 1 CYTOCHROME B5 HEME-BINDING DOMAIN.
 CC -----
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 CC -----
 DR EMBL; L31573; AAA74886.1; -;
 DR EMBL; AY056018; AAL08048.1; -;
 DR PIR; S55874; S55874.
 DR PDB; 1M04; 12-SEP-02.
 DR Genew; HGNC:11460; SUOX.
 DR MIM; 606887; -;
 DR MIM; 272300; -;
 DR GO; GO:0006482; F:sulfite oxidase activity; TAS.
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR000572; Euk_Mb_oxred.
 DR InterPro; IPR005066; Mo-co_dimer.
 DR Pfam; PF00173; heme_1; 1.
 DR Pfam; PF03404; Mo-co_dimer; 1.
 DR Pfam; PF00174; oxidored_mol_yb; 1.
 DR PRINTS; PR00363; CYTOCHROME_B5.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRODOM; PD000612; Cyt_B5.1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
 KM Oxidoreductase; Mitochondrion; Heme; Molybdenum; Transit peptide;
 KW Disease mutation; 3D-structure.
 FT TRANSIT 1 22
 FT CHAIN 23 488
 FT DOMAIN 23 107
 FT DOMAIN 108 124
 FT DOMAIN 125 488
 FT METAL 61 61
 FT METAL 86 86
 FT METAL 207 207
 FT METAL 260 260
 HINGE (BY SIMILARITY).
 MOLYBDENUM-PTERIN DOMAIN (BY SIMILARITY).
 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 MOLYBDENUM-PTERIN (BY SIMILARITY).
 MOLYBDENUM-PTERIN (BY SIMILARITY).

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FT VARIANT 160 160 R -> Q (IN SUOX DEFICIENCY; 2% OF
FT ACTIVITY).
FT /FTID=VAR 002200.
FT VARIANT 208 208 A -> D (IN SUOX DEFICIENCY).
FT /FTID=VAR 002201.
FT VARIANT 370 370 S -> Y (IN SUOX DEFICIENCY).
FT /FTID=VAR 002202.
FT VARIANT 473 473 G -> D (IN SUOX DEFICIENCY).
FT /FTID=VAR 002203.
SQ SEQUENCE 488 AA, 53884 MW, 41EPA367FAB766DA CRC64;

Query Match 0.9%; Score 7; DB 1; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 733 EAEVLLA 739
DB 286 EAEVLLA 292

RESULT 90
K2M2_SHEEP STANDARD; PRT; 491 AA.
ID K2M2_SHEEP
AC P15241;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Keratin, type II microfibrillar, component 7C.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RA MEDLINE=90026244; PubMed=2803211;
RA Sparrow L.G., Robinson C.P., McMahon D.T.W., Rubira M.R.;
RT "The amino acid sequence of component 7c, a type II intermediate-
RL filament protein from wool.";
CC Biochem. J. 261:1015-1022(1989).
CC -I- FUNCTION: WOOL MICROFIBRILLAR KERATIN.
CC -I- MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND
CC MICROFIBRILLAR KERATIN, I AND II (40-55 AND 56-70 KILODALTONS,
CC RESPECTIVELY). AT LEAST ONE TYPE OF CYTOSKELETAL KERATIN IS
CC PRESENT IN ALL VERTEBRATE EPITHELIAL CELLS.
CC -I- MISCELLANEOUS: THE LOW-SULFUR PROTEINS, DERIVED FROM THE
CC MICROFIBRILLAR FRACTION OF WOOL EXTRACTS, ARE COMPOSED OF TWO
CC FAMILIES, EACH CONSISTING OF 4 HOMOLOGOUS SUBUNITS: THE TYPE I
CC COMPONENTS (8C-1, 8C-2, 8A & 8B) AND THE TYPE II COMPONENTS (5,
CC 7A, 7B, AND 7C).
CC -I- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CC DR InterPro: IPR001664; IF.
CC DR InterPro: IPR003054; Keratin_II.
CC DR Pfam: PF00038; filament_1.
CC DR PRINTS: PR01276; TYPE2KERATIN.
CC DR PROSITE: PS00226; IF; 1.
KW Intermediate filament; Coiled coil; Keratin.
FT MOD_RES 1 109 BLOCKED.
FT DOMAIN 1 109 HEAD.
FT DOMAIN 110 416 ROD.
FT DOMAIN 417 491 TAIL.
FT DOMAIN 110 144 COIL 1A.
FT DOMAIN 145 154 COIL 1B.
FT DOMAIN 155 255 COIL 1B.
FT DOMAIN 256 272 LINKER 12.
FT DOMAIN 273 416 COIL 2.
FT VARIANT 74 74 C -> G OR S.
FT VARIANT 80 80 C -> S.
FT VARIANT 144 144 F -> Y.
FT VARIANT 232 232 S -> V.
FT VARIANT 276 276 C -> D OR N.
FT VARIANT 284 284 Q -> H.
FT UNSURE 1 2 CG -> GC.

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SQ SEQUENCE 491 AA, 53681 MW, AB01771FE3831ABE CRC64;

Query Match 0.9%; Score 7; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 RTKEIN 133
DB 320 RTKEIN 326

RESULT 91
K2M3_SHEEP STANDARD; PRT; 502 AA.
ID K2M3_SHEEP
AC P26591;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Keratin, type II microfibrillar, component 5.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RA MEDLINE=92171866; PubMed=1371668;
RA Sparrow L.G., Robinson C.P., Caine J., McMahon D.T.W., Strike P.M.;
RT "Type II intermediate-filament proteins from wool. The amino acid
RL sequence of component 5 and comparison with component 7c.";
CC Biochem. J. 282:291-297(1992).
CC -I- FUNCTION: WOOL MICROFIBRILLAR KERATIN.
CC -I- TISSUE SPECIFICITY: HARD KERATIN WOOL.
CC -I- MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND
CC MICROFIBRILLAR KERATIN, I AND II (40-55 AND 56-70 KILODALTONS,
CC RESPECTIVELY). AT LEAST ONE TYPE OF CYTOSKELETAL KERATIN IS
CC PRESENT IN ALL VERTEBRATE EPITHELIAL CELLS.
CC -I- MISCELLANEOUS: THE LOW-SULFUR PROTEINS, DERIVED FROM THE
CC MICROFIBRILLAR FRACTION OF WOOL EXTRACTS, ARE COMPOSED OF TWO
CC FAMILIES, EACH CONSISTING OF 4 HOMOLOGOUS SUBUNITS: THE TYPE I
CC COMPONENTS (8C-1, 8C-2, 8A & 8B) AND THE TYPE II COMPONENTS (5,
CC 7A, 7B, AND 7C).
CC -I- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CC DR InterPro: IPR001664; IF.
CC DR InterPro: IPR003054; Keratin_II.
CC DR Pfam: PF00038; filament_1.
CC DR PRINTS: PR01276; TYPE2KERATIN.
CC DR PROSITE: PS00226; IF; 1.
KW Intermediate filament; Coiled coil; Keratin.
FT MOD_RES 1 122 BLOCKED.
FT DOMAIN 1 122 HEAD.
FT DOMAIN 123 429 ROD.
FT DOMAIN 430 502 TAIL.
FT DOMAIN 123 157 COIL 1A.
FT DOMAIN 158 167 LINKER 1.
FT DOMAIN 168 268 COIL 1B.
FT DOMAIN 269 285 LINKER 12.
FT DOMAIN 286 429 COIL 2.
FT UNSURE 1 2 SC -> CS.
SQ SEQUENCE 502 AA, 55255 MW, 8734C8230550CE68 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 RTKEIN 133
DB 333 RTKEIN 339

RESULT 92
V56K_PLRV1

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ID V56K_PLRV1 STANDARD; PRT; 508 AA.
AC P17525;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE 56 kDa protein (ORF 6).
OC Potato leafroll virus (strain 1) (PLRV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OC NCBI_TaxID=12046;
RX MEDLINE=89279282; PubMed=2732710;
RA Mayo M.A., Robinson D.J., Jolly C.A., Hyman L.;
RT "Nucleotide sequence of potato leafroll luteovirus RNA.";
RL J. Gen. Virol. 70:1037-1051(1989).
CC -1- SIMILARITY: 59% SIMILARITY TO ORF 6 OF BEET WESTERN YELLOWS
VIRUS AND 45% SIMILARITY TO ORF 4 OF BARLEY YELLOW DWARF VIRUS.
CC -----
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CC -----
DR EMBL; D00530; -; NOT_ANNOTATED_CDS.
DR PIR; S24594; S24594.
DR InterPro; IPR000893; Luteo_ORF6.
DR InterPro; IPR002929; PLRV_ORF5.
DR Pfam; PF01690; PLRV_ORF5; 1.
DR PRINTS; PR00910; LVIRUSORF6.
SQ SEQUENCE 508 AA; 56593 MW; FCB68654EF1E3D7 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 PSPQPTP 355
DB 9 PSPQPTP 15

RESULT 93
V56K_PLRV1 STANDARD; PRT; 508 AA.
ID V56K_PLRV1 STANDARD; PRT; 508 AA.
AC P1626;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE 56 kDa protein (ORF 6).
OC Potato leafroll virus (strain Wageningen) (PLRV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC Polerovirus.
OC NCBI_TaxID=12048;
RX MEDLINE=89171329; PubMed=2466700;
RA van der Wilk F., Huismans M.J., Cornelissen B.J.C., Huttinga H.,
RT Goldbach R.W.;
RT "Nucleotide sequence and organization of potato leafroll virus
RT genomic RNA.";
RL FEBS Lett. 245:51-56(1989).
CC -1- SIMILARITY: 59% SIMILARITY TO ORF 6 OF BEET WESTERN YELLOWS
VIRUS AND 45% SIMILARITY TO ORF 4 OF BARLEY YELLOW DWARF VIRUS.
CC -----
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CC -----
DR EMBL; Y07496; CAA68799.1; ALT_INIT.
DR PIR; S03551; S03551.
DR InterPro; IPR000893; Luteo_ORF6.
DR InterPro; IPR002929; PLRV_ORF5.
DR Pfam; PF01690; PLRV_ORF5; 1.
DR PRINTS; PR00910; LVIRUSORF6.
SQ SEQUENCE 508 AA; 56510 MW; 195A346E9749C8A8 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 PSPQPTP 355
DB 9 PSPQPTP 15

RESULT 94
GUA_CLOPE STANDARD; PRT; 509 AA.
ID GUA_CLOPE STANDARD; PRT; 509 AA.
AC Q8X146;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (Glutamine
DE amidotransferase) (GMP synthetase).
GN GUA OR CPE2275.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OC NCBI_TaxID=1502;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -1- CATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine +
CC H(2)O = AMP + diphosphate + GMP + L-glutamate.
CC -1- PATHWAY: GMP biosynthesis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE GMP SYNTHASE
CC FAMILY.
CC -----
CC -1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
CC -----
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CC -----
DR EMBL; AP003193; BAB81981.1; -.
DR HAMAP; MF_00344; -; 1.
DR InterPro; IPR006220; Anth synthH1.
DR InterPro; IPR001317; CPS_GATase.
DR InterPro; IPR000991; GATase_1.
DR InterPro; IPR001674; GMP_synth_C.
DR InterPro; IPR004739; GMPsynthase_N.
DR Pfam; PF00117; GATase; 1.
DR Pfam; PF00958; GMP_synth_C; 1.
DR PRINTS; PR00097; ANTSYNTHASE1.
DR PRINTS; PR00099; CPSGATASE.
DR PRINTS; PR00096; GATASE.
DR TIGRFAMs; TIGR00884; guaA_Cterm; 1.
DR TIGRFAMs; TIGR00888; guaA_Nterm; 1.
DR PROSITE; PS00442; GATASE_TYPE_1; 1.

```

KM Ligase; GMP biosynthesis; Purine biosynthesis; ATP-binding;
 KW Glutamine amidotransferase; Complete proteome.
 FT DOMAIN 1 193 GLUTAMINE AMIDOTRANSFERASE.
 FT NP_BIND 222 228 ATP (BY SIMILARITY).
 FT DOMAIN 226 385 GMP-BINDING (BY SIMILARITY).
 FT ACT_SITE 81 81 GATASE (BY SIMILARITY).
 FT ACT_SITE 168 168 GATASE (BY SIMILARITY).
 FT ACT_SITE 170 170 GATASE (BY SIMILARITY).
 SQ SEQUENCE 509 AA; 56843 MW; BAA75E1207DB029A CRC64;

Query Match 0.9%; Score 7; DB 1; Length 509;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 IYNEVKG 103
 Db 484 IYNEVKG 490

RESULT 95
 ID GUAA_CLOAB STANDARD; PRT; 510 AA.
 AC Q97FW9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (Glutamine
 amidotransferase) (GMP synthetase).
 GN GUAA OR CAC2700.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 CC Clostridium.
 CX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Brekon G., Omeichenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitt J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum";
 RL J. Bacteriol. 183:4823-4838(2001).
 CC -1- CATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine +
 H(2)O = AMP + diphosphate + GMP + L-glutamate.
 CC -1- PATHWAY: GMP biosynthesis.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE GMP SYNTHASE
 FAMILY.
 CC -1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
 CC -----
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 CC -----
 CC EMBL, AE007767; AAK80646.1; -
 CC PIR: C97232; C97232.
 DR HAMAP, MF_00344; -, 1.
 DR InterPro, IPR006220; Anth_synthII.
 DR InterPro, IPR001317; CPS_GATase.
 DR InterPro, IPR000991; GATase_1.
 DR InterPro, IPR001674; GMP_synth_C.
 DR InterPro, IPR004739; GMPsynthase_N.
 DR InterPro, IPR004506; Tmnd.
 DR Pfam, PF00117; GATase_1.
 DR Pfam, PF00958; GMP_synth_C_1.
 DR Pfam, PF03054; rRNA_Me_trans_1.
 DR PRINTS, PR00097; ANTSNTHASEII.

DR PRINTS, PR00099; CPGATASE.
 DR PRINTS, PR00096; GATASE.
 DR TIGRFAMs, TIGR00884; guaa_Cterm; 1.
 DR TIGRFAMs, TIGR00888; guaa_Nterm; 1.
 DR PROSITE, PS00442; GATASE_TYPE_I; 1.
 KW Ligase; GMP biosynthesis; Purine biosynthesis; ATP-binding;
 FT Glutamine amidotransferase; Complete proteome.
 FT DOMAIN 1 194
 FT NP_BIND 223 229 ATP (BY SIMILARITY).
 FT DOMAIN 226 386 GMP-BINDING (BY SIMILARITY).
 FT ACT_SITE 82 82 GATASE (BY SIMILARITY).
 FT ACT_SITE 169 169 GATASE (BY SIMILARITY).
 FT ACT_SITE 171 171 GATASE (BY SIMILARITY).
 SQ SEQUENCE 510 AA; 57269 MW; 066C9E02F850CAC CRC64;

Query Match 0.9%; Score 7; DB 1; Length 510;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 IYNEVKG 103
 Db 485 IYNEVKG 491

RESULT 96
 ID LYN_HUMAN STANDARD; PRT; 511 AA.
 AC P07948;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
 GN LYN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87172710; PubMed=3561390;
 RA Yananashi Y., Fukushige S.-I., Semba K., Sukegawa J., Miyajima N.,
 RA Matsubara K.-I., Yamamoto T., Toyoshima K.;
 RT "The yes-related cellular gene lyn encodes a possible tyrosine kinase
 RT similar to p56lck";
 RL Mol. Cell. Biol. 7:237-243(1987).
 CC [2]
 CC SEQUENCE FROM N.A.
 RC MEDLINE=94171041; PubMed=8125304;
 RA Rider L.G., Raben N., Miller L., Jelsema C.;
 RT "The cdnas encoding two forms of the lyn protein tyrosine kinase are
 RT expressed in rat mast cells and human myeloid cells";
 RL Gene 138:219-222(1994).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=LYN A;
 CC IsoId=P07948-1; Sequence=displayed;
 CC Name=LYN B;
 CC IsoId=P07948-2; Sequence=VSP_005002;
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC -----

DR EMBL: M16038; AAA59540.1; --
 DR EMBL: M79321; AAB50019.1; --
 DR PIR: A26719; TVHULY.
 DR HSSP: P08631; IAD5.
 DR Gene: HGNC:6735; LYN.
 DR MIM: 165120; --
 DR GO: GO:0004716; F:receptor signaling protein tyrosine kinase . . .; TAS.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00108; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; TYRC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR PROTO-ONCOGENE; Tyrosine-protein kinase; Phosphorylation;
 KW Transferrase; ATP-binding; Myristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 FT INIT MET 0
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 PALMITATE (BY SIMILARITY).
 FT DOMAIN 62 122 SH2.
 FT DOMAIN 128 225 SH2.
 FT DOMAIN 246 500 PROTEIN_KINASE.
 FT NP_BIND 252 260 ATP (BY SIMILARITY).
 FT BINDING 274 274 ATP (BY SIMILARITY).
 FT ACT_SITE 366 366 BY SIMILARITY.
 FT MOD_RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 507 507 PHOSPHORYLATION (BY SIMILARITY).
 FT VARSPIC 22 42 Missing (in isoform LYN B).
 FT FTID=VSP_005002.
 SO SEQUENCE 511 AA; 58442 MW; 8419CD461204B364 CRC64;
 Query Match 0.9%; Score 7; DB 1; Length 511;
 Best Local Similarity 100.0%; Pred. No. 1; le+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 557 GKDSLSD 563
 DB 7 GKDSLSD 13
 RESULT 97
 ID C84A_ARATH STANDARD; PRT; 520 AA.
 AC 042600;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome P450 84A1 (Fenulate-5-hydroxylase) (EC 1.14.-.-) (F5H).
 GN CYP84A1 OR FAH1 OR AFG36220 OR F23E13.110.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosidia II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;

RX MEDLINE=96293440; PubMed=8692910;
 RA Meyer K., Cusumano J.C., Somerville C.R., Chapple C.C.S.;
 RT "Fenulate-5-hydroxylase from Arabidopsis thaliana defines a new
 family of cytochrome P450-dependent monooxygenases.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:6869-6874 (1996).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Landsberg erecta;
 RX MEDLINE=99097044; PubMed=9880351;
 RA Ruegger M., Meyer K., Cusumano J.C., Chapple C.;
 RT "The regulation of fenulate-5-hydroxylase expression in Arabidopsis in
 the context of sinapate ester biosynthesis.";
 RL Plant Physiol. 119:101-110 (1999).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Many strains;
 RX MEDLINE=20580555; PubMed=11141187;
 RA Aguade M.;
 RT "Nucleotide sequence variation at two genes of the phenylpropanoid
 pathway, the FAH1 and F3H genes, in Arabidopsis thaliana.";
 RL Mol. Biol. Evol. 18:1-9 (2001).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Payer K.F.X., Scheller C., Wambutt R., Murphy G., Voelckers G.,
 RA Pohl T., Diestelhorst A., Strickema W., Ertler K.-D., Terry N.,
 RA Harris B., Anesorge W., Brandt P., Grivell L.A., Rieger M.,
 RA Weissegartner M., de Simone V., Obermayer B., Maché R., Mueller M.,
 RA Kreis M., Deleney M., Pilgdomenech P., Watson M., Schmidtke T.,
 RA Reichert B., Portelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hobeisel J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCallagh B., Bilham L., Robben J.,
 RA van der Schueren J., Grymoprez B., Chuang Y.-T., Vandenbusche F.,
 RA Braeken M., Weltyens I., Voet M., Baetiaens I., Aert R., Deloor E.,
 RA Weitzenger T., Bothé G., Rampsperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
 RA Moeljaner P., Klein Lankhorst R., Rose M., Hauf J., Koetler P.,
 RA Bernier A., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA De Keyser A., Buysheert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlroy K., Mayes R.,
 RA Pettett A., Rajandream M.A., Lyne M., Benes V., Reichen S.,
 RA Borkova D., Bloembergen H., Scharfe M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fartmann B., Grandjean K., Danner D., Herzi A.,
 RA Neumann S., Argitrou A., Vitale D., Liguori R., Piravandi E.,
 RA Massenot O., Quigley F., Clabaud G., Mendenhall A., Feilber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Cheifor F., Cooke R., Berger C., Montfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bleike C.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schurz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheel P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Walter A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
 RA Granat S., Shobdy N., Hasegawa A., Hamed A., Lodhi M., Johnson A.,
 RA Chen E., Maria M., Martienssen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:769-777 (1999).
 CC -I- PATHWAY: Phenylpropanoid biosynthesis.
 CC -I- SIMILARITY: Belongs to the cytochrome P450 family.

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CC -----
DR EMBL; U38416; AAC9389.1; -
DR EMBL; AL161589; CAB80293.1; -
DR EMBL; AJ295566; CAC26922.1; -
DR EMBL; AJ295567; CAC26923.1; -
DR EMBL; AJ295568; CAC26924.1; -
DR EMBL; AJ295569; CAC26925.1; -
DR EMBL; AJ295570; CAC26926.1; -
DR EMBL; AJ295571; CAC26927.1; -
DR EMBL; AJ295572; CAC26928.1; -
DR EMBL; AJ295573; CAC26929.1; -
DR EMBL; AJ295574; CAC26930.1; -
DR EMBL; AJ295575; CAC26931.1; -
DR EMBL; AJ295576; CAC26934.1; -
DR EMBL; AJ295579; CAC26935.1; -
DR EMBL; AL022141; CAAL18128.1; -
DR EMBL; AF068574; AAD11580.1; -
DR PIR; T04591; T04591.
DR HSSP; P14779; T04591.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450; 1.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
DR Oxidoreductase; Monooxygenase; Transmembrane; Heme; Multigene family.
FT TRANSMEM 12 32
FT METAL 458 458 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 520 AA; 58720 MW; E812779AF5BF01BC CRC64;

Query Match 0.9%; Score 7; DB 1; Length 520;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 485 VDDLIAP 491
DB 278 VDDLIAP 284

RESULT 98
CP11_CANFA STANDARD; PRT; 524 AA.
AC P56550;
ID 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1) (DAH1).
GN CYP1A1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Beagle; TISSUE=Liver;
RX MEDLINE=91042464; PubMed=2122230;
RA Uchida T., Komori M., Kitada M., Kamataki T.;
RT "Isolation of cDNAs coding for three different forms of liver
RT microsomal cytochrome P-450 from polychlorinated biphenyl-treated
RT beagle-dogs."
RL Mol. Pharmacol. 38:644-651(1990).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. THIS ISOLYME SEEMS
CC RESPONSIBLE FOR METABOLISM OF 2,2',4,4',5,5'-HEXACHLOROBIPHENYL.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.

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CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- SIMILARITY: BY POLYCHLORINATED BIPHENYL (PCB) IN LIVER AND KIDNEY.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-2 OR MET-4 IS THE
CC INITIATOR.
DR PIR; C37222; C37222.
DR HSSP; P00179; ID16.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
DR Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
DR Microsome; Endoplasmic reticulum.
FT METAL 461 461 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 524 AA; 59209 MW; 0BBD2C651C13BB40 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 732 KEAEVL 738
DB 169 KEAEVL 175

RESULT 99
GCR2_YEAST STANDARD; PRT; 534 AA.
ID GCR2_YEAST
AC Q01722;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Glycolytic genes transcriptional activator GCR2.
GN GCR2 OR YNL199C OR N1374.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A. PubMed=1508187;
RX MEDLINE=92375051; PubMed=1508187;
RA Uemura H., Jigami Y.;
RT "Role of GCR2 in transcriptional activation of yeast glycolytic
RT genes."
RL Mol. Cell. Biol. 12:3834-3842(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=95242839; PubMed=7725799;
RA Joniaux J.-L., Coester F., Purnelle B., Goffeau A.;
RT "A 21.7 kb DNA segment on the left arm of yeast chromosome XIV
RT carries WHI3, GCR2, SPX18, SPX19, an homologue to the heat shock gene
RT SSB1 and 8 new open reading frames of unknown function."
RL Yeast 10:1639-1645(1994).
CC -1- FUNCTION: REQUIRED FOR THE EXPRESSION OF MOST GLYCOLYTIC GENES.
CC GCR1 AND GCR2 PROBABLY FUNCTION AS A TRANSCRIPTIONAL ACTIVATION
CC COMPLEX, GCR1 PROVIDING THE SPECIFIC DNA-BINDING FUNCTION AND
CC GCR2 PROVIDING THE ACTIVATION FUNCTION.
CC -1- SUBUNIT: FORMS A GCR1/GCR2 COMPLEX.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: SOME, TO GCR1.
CC -----
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CC -----
DR EMBL; D10104; BAA00985.1; -
DR EMBL; X78898; CAA55509.1; -
DR EMBL; Z71475; CAA96097.1; -

```

DR PIR; S31300; S31300.
 DR TRANSFAC; T03370; -.
 DR SGD; S0005143; GCR2.
 DR GO; GO:0016563; F:transcriptional activator activity; IDA.
 DR GO; GO:0045821; P:positive regulation of glycolysis; IMP.
 KM Transcription regulation; Activator; Nuclear protein.
 FT DOMAIN 281 288 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 255 283 ASN-RICH.
 SQ SEQUENCE 534 AA; 58062 MW; 958D4A393255B1B CRC64;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 1; Length 534;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 75_YDAIISE 81
 |||||
 Db 486_YDAIISE 492

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 353_PTPESP 359
 |||||
 Db 33_PTPESP 39

Search completed: November 14, 2003, 10:59:21
 Job time : 35 secs

RESULT 100
 GLE1_YEAST
 ID GLE1_YEAST STANDARD; PRT; 538 AA.
 AC 012315;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE RNA export factor GLE1.
 GN GLE1 OR BRR3 OR YDL207W OR D1049.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS.
 RX MEDLINE=96404361; PubMed=8848052;
 RA Murphy R., Wente S.R.;
 RT "An RNA-export mediator with an essential nuclear export signal.";
 RL Nature 383:357-360 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=S288c / FY1679;
 RA Bahr A., Moeller-Rieker S., Hankeln T., Kraemer C., Schmidt E.R.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RNA EXPORT FACTOR. THE MECHANISM MAY INVOLVE THE DIRECT
 TARGETING OF RNA/RNP MOLECULES TO OR THROUGH THE NUCLEAR PORE
 COMPLEX BY MEANS OF R1P1 AND NUP100 INTERACTIONS.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR. LOCALIZED PREDOMINANTLY AT THE
 NUCLEAR PORE COMPLEXES.
 CC
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 CC
 CC EMBL; U68475; AAC9444.1; -;
 CC EMBL; X99000; CAA67484.1; -;
 CC EMBL; Z74255; CAA98785.1; -;
 DR PIR; S67766; S67766.
 DR SGD; S0002366; GLE1.
 DR GO; GO:0016973; P:poly(A)+ mRNA-nucleus export; IMP.
 KM Nuclear protein; mRNA processing.
 FT DOMAIN 351 358 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MUTAGEN 351 351 L->A: PARTIAL LOSS OF ACTIVITY.
 FT MUTAGEN 353 353 L->A: PARTIAL LOSS OF ACTIVITY.
 FT MUTAGEN 356 356 L->A: TEMPERATURE SENSITIVE.
 FT MUTAGEN 358 358 L->A: PARTIAL LOSS OF ACTIVITY.
 SQ SEQUENCE 538 AA; 62073 MW; C9C6B1513AF95711 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 1; Length 538;
 Pred. No. 1.2e+02;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 10:45:15 ; Search time 88 Seconds
(without alignments)
2334.203 Million cell updates/sec

Title: US-09-765-271-56

Perfect score: 796

Sequence: 1 SYELGIYQARTVKENNRVSY.....KLIALIKGSPSSVSKEKIN 796

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 200 summaries

Database :

SPREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	795	99.9	816	2 Q9AHT9	Q9AHT9 streptococc
2	695	87.3	802	16 Q97QM8	Q97QM8 streptococc
3	616	77.4	828	16 Q8DPQ2	Q8DPQ2 streptococc
4	107	13.4	844	2 Q9AG74	Q9AG74 streptococc
5	107	13.4	855	16 Q8CNR4	Q8CNR4 streptococc
6	60	7.5	819	2 Q9ANY3	Q9ANY3 streptococc
7	60	7.5	819	16 Q97QM9	Q97QM9 streptococc
8	60	7.5	839	16 Q9ANY2	Q9ANY2 streptococc
9	60	7.5	853	16 Q8DQ08	Q8DQ08 streptococc
10	32	4.0	1039	16 Q9ANY1	Q9ANY1 streptococc
11	32	4.0	1039	16 Q8DQ07	Q8DQ07 streptococc
12	27	3.4	481	16 Q8E338	Q8E338 streptococc
13	17	2.1	289	2 Q9AE21	Q9AE21 streptococc
14	17	2.1	822	2 Q9ZHG7	Q9ZHG7 streptococc
15	17	2.1	822	16 Q8E4U1	Q8E4U1 streptococc
16	17	2.1	822	16 Q8D281	Q8D281 streptococc

17	17	2.1	823	16 Q8N282	Q8N282 streptococc
18	17	2.1	823	16 Q8K5Q1	Q8K5Q1 streptococc
19	17	2.1	825	2 Q93GTS	Q93GTS streptococc
20	17	2.1	825	16 Q99XV4	Q99XV4 streptococc
21	10	1.3	182	16 Q8DQ06	Q8DQ06 streptococc
22	9	1.1	791	16 Q9CLO1	Q9CLO1 pasteurella
23	8	1.0	71	12 Q8B9M0	Q8B9M0 rachidiplusia
24	8	1.0	147	16 Q8EHD8	Q8EHD8 shewanella
25	8	1.0	152	5 Q8IIB9	Q8IIB9 plasmodium
26	8	1.0	154	5 P91742	P91742 hydra atten
27	8	1.0	181	5 Q44095	Q44095 drosophila
28	8	1.0	270	5 Q9NCF0	Q9NCF0 cryptocercu
29	8	1.0	284	5 Q22866	Q22866 caenorhabdi
30	8	1.0	284	5 Q22865	Q22865 caenorhabdi
31	8	1.0	284	5 Q27284	Q27284 caenorhabdi
32	8	1.0	294	5 Q46010	Q46010 caenorhabdi
33	8	1.0	301	5 Q95Q31	Q95Q31 caenorhabdi
34	8	1.0	319	16 Q8FLF7	Q8FLF7 corynebacte
35	8	1.0	436	3 Q9P8N1	Q9P8N1 coriolus ve
36	8	1.0	484	16 Q9K5S1	Q9K5S1 vibrio chol
37	8	1.0	485	10 Q80401	Q80401 oryza sativ
38	8	1.0	488	16 Q99TD8	Q99TD8 staphylococ
39	8	1.0	488	16 Q8NW40	Q8NW40 staphylococ
40	8	1.0	490	16 Q8CNW2	Q8CNW2 staphylococ
41	8	1.0	673	6 Q95LI9	Q95LI9 oryctolagus
42	8	1.0	840	16 Q9RSJ4	Q9RSJ4 deinococcus
43	8	1.0	945	16 Q26077	Q26077 helicobacte
44	8	1.0	1233	17 Q8TMX4	Q8TMX4 methanosarc
45	8	1.0	1646	2 Q93HW0	Q93HW0 streptococc
46	8	1.0	1659	16 Q97S90	Q97S90 streptococc
47	8	1.0	1659	16 Q8C252	Q8C252 streptococc
48	8	1.0	2621	5 Q8SSW5	Q8SSW5 dictyostell
49	7	0.9	42	15 Q87936	Q87936 chimpanzee
50	7	0.9	42	15 Q87948	Q87948 chimpanzee
51	7	0.9	42	15 Q87938	Q87938 chimpanzee
52	7	0.9	42	15 Q88084	Q88084 chimpanzee
53	7	0.9	42	15 Q87952	Q87952 chimpanzee
54	7	0.9	42	15 Q87946	Q87946 chimpanzee
55	7	0.9	42	15 Q88080	Q88080 chimpanzee
56	7	0.9	43	15 Q87944	Q87944 chimpanzee
57	7	0.9	44	15 Q87942	Q87942 chimpanzee
58	7	0.9	49	15 Q87940	Q87940 chimpanzee
59	7	0.9	49	16 Q45596	Q45596 bacillus su
60	7	0.9	50	2 Q9AGM9	Q9AGM9 clostridium
61	7	0.9	51	16 Q8EHT0	Q8EHT0 escherichia
62	7	0.9	68	15 Q90VA0	Q90VA0 human immun
63	7	0.9	68	16 Q9A3B0	Q9A3B0 caulobacter
64	7	0.9	71	1 Q977L2	Q977L2 uncultured
65	7	0.9	71	17 Q96YD8	Q96YD8 sulfobolus
66	7	0.9	80	3 Q9HGR7	Q9HGR7 gilbertella
67	7	0.9	83	5 Q8MYJ9	Q8MYJ9 dictyostell
68	7	0.9	86	15 Q73850	Q73850 human immun
69	7	0.9	86	15 Q73851	Q73851 human immun
70	7	0.9	86	15 Q73852	Q73852 human immun
71	7	0.9	90	17 Q97W98	Q97W98 sulfobolus
72	7	0.9	93	16 Q9RUC5	Q9RUC5 deinococcus
73	7	0.9	94	16 Q9RY27	Q9RY27 deinococcus
74	7	0.9	96	16 Q8FAP6	Q8FAP6 escherichia
75	7	0.9	104	17 Q8U029	Q8U029 pyrococcus
76	7	0.9	108	15 P88557	P88557 human immun
77	7	0.9	109	2 Q8VR72	Q8VR72 escherichia
78	7	0.9	110	16 Q9A654	Q9A654 caulobacter
79	7	0.9	110	16 Q9CDT0	Q9CDT0 lactococcus
80	7	0.9	111	16 Q8FC10	Q8FC10 escherichia
81	7	0.9	115	16 Q8CMN4	Q8CMN4 staphylococ
82	7	0.9	116	5 Q8T427	Q8T427 plasmodium
83	7	0.9	117	10 Q8I494	Q8I494 oryza sativ
84	7	0.9	117	16 Q8YCC21	Q8YCC21 bruceella me
85	7	0.9	120	12 Q8QUR7	Q8QUR7 infectious
86	7	0.9	124	16 Q8FDX0	Q8FDX0 escherichia
87	7	0.9	126	2 Q9X6J3	Q9X6J3 bacillus st
88	7	0.9	128	16 Q8FWA2	Q8FWA2 bruceella su
89	7	0.9	128	16 Q8EMH6	Q8EMH6 oceanobacill

90	7	0.9	128	17	O9YAF7	O9YAF7 aeropyrum p
91	7	0.9	129	16	O9XBD3	O9XBD3 streptomyce
92	7	0.9	130	16	P74726	P74726 synechocyst
93	7	0.9	131	2	O69802	O69802 streptomyce
94	7	0.9	131	16	O92P78	O92P78 rhizobium m
95	7	0.9	131	16	O86762	O86762 streptomyce
96	7	0.9	134	12	O9YL97	O9YL97 human adeno
97	7	0.9	134	15	O90640	O90640 smian-huma
98	7	0.9	134	15	O8PN57	O8PN57 xanthomonas
99	7	0.9	136	2	O8V819	O8V819 shigella fl
100	7	0.9	136	5	O17947	O17947 caenorhabdi
101	7	0.9	136	16	O9JMT0	O9JMT0 escherichia
102	7	0.9	137	15	O8QDG8	O8QDG8 chimpanzee
103	7	0.9	137	15	O8QDG9	O8QDG9 chimpanzee
104	7	0.9	137	15	O8QDG3	O8QDG3 chimpanzee
105	7	0.9	137	15	O8QDH0	O8QDH0 chimpanzee
106	7	0.9	137	15	O8QDH5	O8QDH5 chimpanzee
107	7	0.9	137	15	O8QDH1	O8QDH1 chimpanzee
108	7	0.9	137	15	O8QDH3	O8QDH3 chimpanzee
109	7	0.9	137	15	O8QDH2	O8QDH2 chimpanzee
110	7	0.9	137	15	O8QDG5	O8QDG5 chimpanzee
111	7	0.9	137	15	O8QDG4	O8QDG4 chimpanzee
112	7	0.9	137	15	O8QDG6	O8QDG6 chimpanzee
113	7	0.9	139	16	O9PMP7	O9PMP7 campylobact
114	7	0.9	143	16	O98J01	O98J01 rhizobium l
115	7	0.9	144	6	O9BH14	O9BH14 antilocapra
116	7	0.9	145	16	O8Y7M1	O8Y7M1 listeria mo
117	7	0.9	147	16	O9HZE1	O9HZE1 pseudomonas
118	7	0.9	148	16	O8X8A4	O8X8A4 escherichia
119	7	0.9	149	16	O8DL26	O8DL26 synechococc
120	7	0.9	151	2	O9AFN4	O9AFN4 shigella fl
121	7	0.9	152	5	O8N052	O8N052 drosophila
122	7	0.9	152	5	O8N052	O8N052 drosophila
123	7	0.9	152	16	O8P1G4	O8P1G4 xanthomonas
124	7	0.9	152	16	O8P749	O8P749 xanthomonas
125	7	0.9	153	5	O8N050	O8N050 drosophila
126	7	0.9	153	5	O9LVZ0	O9LVZ0 arabidopsis
127	7	0.9	154	5	O8N041	O8N041 drosophila
128	7	0.9	154	5	O8N048	O8N048 drosophila
129	7	0.9	154	5	O8N051	O8N051 drosophila
130	7	0.9	155	5	O8N042	O8N042 drosophila
131	7	0.9	155	5	O8N039	O8N039 drosophila
132	7	0.9	155	5	O8N013	O8N013 drosophila
133	7	0.9	155	5	O8N040	O8N040 drosophila
134	7	0.9	155	5	O8N047	O8N047 drosophila
135	7	0.9	155	5	O8N053	O8N053 drosophila
136	7	0.9	156	11	O9JUF0	O9JUF0 mus musculu
137	7	0.9	157	5	O9Y064	O9Y064 taenia soli
138	7	0.9	157	5	O8N043	O8N043 drosophila
139	7	0.9	157	5	O8N054	O8N054 drosophila
140	7	0.9	157	5	O8N049	O8N049 drosophila
141	7	0.9	157	5	O8N045	O8N045 drosophila
142	7	0.9	157	16	O8UB40	O8UB40 agrobacteri
143	7	0.9	157	16	O8U631	O8U631 agrobacteri
144	7	0.9	157	16	O8PM65	O8PM65 xanthomonas
145	7	0.9	158	10	O8GWR9	O8GWR9 arabidopsis
146	7	0.9	159	2	O86437	O86437 escherichia
147	7	0.9	160	2	O8GHN8	O8GHN8 pseudomonas
148	7	0.9	160	5	O8N046	O8N046 drosophila
149	7	0.9	161	5	O8N030	O8N030 drosophila
150	7	0.9	161	5	O8N032	O8N032 drosophila
151	7	0.9	161	5	O8N015	O8N015 drosophila
152	7	0.9	162	5	O8N035	O8N035 drosophila
153	7	0.9	162	5	O8N020	O8N020 drosophila
154	7	0.9	163	5	O8N036	O8N036 drosophila
155	7	0.9	164	5	O8N017	O8N017 drosophila
156	7	0.9	164	5	O8N033	O8N033 drosophila
157	7	0.9	164	5	O8N029	O8N029 drosophila
158	7	0.9	164	5	O8N023	O8N023 drosophila
159	7	0.9	164	5	O8N028	O8N028 drosophila
160	7	0.9	164	5	O8N027	O8N027 drosophila
161	7	0.9	165	5	O8N026	O8N026 drosophila
162	7	0.9	165	5		

163	7	0.9	165	5	O8N024	O8N024 drosophila
164	7	0.9	165	5	O8N019	O8N019 drosophila
165	7	0.9	165	5	O8N034	O8N034 drosophila
166	7	0.9	165	5	O8N016	O8N016 drosophila
167	7	0.9	165	5	O8N031	O8N031 drosophila
168	7	0.9	165	5	O8N022	O8N022 drosophila
169	7	0.9	165	16	O9I2Q4	O9I2Q4 pseudomonas
170	7	0.9	165	5	O8N037	O8N037 drosophila
171	7	0.9	166	5	O8N021	O8N021 drosophila
172	7	0.9	166	16	O8NR4	O8NR4 corynebacte
173	7	0.9	167	5	O8N057	O8N057 drosophila
174	7	0.9	167	5	O8N025	O8N025 drosophila
175	7	0.9	167	5	O8N044	O8N044 drosophila
176	7	0.9	167	5	O8N038	O8N038 drosophila
177	7	0.9	167	16	O8DBU1	O8DBU1 vibrio vuln
178	7	0.9	168	2	O8GCH0	O8GCH0 chlamydomo
179	7	0.9	168	5	O8N018	O8N018 drosophila
180	7	0.9	169	5	O8N059	O8N059 drosophila
181	7	0.9	169	5	O8N055	O8N055 drosophila
182	7	0.9	169	5	O8N060	O8N060 drosophila
183	7	0.9	169	5	O8N058	O8N058 drosophila
184	7	0.9	171	5	O8N056	O8N056 drosophila
185	7	0.9	177	16	O8RIJ7	O8RIJ7 fusobacteri
186	7	0.9	181	4	O5I571	O5I571 borrelia bu
187	7	0.9	184	16	O96RK1	O96RK1 homo sapien
188	7	0.9	184	16	O8PBK5	O8PBK5 xanthomonas
189	7	0.9	184	16	O8FS32	O8FS32 corynebacte
190	7	0.9	186	2	O49530	O49530 mycoplasma
191	7	0.9	186	10	O9LID5	O9LID5 arbidopsis
192	7	0.9	186	17	O96Z27	O96Z27 sulfolobus
193	7	0.9	187	2	O8LRF4	O8LRF4 oryza sativ
194	7	0.9	189	2	O8VBE6	O8VBE6 salmonella
195	7	0.9	189	10	O8H341	O8H341 oryza sativ
196	7	0.9	190	16	O8CK90	O8CK90 yersinia pe
197	7	0.9	192	10	O9FIT9	O9FIT9 arbidopsis
198	7	0.9	192	11	O9DA99	O9DA99 mus musculu
199	7	0.9	198	4	O9NPS2	O9NPS2 homo sapien
200	7	0.9	198	17	O8ZV93	O8ZV93 pyrobaculum

ALIGNMENTS

RESULT 1

ID	Q9AHT9	PRELIMINARY:	PRT:	816 AA.
AC	O9AHT9			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Pneumococcal histidine triad A protein.			
GN	PTHA.			
OS	Streptococcus pneumoniae.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
CC	Streptococcus.			
OX	NCBI_TaxID=1313;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=N4;			
RX	MEDLINE=21116976; PubMed=1179332;			
RA	Wizemann T.M., Heinrichs J.H., Adamou J.E., Erwin A.L., Kunsch C.,			
RA	Choi G.H., Barash S.C., Rosen C.A., Masure H.R., Tuomanen E.,			
RA	Cayle A., Brewah Y.A., Walsh W., Barron P., Lathigra R., Hanson M.,			
RA	Langemann S., Johnson S., Koenig S.,			
RT	"Use of a Whole Genome Approach To Identify Vaccine Molecules			
RT	Affording Protection Against Streptococcus pneumoniae Infection."			
RL	Infect. Immun. 69:1593-1598(2001).			
DR	EMBL: AF291695; AAK19155.1; "			
DR	InterPro: IPR006270; Strep_his_triad.			
DR	TIGRFAWS: TIGR01363; strep_his_triad; 2			
SQ	SEQUENCE 816 AA; 91519 MW; 5359126A61D27ED CRC64;			

Query Match 99.9%; Score 795; DB 2; Length 816;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYELGLYQARTVKNRRVSYIDGKQATQKTEMLTPDEVSKREGINAEQIVIKITDGGYVT 60
DB 21 SYELGLYQARTVKNRRVSYIDGKQATQKTEMLTPDEVSKREGINAEQIVIKITDGGYVT 80
QY 61 SHGDHYYNGKVPYDAIISEELMKDPNYLKDEDIVNEVKGQYVIRKDGKYYVYLKDA 120
DB 81 SHGDHYYNGKVPYDAIISEELMKDPNYLKDEDIVNEVKGQYVIRKDGKYYVYLKDA 140
QY 121 AAHDNVRKTEINRQKQESHQHEGTPRNDGVALARSQGYTTDDGYIFNADIIEDT 180
DB 141 AAHDNVRKTEINRQKQESHQHEGTPRNDGVALARSQGYTTDDGYIFNADIIEDT 200
QY 181 GDAYIVPHGDHYHIFPKNELSASELAFAFLSGRGLNSRTRYRQNSDNTSRTWVPS 240
DB 201 GDAYIVPHGDHYHIFPKNELSASELAFAFLSGRGLNSRTRYRQNSDNTSRTWVPS 260
QY 241 VSNPGTTNTNTSNNSNTNSQASQNDIDSLKQLYKLPSQRHVESDGLVFPDAQITSTRT 300
DB 261 VSNPGTTNTNTSNNSNTNSQASQNDIDSLKQLYKLPSQRHVESDGLVFPDAQITSTRT 320
QY 301 ARGVAVPHGDHYHIFIPYSQMSLEERIIARIIPLRYSNMHWDPDSRPPSPQPTPEPSPG 360
DB 321 ARGVAVPHGDHYHIFIPYSQMSLEERIIARIIPLRYSNMHWDPDSRPPSPQPTPEPSPG 380
QY 361 POPAPVPLKIDSNSLSVQLVRKVGEGYVEEKGISRYVFAKDLPSFTVKNLESKLSKQES 420
DB 381 POPAPVPLKIDSNSLSVQLVRKVGEGYVEEKGISRYVFAKDLPSFTVKNLESKLSKQES 440
QY 421 VSHITLAKKENVAAPROEFYDKAYNLLTEAHKALFNKGRNSDFOLADKLELNDESTN 480
DB 441 VSHITLAKKENVAAPROEFYDKAYNLLTEAHKALFNKGRNSDFOLADKLELNDESTN 500
QY 481 KEKLVDDLAFAPITHPERLGRKPSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD 540
DB 501 KEKLVDDLAFAPITHPERLGRKPSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD 560
QY 541 EGDAYVTPHMGSHHWGKSLSDKEKVAQAATYKKGILPPSPDADVKNPFGDSAAAY 600
DB 561 EGDAYVTPHMGSHHWGKSLSDKEKVAQAATYKKGILPPSPDADVKNPFGDSAAAY 620
QY 601 NRKVGKRIPLVRLPMVHEHTEVKNGNLIIIPKDHYNHKKFAMPFDHTYKAPNGYTLSD 660
DB 621 NRKVGKRIPLVRLPMVHEHTEVKNGNLIIIPKDHYNHKKFAMPFDHTYKAPNGYTLSD 680
QY 661 LFATIKYYVEHPDERPHSNDGNGNASEHVLGKKHSDPNKPKADEEVEETPAPEVP 720
DB 681 LFATIKYYVEHPDERPHSNDGNGNASEHVLGKKHSDPNKPKADEEVEETPAPEVP 740
QY 721 QVTEKEVAQLKAEVLLAVYTSSSLKAAATEFLAGLRNNLTLOIMDNNSIMAEKELA 780
DB 741 QVTEKEVAQLKAEVLLAVYTSSSLKAAATEFLAGLRNNLTLOIMDNNSIMAEKELA 800
QY 781 LKGSNPPSSVSKKIN 796
DB 801 LKGSNPPSSVSKKIN 816

RESULT 2
Q970M8 PRELIMINARY; PRT; 802 AA.
AC Q970M8; 01-OCT-2001 (Tremblrel. 18, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
GN SP1175.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
NCBI_TaxID=1313;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettein H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwin M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holzapfel E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Lotens B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.,
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae."
RL Science 293:498-506(2001).
DR EMBL: AE007418; AKK75284.1; -.
DR TIGR: SP1175; -.
DR InterPro: IPR006270; Strept_his_triad.
DR TIGRfams: TIGR01363; strep_his_triad; 2.
KW Complete proteome.
SQ SEQUENCE 802 AA; 90080 MW; 4E5CB8364EBA1833 CRC64;

Query Match 87.3%; Score 695; DB 16; Length 802;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYELGLYQARTVKNRRVSYIDGKQATQKTEMLTPDEVSKREGINAEQIVIKITDGGYVT 60
DB 7 SYELGLYQARTVKNRRVSYIDGKQATQKTEMLTPDEVSKREGINAEQIVIKITDGGYVT 66
QY 61 SHGDHYYNGKVPYDAIISEELMKDPNYLKDEDIVNEVKGQYVIRKDGKYYVYLKDA 120
DB 67 SHGDHYYNGKVPYDAIISEELMKDPNYLKDEDIVNEVKGQYVIRKDGKYYVYLKDA 126
QY 121 AAHDNVRKTEINRQKQESHQHEGTPRNDGVALARSQGYTTDDGYIFNADIIEDT 180
DB 127 AAHDNVRKTEINRQKQESHQHEGTPRNDGVALARSQGYTTDDGYIFNADIIEDT 186
QY 181 GDAYIVPHGDHYHIFPKNELSASELAFAFLSGRGLNSRTRYRQNSDNTSRTWVPS 240
DB 187 GDAYIVPHGDHYHIFPKNELSASELAFAFLSGRGLNSRTRYRQNSDNTSRTWVPS 246
QY 241 VSNPGTTNTNTSNNSNTNSQASQNDIDSLKQLYKLPSQRHVESDGLVFPDAQITSTRT 300
DB 247 VSNPGTTNTNTSNNSNTNSQASQNDIDSLKQLYKLPSQRHVESDGLVFPDAQITSTRT 306
QY 301 ARGVAVPHGDHYHIFIPYSQMSLEERIIARIIPLRYSNMHWDPDSRPPSPQPTPEPSPG 360
DB 307 ARGVAVPHGDHYHIFIPYSQMSLEERIIARIIPLRYSNMHWDPDSRPPSPQPTPEPSPG 366
QY 361 POPAPVPLKIDSNSLSVQLVRKVGEGYVEEKGISRYVFAKDLPSFTVKNLESKLSKQES 420
DB 367 POPAPVPLKIDSNSLSVQLVRKVGEGYVEEKGISRYVFAKDLPSFTVKNLESKLSKQES 426
QY 421 VSHITLAKKENVAAPROEFYDKAYNLLTEAHKALFNKGRNSDFOLADKLELNDESTN 480
DB 427 VSHITLAKKENVAAPROEFYDKAYNLLTEAHKALFNKGRNSDFOLADKLELNDESTN 486
QY 481 KEKLVDDLAFAPITHPERLGRKPSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD 540
DB 487 KEKLVDDLAFAPITHPERLGRKPSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD 546
QY 541 EGDAYVTPHMGSHHWGKSLSDKEKVAQAATYKKGILPPSPDADVKNPFGDSAAAY 600
DB 547 EGDAYVTPHMGSHHWGKSLSDKEKVAQAATYKKGILPPSPDADVKNPFGDSAAAY 606
QY 601 NRKVGKRIPLVRLPMVHEHTEVKNGNLIIIPKDHYNHKKFAMPFDHTYKAPNGYTLSD 660
DB 607 NRKVGKRIPLVRLPMVHEHTEVKNGNLIIIPKDHYNHKKFAMPFDHTYKAPNGYTLSD 666
QY 661 LFATIKYYVEHPDERPHSNDGNGNASEHVLGKKHSDPNKPKADEEVEETPAPEVP 720
DB 667 LFATIKYYVEHPDERPHSNDGNGNASEHVLGKKHSDPNKPKADEEVEETPAPEVP 726

OY 721 OVEETEKEVAQLKEAEVLLAKVTDSLLKANATETTLAGLRNNLTLOIMDNNSIMAEAKLLA 780
 DB 727 OVEETEKEVAQLKEAEVLLAKVTDSLLKANATETTLAGLRNNLTLOIMDNNSIMAEAKLLA 786
 OY 781 LKGSNPSSVSKEKIN 796
 DB 787 LKGSNPSSVSKEKIN 802

RESULT 3

Q8DPQ2 PRELIMINARY; PRT; 828 AA.
 AC Q8DPQ2:
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Pneumococcal histidine triad protein A.
 GN PHTA OR SPRI061.
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 NCBI_TaxID=171101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21429245; PubMed=11544234;
 RA Hoskins J., Alborn W.E., Jr., Arnold J., Blaszczak L.C., Burgett S.,
 Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
 Gilmour R., Glas J.S., Khoja H., Kraft A.R., Lagace R.E.,
 Leblanc D.J., Lee L.N., Leikowitz E.J., Lu J., Matsumura P.,
 McAhren S.M., McNamey M., McLeaster K., Mundy C.W., Nices T.I.,
 Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rocky P.,
 Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
 Zook C.A., Baltz R.H., Jaskunas S.R., Kosteck P.R., Jr., Skatrud P.L.,
 RA Glas J.I.;
 RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
 RL J. Bacteriol. 183:5709-5717(2001).
 DR EMBL: AE008479; AAK9865.1; -.
 KW Complete proteome.
 SQ SEQUENCE 828 AA; 93015 MW; 12CCCF407B550CID CRC64;

Query Match 77.4%; Score 616; DB 16; Length 828;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 716; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 80 SEELMKDPNYKLKDEDIVNEVKGIVIKVDGKYVYLKDAHADNVRTKEINRQKOE 139
 DB 112 SEELMKDPNYKLKDEDIVNEVKGIVIKVDGKYVYLKDAHADNVRTKEINRQKOE 171
 OY 140 SOHREGCPRNDGAVALARSOGRYTTDDGYIFNADIIEDTGDAYIVPHGDHYHPIKNE 199
 DB 172 SOHREGCPRNDGAVALARSOGRYTTDDGYIFNADIIEDTGDAYIVPHGDHYHPIKNE 231
 OY 200 LSASELAALAEAFLSGRNLNSNRTYRONSNDTSRTNWPSVSNFGTTNTNNTS 259
 DB 232 LSASELAALAEAFLSGRNLNSNRTYRONSNDTSRTNWPSVSNFGTTNTNNTS 291
 OY 260 QASOSNDIDSLKQLYKPLPSORHVESDGLVDPDQITSRTRAGVAVPHGDHYHPIYSQ 319
 DB 292 QASOSNDIDSLKQLYKPLPSORHVESDGLVDPDQITSRTRAGVAVPHGDHYHPIYSQ 351
 OY 320 MSELERARITPLPYRSNHWVPSRPOSPQPTPEPSPGOPAPNLIKIDNSLSVQL 379
 DB 352 MSELERARITPLPYRSNHWVPSRPOSPQPTPEPSPGOPAPNLIKIDNSLSVQL 411
 OY 380 VRKVEGVVFEKGIISRYVFAKDLPSYTKNLESLSKQESVSHLTAKKEVAPRDOEF 439
 DB 412 VRKVEGVVFEKGIISRYVFAKDLPSYTKNLESLSKQESVSHLTAKKEVAPRDOEF 471
 OY 440 YDKAVNLTFAHAKLPXNKGNSDPQALDKLIERLNDSSTNKEKLVDDLAFAPITPHE 499
 DB 472 YDKAVNLTFAHAKLPXNKGNSDPQALDKLIERLNDSSTNKEKLVDDLAFAPITPHE 531

OY 500 RLGRPNQISEYTEDEVEVIAQLADKYTTSDGYIPDEHDIISDEGDAYVTPHNGSHMTGKD 559
 DB 532 RLGRPNQISEYTEDEVEVIAQLADKYTTSDGYIPDEHDIISDEGDAYVTPHNGSHMTGKD 591
 OY 560 SLSDKEKVAQAAYTEKGIILPPSPDADVKANPTGDSAAAIYNRVKGKRIPLVRLPYVE 619
 DB 592 SLSDKEKVAQAAYTEKGIILPPSPDADVKANPTGDSAAAIYNRVKGKRIPLVRLPYVE 651
 OY 620 HTVEVKGNLIIIPKDHVHNIKFPMPDHTYKANGTYLEDLPATIKYVEHPERPHSN 679
 DB 652 HTVEVKGNLIIIPKDHVHNIKFPMPDHTYKANGTYLEDLPATIKYVEHPERPHSN 711
 OY 680 DGMGNASEHVLAGKDHSEDPKNFKADEEPYEETPAEBEVPQVETKEVAQLKEAEVLLA 739
 DB 712 DGMGNASEHVLAGKDHSEDPKNFKADEEPYEETPAEBEVPQVETKEVAQLKEAEVLLA 771
 OY 740 KVTDSLLKANATETTLAGLRNNLTLOIMDNNSIMAEAKLLALKGSNPSSVSKEKIN 796
 DB 772 KVTDSLLKANATETTLAGLRNNLTLOIMDNNSIMAEAKLLALKGSNPSSVSKEKIN 828

RESULT 4

Q9AG74 PRELIMINARY; PRT; 844 AA.
 AC Q9AG74:
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE PhpA.
 GN PHPA.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21246685; PubMed=11349048;
 RA Zhang Y., Masi A.W., Barniak V., Mountzouros K., Hostetter M.K.,
 RA Green B.A.;
 RT "Recombinant PhpA Protein, a Unique Histidine Motif-Containing Protein
 from Streptococcus pneumoniae, Protects Mice against Intranasal
 RT from Streptococcus pneumoniae, Protects Mice against Intranasal
 RT Infect. Immun. 69:3827-3836(2001).
 RL EMBL: AF340221; AAK26629.1; -.
 DR InterPro: IPR006270; Strep_his_triad.
 DR TIGRFAMs: TIGR01363; Strep_his_triad; 2
 SQ SEQUENCE 844 AA; 94769 MW; D738A55290FF8902 CRC64;

Query Match 13.4%; Score 107; DB 2; Length 844;
 Best Local Similarity 100.0%; Pred. No. 1,2e-96;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 102 KGGYIVKDGKYVYLKDAHADNVRTKEINRQKQHSQHREGCTPRNDGAVALARSO 161
 DB 122 KGGYIVKDGKYVYLKDAHADNVRTKEINRQKQHSQHREGCTPRNDGAVALARSO 181
 OY 162 RYTTDDGYIFNADIIEDTGDAYIVPHGDHYHPIKNELSASELAA 208
 DB 182 RYTTDDGYIFNADIIEDTGDAYIVPHGDHYHPIKNELSASELAA 228

RESULT 5

Q8CWR4 PRELIMINARY; PRT; 855 AA.
 AC Q8CWR4:
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Histidine motif-containing protein.
 GN PHPA OR SPRI060.
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.

OK NCBI_TaxID=171101;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21429245; PubMed=11544234;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., BURGESS S.,
RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McArthur S.M., McHenry M., Mcleaster K., Mundy C.W., Nicot T.I.,
RA Norris F.H., O'Garra M., Peery R.B., Robertson G.T., Rokey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Kosteck P.R. Jr., Skatrud P.L.,
RA Glass J.I.,
RT "Genome of the bacterium Streptococcus pneumoniae strain R6,"
RL J. Bacteriol. 183:5709-5717(2001).
DR EMBL: AE008479; AAK99864.1; -.
KW Complete proteome.
SQ SEQUENCE 855 AA; 96177 MW; 4350E82A3F97089A CRC64;

Query Match 13.4%; Score 107; DB 16; Length 855;
Best Local Similarity 100.0%; Pred. No. 1.2e-96;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 KGGYIKDYGKYYVYIKDAADNVTKEINRQKQSHQRBGGTPRNDGVALARSG 161
DB 133 KGGYIKDYGKYYVYIKDAADNVTKEINRQKQSHQRBGGTPRNDGVALARSG 192

QY 162 RYTTDDGYIFNADIIEDTDGAYIVPHGDHYHYIPKNELSASELAA 208
DB 193 RYTTDDGYIFNADIIEDTDGAYIVPHGDHYHYIPKNELSASELAA 239

RESULT 6
Q9ANY3 PRELIMINARY; PRT; 819 AA.
ID Q9ANY3;
AC Q9ANY3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pneumococcal histidine triad protein B precursor (Fragment).
GN PHTB.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21101045; PubMed=11159990;
RA Adamou J.E., Heinrichs J.H., Erwin A.L., Walsh W., Gayle T.,
RA Dornitzer M., Dagan R., Brewah Y.A., Barren P., Lathigra R.,
RA Langemann S., Koenig S., Johnson S.;
RT "Identification and characterization of a novel family of pneumococcal
RT proteins (the Pht family) that are protective against sepsis,"
RL Infect. Immun. 69:949-958(2001).
DR EMBL: AF318954; AAK06759.1; -.
DR InterPro: IPR006270; Strep_his_triad.
DR TIGRFAMs: TIGR01363; strep_his_triad; 2.
KW SIGNAL.
FT SIGNAL 1 29 POTENTIAL.
FT NON_TER 819
SQ SEQUENCE 819 AA; 92108 MW; E602CFC16CC28A5F CRC64;

Query Match 7.5%; Score 60; DB 2; Length 819;
Best Local Similarity 100.0%; Pred. No. 4.6e-50;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 ENLTPDEVSKREGINAEOIVIKITDGYVTSHGHHYNGKVPYDAIISELLMKDPNY 90
DB 52 ENLTPDEVSKREGINAEOIVIKITDGYVTSHGHHYNGKVPYDAIISELLMKDPNY 111

RESULT 7
Q97OM9

ID Q97OM9 PRELIMINARY; PRT; 819 AA.
AC Q97OM9;
DT 01-OCT-2001 (TrEMBLrel. 19, Created)
DT 01-OCT-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Conserved domain protein.
GN SP1174.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tetelcin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., Deboy R.T., Hatt D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapfel E., Khouri H., Wolf A.M., Utecherback T.R., Hansen C.L.,
RA McDonald L.A., Feldhlyum T.V., Angiolini S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Frazer C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae,"
RL Science 293:498-506(2001).
DR EMBL: AE007418; AAK75283.1; -.
DR TIGR: SP1174; -.
DR InterPro: IPR006270; Strep_his_triad.
DR TIGRFAMs: TIGR01363; strep_his_triad; 2.
KW Complete proteome.
SQ SEQUENCE 819 AA; 92228 MW; 43852B7E8163BDE CRC64;

Query Match 7.5%; Score 60; DB 16; Length 819;
Best Local Similarity 100.0%; Pred. No. 4.6e-50;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 ENLTPDEVSKREGINAEOIVIKITDGYVTSHGHHYNGKVPYDAIISELLMKDPNY 90
DB 52 ENLTPDEVSKREGINAEOIVIKITDGYVTSHGHHYNGKVPYDAIISELLMKDPNY 111

RESULT 8
Q9ANY2 PRELIMINARY; PRT; 839 AA.
ID Q9ANY2;
AC Q9ANY2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pneumococcal histidine triad protein D precursor (Hypothetical protein
DE SP1003) (Fragment).
GN PHTD OR SP1003.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21101045; PubMed=11159990;
RA Adamou J.E., Heinrichs J.H., Erwin A.L., Walsh W., Gayle T.,
RA Dornitzer M., Dagan R., Brewah Y.A., Barren P., Lathigra R.,
RA Langemann S., Koenig S., Johnson S.;
RT "Identification and characterization of a novel family of pneumococcal
RT proteins (the Pht family) that are protective against sepsis,"
RL Infect. Immun. 69:949-958(2001).
RN (2)
RP SEQUENCE FROM N.A.
RX STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tetelcin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., Deboy R.T., Hatt D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,

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RA Holtzapfle E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiolini S., Dickson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.,
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae."
RL Science 293:498-506(2001).
DR EMBL: AF318955; AAK06760.1; -.
DR EMBL: AE007403; AAK75120.1; -.
DR TIGR: SP1003; -.
DR InterPro: IPR006270; Strep_his_triad.
DR SignalFAMS; TIGR01363; strep_his_triad; 2.
KW Signal, Hypothetical protein; Complete proteome.
FT SIGNAL 1 29
FT NON TER 839 839
SQ SEQUENCE 839 AA; 93672 MW; 713B180D5E03BDCA CRC64;

Query Match 7.5%; Score 60; DB 16; Length 839;
Best Local Similarity 100.0%; Pred. No. 4.7e-50;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ENLTPDEVSKRGIAEIOIVKITDQGYVTSFGDHYHYNGKVPYDAIISBELMKDPNY 90
Db 52 ENLTPDEVSKRGIAEIOIVKITDQGYVTSFGDHYHYNGKVPYDAIISBELMKDPNY 111

RESULT 9
QSD008 PRELIMINARY; PRT; 853 AA.
AC QSD008;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Pneumococcal histidine triad protein D.
GN PHTD OR SPR0907.
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=171101;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21429245; PubMed=11544234;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmour R., Glas J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA Leblanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushina P.,
RA McAhren S.M., McHenry M., Mcleaster K., Mundy C.W., Niclas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,
RA Glas J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6."
RL J. Bacteriol. 183:5709-5717(2001).
DR EMBL: AE008464; AAK99711.1; -.
KW Complete proteome.
SQ SEQUENCE 853 AA; 95225 MW; 98F06A1EDE990CFS CRC64;

Query Match 7.5%; Score 60; DB 16; Length 853;
Best Local Similarity 100.0%; Pred. No. 4.7e-50;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ENLTPDEVSKRGIAEIOIVKITDQGYVTSFGDHYHYNGKVPYDAIISBELMKDPNY 90
Db 52 ENLTPDEVSKRGIAEIOIVKITDQGYVTSFGDHYHYNGKVPYDAIISBELMKDPNY 111

RESULT 10
QSD007 PRELIMINARY; PRT; 1039 AA.
AC QSD007;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)

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DE Pneumococcal histidine triad protein E precursor (Hypothetical protein
DE SPI004).
GN PHTD OR SPI004.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21101045; PubMed=11159990;
RA Adamou J.E., Heinrichs J.H., Erwin A.L., Walsh W., Gayle T.,
RA Dornitzner M., Degan R., Brewah Y.A., Barren P., Lathigra R.,
RA Langemann S., Koenig S., Johnson S.,
RT "Identification and characterization of a novel family of pneumococcal
RT proteins (the Pht family) that are protective against sepsis."
RL Infect. Immun. 69:949-958(2001).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tetteijn H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radebe D.,
RA Holtzapfle E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiolini S., Dickson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.,
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae."
RL Science 293:498-506(2001).
DR EMBL: AF318955; AAK06761.1; -.
DR EMBL: AE007403; AAK75121.1; -.
DR TIGR: SP1004; -.
DR InterPro: IPR006270; Strep_his_triad.
DR SignalFAMS; TIGR01363; strep_his_triad; 4.
KW Signal, Hypothetical protein; Complete proteome.
FT SIGNAL 1 29
FT NON TER 1039 1039
SQ SEQUENCE 1039 AA; 114631 MW; 81A563FC080625C4 CRC64;

Query Match 4.0%; Score 32; DB 16; Length 1039;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 AEOIVKITDQGYVTSFGDHYHYNGKVPYDA 77
Db 67 AEOIVKITDQGYVTSFGDHYHYNGKVPYDA 98

RESULT 11
QSD007 PRELIMINARY; PRT; 1039 AA.
AC QSD007;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Pneumococcal histidine triad protein E.
GN PHTD OR SPR0908.
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=171101;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21429245; PubMed=11544234;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmour R., Glas J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA Leblanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushina P.,
RA McAhren S.M., McHenry M., Mcleaster K., Mundy C.W., Niclas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,

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RA Class U.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6."
RL J. Bacteriol. 183:5709-5717(2001).
DR EMBL; AE008464; AAK9712.1; -
KW Complete proteome.
SQ SEQUENCE 1039 AA, 114625 MW, 05CC226D2028F551 CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 16; Length 1039;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AEOIVIKITDQGVYTSHGHHYNGKVPYDA 77
DB 67 AEOIVIKITDQGVYTSHGHHYNGKVPYDA 98

RESULT 12

Q8E338 PRELIMINARY; PRT; 481 AA.
AC Q8E338;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN GBS1925.
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_Taxid=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=2242508; PubMed=12354221;
RA Glaeser P., Rumsick C., Buchrieser C., Chevalier F., Frangoul L.,
RA Meadek T., Zouine M., Couve E., Lalioui L., Poyart C., Tlieu-Cuot P.,
RT Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease."
RL Mol. Microbiol. 45:1499-1513(2002).
DR EMBL; AL766854; CAD47584.1; -
DR Sagalier; gbs1925; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 481 AA; 53326 MW, DFDFO453DA929BE CRC64;

Query Match
Best Local Similarity 100.0%; Score 27; DB 16; Length 481;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 GYVTSBGHHYNGKVPYDAISEEL 83
DB 81 GYVTSBGHHYNGKVPYDAISEEL 107

RESULT 13

Q9AE21 PRELIMINARY; PRT; 289 AA.
AC Q9AE21;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 32.0 kDa protein (Fragment).
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_Taxid=1311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5531;
RX MEDLINE=21172873; PubMed=11274116;
RA Granlund M., Michel F., Norgren M.,
RT "Mutually exclusive distribution of IS1548 and GBSII, an active group
RT II intron identified in human isolates of group b streptococci."
RT J. Bacteriol. 183:2560-2569(2001).

DR EMBL; AJ290952; CAC35985.1; -
DR InterPro; IPR006270; strep_his_triad.
DR TIGRPMs; TIGR01363; strep_his_triad; 1.
KW Hypothetical protein.
FT NON_TER 289
SQ SEQUENCE 289 AA; 32043 MW, A15A8588EA8140E4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 17; DB 2; Length 289;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 YNGKVPYDAIISEELM 85
DB 92 YNGKVPYDAIISEELM 108

RESULT 14

Q9ZHG7 PRELIMINARY; PRT; 822 AA.
AC Q9ZHG7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 92.4 kDa protein.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_Taxid=1311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R268;
RX MEDLINE=99115568; PubMed=9916102;
RA Spellerberg B., Rozdzinski E., Martin S., Weber-Heymann J.,
RA Schmitz N., Luetticken R., Podbielski A.,
RT "Lmo, a protein with similarities to the Lrai adhesin family, mediates
RT attachment of Streptococcus agalactiae to human laminin."
RL Infect. Immun. 67:871-878(1999).
DR EMBL; AF062533; MAD13797.1; -
DR InterPro; IPR006270; strep_his_triad.
DR TIGRPMs; TIGR01363; strep_his_triad; 4.
KW Hypothetical protein.
SQ SEQUENCE 822 AA; 92386 MW, 80E4EDF313481F98 CRC64;

Query Match
Best Local Similarity 100.0%; Score 17; DB 2; Length 822;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 YNGKVPYDAIISEELM 85
DB 92 YNGKVPYDAIISEELM 108

RESULT 15

Q8E4U1 PRELIMINARY; PRT; 822 AA.
AC Q8E4U1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN GBS1306.
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_Taxid=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=2242508; PubMed=12354221;
RA Glaeser P., Rumsick C., Buchrieser C., Chevalier F., Frangoul L.,
RA Meadek T., Zouine M., Couve E., Lalioui L., Poyart C., Tlieu-Cuot P.,
RT Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing

RT invasive neonatal disease.";
 RL Mol. Microbiol. 45:1499-1513 (2002).
 DR EMBL: AL766850; CAD46965.1; -.
 DR Sagalistic; gbs1306; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 822 AA; 92393 MW; 2929A97C8AFCD78F CRC64;

Query Match 2.1%; Score 17; DB 16; Length 822;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 YNGKVPYDAIISEBLM 85
 |||||
 DB 92 YNGKVPYDAIISEBLM 108

RESULT 16

OBD281 PRELIMINARY; PRT; 822 AA.

AC OBD281;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DE Streptococcal histidine triad family protein.
 GN SAG1233.
 OS Streptococcus agalactiae (serotype V).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216466;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=2603 V/R / Serotype V;
 RX MEDLINE=22222988; PubMed=12200547;
 RA Tettelein H., Maignan V., Cieslewicz M.J., Eisen J.A., Peterson S.,
 Wesels M.R., Paulsen I.T., Nelson K.E., Margalit I., Read T.D.,
 Madoff L.C., Wolf A.M., Beaman M.J., Brinkac L.M., Daugherty S.C.,
 DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
 Radu D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
 Caray H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
 Jacobini E.T., Breton C., Galli G., Mariotti M., Vanni F., Malone D.,
 Rinaudo C., Rappaport R., Telford J.L., Kasper D.L., Grandi G.,
 Fraser C.M.;
 RA "Complete genome sequence and comparative genomic analysis of an
 RT emerging human pathogen, serotype V Streptococcus agalactiae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
 DR EMBL: AE014246; AAN0111.1; -.
 DR TIGR: SAG1233; -.
 KW Complete proteome.
 SQ SEQUENCE 822 AA; 92400 MW; 8CC8DF316727F98 CRC64;

Query Match 2.1%; Score 17; DB 16; Length 822;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 YNGKVPYDAIISEBLM 85
 |||||
 DB 92 YNGKVPYDAIISEBLM 108

RESULT 17

OBN282 PRELIMINARY; PRT; 823 AA.

AC OBN282;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DE Hypothetical protein spyM18_2072.
 GN SPYM18_2072.
 OS Streptococcus pyogenes (serotype M18).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=186103;
 RN (1)

RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS8232 / Serotype M18;
 RX MEDLINE=21927593; PubMed=11917108;
 RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
 RA Sylva G.L., Sturtevant D.E., Ricklets S.M., Porcella S.F.,
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
 RA Kapur V., Daly J.A., Vasey L.G., Musser J.M.;
 RT "Genome sequence and comparative microarray analysis of serotype M18
 RT group A Streptococcus strains associated with acute rheumatic fever
 RT outbreaks.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
 DR EMBL: AE010110; AAL98543.1; -.
 DR InterPro: IPR006270; Strep_his_triad.
 DR TIGRFAMs: TIGR01363; strep_his_triad; 4.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 823 AA; 92585 MW; C79EB30CEBDFC CRC64;

Query Match 2.1%; Score 17; DB 16; Length 823;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 YNGKVPYDAIISEBLM 85
 |||||
 DB 92 YNGKVPYDAIISEBLM 108

RESULT 18

OBSQ1 PRELIMINARY; PRT; 823 AA.

AC OBSQ1;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Histidine triad protein.
 GN SPYM3_1724.
 OS Streptococcus pyogenes (serotype M3).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=198466;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS315 / Serotype M3;
 RX MEDLINE=22133808; PubMed=12122206;
 RA Beres S.B., Sylva G.L., Barbican K.D., lei B., Hoff J.S.,
 RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
 RA Campbell D.S., Smith T.M., McCormack J.K., Leung D.Y.M.,
 RA Schlievert P.M., Musser J.M.;
 RA "Genome sequence of a serotype M3 strain of group A Streptococcus:
 RT phase-encoded toxins, the high-virulence phenotype, and clone
 RT emergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
 DR EMBL: AE014169; AAM80331.1; -.
 DR InterPro: IPR006270; Strep_his_triad.
 DR TIGRFAMs: TIGR01363; strep_his_triad; 1.
 KW Complete proteome.
 SQ SEQUENCE 823 AA; 92431 MW; 8C6CB517A2DD616 CRC64;

Query Match 2.1%; Score 17; DB 16; Length 823;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 YNGKVPYDAIISEBLM 85
 |||||
 DB 92 YNGKVPYDAIISEBLM 108

RESULT 19

O93GTS PRELIMINARY; PRT; 825 AA.

AC O93GTS;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)


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DE Histidine triad protein of group A streptococci.
GN HTPA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxId=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-9;
RA Terao Y., Kawabata S., Hamada S.;
RT "Characterization of a novel histidine triad protein of group A
RL streptococci."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073859; BAB71774.1; -.
DR InterPro; IPR006270; Strep_his_triad.
DR TIGRFAMs; TIGR01363; strep_his_triad; 4.
SQ SEQUENCE 825 AA; 92623 MW; DEAFCC199181DFB CRC64;

Query Match
Best Local Similarity 2.1%; Score 17; DB 2; Length 825;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 YNGKVPYDAIISELLM 85
DB 92 YNGKVPYDAIISELLM 108

RESULT 20
Q09XV4 PRELIMINARY; PRT; 825 AA.
AC Q09XV4;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein SPY2006.
GN SPY2006.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxId=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
DR EMBL; AE006623; AAK34688.1; -.
DR InterPro; IPR006270; Strep_his_triad.
DR TIGRFAMs; TIGR01363; strep_his_triad; 4.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 825 AA; 92649 MW; 57DF509656D50F4 CRC64;

Query Match
Best Local Similarity 2.1%; Score 17; DB 16; Length 825;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 YNGKVPYDAIISELLM 85
DB 92 YNGKVPYDAIISELLM 108

RESULT 21
Q08D06 PRELIMINARY; PRT; 182 AA.
AC Q08D06;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Pneumococcal histidine triad protein E, truncation.

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GN PHE-TRUNCATION OR SPR0910.
OS Streptococcus pneumoniae (strain ATCC BAA-295 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxId=171101;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21429245; PubMed=11544234;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczyk L.C., Burgett S.,
RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmore R., Glase J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Letkowitz E.J., Lu J., Matsushima P.,
RA McAnren S.M., McInerney M., McLeaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rokey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,
RA Glase J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717 (2001).
DR EMBL; AE008464; AAK99714.1; -.
KW Complete proteome.
SQ SEQUENCE 182 AA; 20145 MW; 29E12D653313A343 CRC64;

Query Match
Best Local Similarity 1.3%; Score 10; DB 16; Length 182;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 HGDHYHYIPK 197
DB 35 HGDHYHYIPK 44

RESULT 22
Q09CLO1 PRELIMINARY; PRT; 791 AA.
AC Q09CLO1;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein PM1448.
GN PM1448.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxId=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whitlam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).
DR EMBL; AE006181; AAK03532.1; -.
DR HSSP; P05055; ISRO.
DR InterPro; IPR003583; HHH_1.
DR InterPro; IPR003029; SL_1.
DR InterPro; IPR006641; YGFC.
DR Pfam; PF00575; SL_1.
DR SMART; SM00278; Hhh1; 2.
DR SMART; SM00316; SL_1.
DR SMART; SM00732; YGFC; 1.
DR PROSITE; PS50126; SL_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 791 AA; 87498 MW; 8C5D16C5401255C0 CRC64;

Query Match
Best Local Similarity 1.1%; Score 9; DB 16; Length 791;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 SASSELAANE 209
DB 443 SASSELAANE 451

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RESULT 23

Q8B9W0 PRELIMINARY; PRT; 71 AA.
 AC Q8B9W0: PRELIMINARY; PRT; 71 AA.
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Rachiplusia ou multiple nucleopolyhedrovirus.
 CC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 CC Nucleopolyhedrovirus.
 OX NCBI_TaxID=80366;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bonning B.C., Harrison R.L.;
 RT "The Rachiplusia ou multiple nucleopolyhedrovirus genome sequence."
 RL Submitted (Aug-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY145471; AAN28126.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 71 AA; 8522 MW; 924875A256D163ED CRC64;

Query Match 1.0%; Score 8; DB 12; Length 71;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 24

Q8EHD8 PRELIMINARY; PRT; 147 AA.
 AC Q8EHD8: PRELIMINARY; PRT; 147 AA.
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Conserved hypothetical protein.
 GN SO1287.
 OS Shewanella oneidensis.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 CC Alteromonadaceae; Shewanella.
 OX NCBI_TaxID=70863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=MR-1;
 RC MEDLINE=22297686; PubMed=12368813;
 RX Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
 RA Read T.D., Eisen J.A., Seshadri R., Ward N., Meche B., Clayton R.A.,
 RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
 RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
 RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
 RA Mueller J., Khouri H., Gill J., Uterback T.R., McDonald L.A.,
 RA Feldblyum T.V., Smith H.O., Venter J.C., Neilson K.H., Fraser C.M.;
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
 Shewanella oneidensis."
 RL Nat. Biotechnol. 20:1118-1123(2002).
 DR EMBL; AE015573; AAN54354.1; -
 DR TIGR; SO1287; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 147 AA; 15926 MW; 659276DA5626367 CRC64;

Query Match 1.0%; Score 8; DB 16; Length 147;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 SELAAEA 210
 DB 73 SELAAEA 80

RESULT 25

O811B9 PRELIMINARY; PRT; 152 AA.
 AC O811B9: PRELIMINARY; PRT; 152 AA.
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN Pfl1.0255.
 OS Plasmodium falciparum (isolate 3D7).
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 CC NCBI_TaxID=36329;
 OX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=3D7;
 RC MEDLINE=22255705; PubMed=12368864;
 RX Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
 RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
 RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Anguillo S.,
 RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
 RA Martin D.M.A., Fairhead A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McRadden G.I., Cummings L.M., Sudramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrall B.;
 RT "Genome sequence of the human malaria parasite Plasmodium
 falciparum."
 RL Nature 419:498-511(2002).
 DR EMBL; AE014839; AAN35839.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 152 AA; 17868 MW; CAEB34CE325F7800 CRC64;

Query Match 1.0%; Score 8; DB 5; Length 152;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 26

P91742 PRELIMINARY; PRT; 154 AA.
 AC P91742: PRELIMINARY; PRT; 154 AA.
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Transposase (Fragment).
 OS Hydra attenuata (Hydra) (Hydra vulgaris).
 CC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroids; Anthomedusae;
 CC Hydridae; Hydra.
 OX NCBI_TaxID=6087;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TRANSPONSON=mariner;
 RX MEDLINE=97327060; PubMed=9183847;
 RA Robertson H.M.;
 RT "Multiple Mariner transposons in flatworms and hydras are related to
 those of insects."
 RL J. Hered. 88:195-201(1997).
 DR EMBL; U51185; AAB61389.1; -
 DR InterPro; IPR001888; Transposase_1.
 DR Pfam; PF01359; Transposase_1; 1.
 FT NON_TER 1 154
 FT NON_TER 1 154
 SQ SEQUENCE 154 AA; 18179 MW; 955FB7091FA434F57 CRC64;

Query Match 1.0%; Score 8; DB 5; Length 154;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 LLERLNDE 477

Db 103 LBLRLNDE 110

RESULT 27

ID 044095 PRELIMINARY; PRT; 181 AA.

AC 044095;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Adenine phosphoribosyltransferase (Fragment).
GN APT.

OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OK NCBI_TaxID=7241;

RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeran J.M., Chen B., Kreitman M.;
RL Genetics 0:0-0(1997).
CC -1- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.

DR EMBL; AF025800; AAB87885.1; -.
DR FlyBase; FBgn0023247; Dsub\Apt.
DR InterPro; IPR005764; Ade.phapho.trans.
DR InterPro; IPR002375; Pr/PY_rp.transf.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01090; apt; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
DR GN Glycosyltransferase; Transferase.
FT NON_TER 181

SQ SEQUENCE 181 AA; 1986 MW; F34786596C31F726 CRC64;

Query Match 1.0%; Score 8; DB 5; Length 181;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 SOLVRKVG 384
Db 143 SOLVRKVG 150

RESULT 28

ID 09NCF0 PRELIMINARY; PRT; 270 AA.

AC 09NCF0;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Beta-1,4-glucanase 2 (Fragment).
GN EG2.

OS Cryptocercus cleavelandi.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Cryptocercidae; Cryptocercus.
OK NCBI_TaxID=119679;

RP SEQUENCE FROM N.A.
RA TISSUE=Salivary gland;
RX MEDLINE=20360158; PubMed=10898984;
RA Lo N., Tokuda G., Watanabe H., Rose H., Slaytor M., Maekawa K.,
RA Bandi C., Noda H.;
RT "Evidence from multiple gene sequences indicated that termites evolved
RT from wood-feeding cockroaches";
RL Curr. Biol. 10:801-804(2000).
DR EMBL; AF220589; AAF63720.1; -.
DR HSSP; P26221; ITFA.
DR InterPro; IPR001701; Glyco_hydro_9;
DR Pfam; PF00759; Glyco_hydro_9; 1.
FT NON_TER 1

FT NON_TER 270 270
SQ SEQUENCE 270 AA; 29875 MW; B03BF2A7ABF0547C CRC64;

Query Match 1.0%; Score 8; DB 5; Length 270;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 EVLLAKVT 742
Db 223 EVLLAKVT 230

RESULT 29

ID 022866 PRELIMINARY; PRT; 284 AA.

AC 022866;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE CetMI (Y105EBB.1a protein).
GN Y105EBB.1 OR TMY-1 OR Y105EBB.1A.

OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodertinae; Caenorhabditis.
OK NCBI_TaxID=6239;

RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RX MEDLINE=95395840; PubMed=7666414;
RA Kagawa H., Sugimoto K., Matsumoto H., Inoue T., Imadzu H., Takuwa K.,
RA Sakabe Y.;
RT "Genome structure, mapping and expression of the tropomyosin gene tmy-
RT 1 of Caenorhabditis elegans";
RL J. Mol. Biol. 251:603-613(1995).
RN [2]

RP SEQUENCE FROM N.A.
RA Sulston J.E.;
RL Submitted (Oct-2001) to the EMBL/Genbank/DBJ databases.
RN [3]

RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology";
RL Science 282:2012-2018(1998).
DR EMBL; D38540; BAA07543.1; -.
DR EMBL; AL132877; CAC70114.1; -.
DR HSSP; P42639; ICIG.
DR WormBEP; Y105EBB.1a; CE28782.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00261; Tropomyosin; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS00326; TROPOMYOSIN; 1.
SQ SEQUENCE 284 AA; 33003 MW; 02271C870E23D2AB CRC64;

Query Match 1.0%; Score 8; DB 5; Length 284;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 VEAQLKEA 734
Db 144 VEAQLKEA 151

RESULT 30

ID 022865 PRELIMINARY; PRT; 284 AA.

AC 022865;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE CetMI.
GN TMY-1.

OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OK NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=95395840; PubMed=7666414;
 RA Kagawa H., Sugimoto K., Matsumoto H., Inoue T., Imadzu H., Takuwa K.,
 RA Sakube Y.;
 RT "Genome structure, mapping and expression of the tropomyosin gene tmy-
 1 of Caenorhabditis elegans.";
 RL J. Mol. Biol. 251:603-613(1995).
 DR EMBL; D38539; BAA07540.1; -;
 DR HSSP; P42639; ICIG.
 DR InterPro; IPR000533; Tropomyosin.
 DR Pfam; PF00261; Tropomyosin.1.
 DR PRINTS; PR00194; TROPOMYOSIN.
 DR PROSITE; PS00326; TROPOMYOSIN; 1.
 SQ SEQUENCE 284 AA; 32951 MW; 80271C870E26C5E CRC64;
 Query Match 1.0%; Score 8; DB 5; Length 284;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 727 VEAOLKEA 734
 DB 144 VEAOLKEA 151
 RESULT 31
 Q27284 PRELIMINARY; PRT; 284 AA.
 AC Q27284;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE CETMII (Y105EBB.1D protein).
 GN Y105EBB.1 OR TMY-1 OR Y105EBB.1D.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OK NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=95395840; PubMed=7666414;
 RA Kagawa H., Sugimoto K., Matsumoto H., Inoue T., Imadzu H., Takuwa K.,
 RA Sakube Y.;
 RT "Genome structure, mapping and expression of the tropomyosin gene tmy-
 1 of Caenorhabditis elegans.";
 RL J. Mol. Biol. 251:603-613(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sulston J.E.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; D38541; BAA07544.1; -;
 DR EMBL; D38539; BAA07541.1; -;
 DR EMBL; AL132877; CAC70112.1; -;
 DR HSSP; P42639; ICIG.
 DR WormPep; Y105EBB.1D; CE29060.
 DR InterPro; IPR000533; Tropomyosin.
 DR Pfam; PF00261; Tropomyosin.1.
 DR PRINTS; PR00194; TROPOMYOSIN.
 DR PROSITE; PS00326; TROPOMYOSIN; 1.
 KW Alternative splicing.

SQ SEQUENCE 284 AA; 32936 MW; D8D32CC6FB4E78F7 CRC64;
 Query Match 1.0%; Score 8; DB 5; Length 284;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 727 VEAOLKEA 734
 DB 144 VEAOLKEA 151
 RESULT 32
 Q46010 PRELIMINARY; PRT; 294 AA.
 AC Q46010;
 DT 01-JUN-1998 (TRENBLREL. 06, Created)
 DT 01-JUN-1998 (TRENBLREL. 06, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE ZK228.4 protein.
 GN ZK228.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OK NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Baeham V.M.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; Z82086; CAB04996.1; -;
 DR WormPep; ZK228.4; CE16713.
 DR InterPro; IPR000182; GCN5acetyltransf.
 DR Pfam; PF00583; Acetyltransf.1.
 SQ SEQUENCE 294 AA; 34067 MW; D91875015FBD9976 CRC64;
 Query Match 1.0%; Score 8; DB 5; Length 294;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 TVKENRV 18
 DB 262 TVKENRV 269
 RESULT 33
 Q95031 PRELIMINARY; PRT; 301 AA.
 AC Q95031;
 DT 01-DEC-2001 (TRENBLREL. 19, Created)
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Y105EBB.1D protein.
 GN Y105EBB.1 OR Y105EBB.1B.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OK NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sulston J.E.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 investigating biology.";

RL Science 282:2012-2018(1998).
 DR EMBL; AL132877; CAC70113.1; -.
 DR HSSP; P04268; 1IC2.
 DR WormRep; Y105EBB.1b; CE29058.
 DR InterPro; IPR000533; Tropomyosin.
 DR Pfam; PF00261; Tropomyosin; 1.
 DR PRINTS; PR00194; TROPOMYOSIN.
 DR PROSITE; PS00326; TROPOMYOSIN; 1.
 SQ SEQUENCE 301 AA; 34832 MW; B6E190C25171D32F CRC64;

Query Match
 Best Local Similarity 100.0%; Score 8; DB 5; Length 301;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 VEAOLKEA 734
 |||||
 Db 161 VEAOLKEA 168

RESULT 34
 Q8FLF7 PRELIMINARY; PRT; 319 AA.

AC Q8FLF7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE Hypothetical protein.
 GN CE3P025.
 OS Corynebacterium efficiens.
 OG Plasmid pCE3.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 RX NCBI_TaxID=152794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
 RA Kawarayashi Y., Yamazaki J., Hino Y., Kikuchi H.;
 RT "The entire sequence of plasmid maintained by Corynebacterium
 RT efficiens YS-314.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF005326; BAC19600.1; -.
 KW Hypothetical protein; Plasmid; Complete proteome.
 SQ SEQUENCE 319 AA; 32777 MW; 38DA547FCB648122 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 8; DB 16; Length 319;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 708 EPVEETPA 715
 |||||
 Db 267 EPVEETPA 274

RESULT 35
 Q9P8N1 PRELIMINARY; PRT; 436 AA.

AC Q9P8N1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE Cellulohydrolase.
 OS Coriolus versicolor.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Coriolus.
 OX NCBI_TaxID=57466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Novo C., Clemente A., Simoes F., Mendonca D., Matos J.;
 RT "Coriolus versicolor cellulohydrolase-like cDNA sequence.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF233583; AAF35251.1; -.
 DR HSSP; P00725; 2CBH.
 DR InterPro; IPR000254; CBD_fungal.

DR InterPro; IPR001524; Glyco_hydro_6.
 DR Pfam; PF00734; CBM.1; 1.
 DR Pfam; PF01341; Glyco_hydro_6; 1.
 DR PRINTS; PR00733; GLYDRLASES.
 DR ProDom; PD001821; CBD_fungal; 1.
 DR ProDom; PD003733; Glyco_hydro_6; 1.
 DR SMART; SM00236; fCBD; 1.
 DR PROSITE; PS00562; CBD_FUNGAL; 1.
 DR PROSITE; PS00655; GLYCOSYL_HYDROL_F6_1; 1.
 DR PROSITE; PS00656; GLYCOSYL_HYDROL_F6_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 436 AA; 46170 MW; E0BC5AFBCA324D4 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 8; DB 3; Length 436;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 741 VTDSLSKA 748
 |||||
 Db 107 VTDSLSKA 114

RESULT 36
 Q9KS51 PRELIMINARY; PRT; 484 AA.

AC Q9KS51;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Multidrug resistance protein, putative.
 GN VC1409.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 RX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Ginn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bases S., Qin H., Disgoli I., Sellers P.,
 RA McDonald L., Ueberback T., Fleischmann R.D., Niernann W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae.";
 RL Nature 406:477-483(2000).
 DR EMBL; AE004219; AAF94566.1; -.
 DR TIGR; VC1409; .
 DR InterPro; IPR003423; OEP.
 DR InterPro; IPR001440; TPR.
 DR Pfam; PF02321; OEP; 2.
 KW Complete proteome.
 SQ SEQUENCE 484 AA; 52131 MW; 1C53BD09B969F203 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 8; DB 16; Length 484;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 SELAAEA 210
 |||||
 Db 169 SELAAEA 176

RESULT 37
 O80401 PRELIMINARY; PRT; 485 AA.

AC O80401;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE SAR DNA binding protein (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OK NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hatton D., Gray J.C.;
 RT "Rice cDNA encoding a protein homologous to a SAR DNA-binding protein
 from pea."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB015431; BAA31260.1; -.
 DR Gramene; O80401; -.
 DR InterPro; IPR002687; Nop.
 DR Pfam; PF01798; Nop; 1.
 DR ProDom; PD004104; Nop; 1.
 DR NON_TER 485 485
 SQ SEQUENCE 485 AA; 5334 MW; 61A2986F7856D56D CRC64;

Query Match 1.0%; Score 8; DB 10; Length 485;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 727 VEAQLKEA 734
 |||||
 Db 229 VEAQLKEA 236

RESULT 38

ID 099TDB PRELIMINARY; PRT; 488 AA.
 AC 099TDB;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE PTS system, N-acetylglucosamine-specific IIABC component.
 GN PTA OR SA11726 OR SA1547.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OK NCBI_TaxID=158878; 158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
 RA MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hatton D., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003363; BAB57888.1; -.
 DR EMBL; AP003134; BAB42815.1; -.
 DR HSSP; P05053; 11BA.
 DR InterPro; IPR001996; PTS_EIIB.
 DR InterPro; IPR003352; PTS_EIIC.
 DR Pfam; PF00367; PTS_EIIB; 1.
 DR Pfam; PF02378; PTS_EIIC; 1.
 DR ProDom; PD001476; PTS_EIIB; 1.
 DR PROSITE; PS01035; PTS_EIIB_CYS; 1.
 KW Complete proteome.
 SQ SEQUENCE 488 AA; 53086 MW; 4A669EF1ACB5ED4E CRC64;

Query Match 1.0%; Score 8; DB 16; Length 488;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 150 NDGAVALA 157

Db 72 NDGAVALA 79
 |||||

RESULT 39

ID 08NCW2 PRELIMINARY; PRT; 488 AA.
 AC 08NCW2;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE PTS system N-acetylglucosamine-specific IIABC component.
 GN PTA OR MW1668.
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OK NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 acquired MRSA."
 RL Lancet 359:1819-1827(2002).
 DR EMBL; AP004827; BAB95533.1; -.
 DR InterPro; IPR001996; PTS_EIIB.
 DR InterPro; IPR003352; PTS_EIIC.
 DR Pfam; PF00367; PTS_EIIB; 1.
 DR Pfam; PF02378; PTS_EIIC; 1.
 DR ProDom; PD001476; PTS_EIIB; 1.
 DR PROSITE; PS01035; PTS_EIIB_CYS; 1.
 KW Complete proteome.
 SQ SEQUENCE 488 AA; 53098 MW; 52887CE71A4F39F CRC64;

Query Match 1.0%; Score 8; DB 16; Length 488;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 150 NDGAVALA 157
 |||||
 Db 72 NDGAVALA 79

RESULT 40

ID 08CNW2 PRELIMINARY; PRT; 490 AA.
 AC 08CNW2;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE PTS system N-acetylglucosamine-specific IIIC component.
 GN SE1403.
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OK NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
 RA Chen Z., Wen Y.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE016748; AA005002.1; -.
 KW Complete proteome.
 SQ SEQUENCE 490 AA; 53646 MW; D1DE11C5EC289E3D CRC64;

Query Match 1.0%; Score 8; DB 16; Length 490;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 150 NDGAVALA 157
 |||||
 Db 72 NDGAVALA 79

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RESULT 41
ID 095LH9 PRELIMINARY; PRT; 673 AA.
AC 095LH9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Rab11 family interaction protein 1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP MEDLINE=21486449; PubMed=11495908;
RX Hales C.M., Griner R., Hobby-Henderson K.C., Dorn M.C., Hardy D.,
RA Kumar R., Navarre J., Chan E.K., Lapierre L.A., Goldenring J.R.;
RT "Identification and characterization of a family of Rab11-interacting
RT proteins."
RL J. Biol. Chem. 276:39067-39075(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Griner R.D., Kumar R., Goldenring J.R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF237668; AAL02425.2; -.
SQ SEQUENCE 673 AA; 69892 MW; A1B8FCDD6998B192 CRC64;

Query Match
Best Local Similarity 1.0%; Score 8; DB 6; Length 673;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 591 PRTGDSAAA 598
DB 69 PRTGDSAAA 76

RESULT 42
ID 09RSJ4 PRELIMINARY; PRT; 840 AA.
AC 09RSJ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protease, putative.
GN DR2130.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Uyang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.D., Lam P., McDonald L., Utecherback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577(1999).
DR EMBL; AE002047; AAF1680.1; -.
DR TIGR; DR2130; -.
DR InterPro; IPR001539; Peptidase_U32.
DR Pfam; PF01136; Peptidase_U32.1.
DR ProDom; PD004398; Peptidase_U32; 1.
KW Protease; Complete proteome.
SQ SEQUENCE 840 AA; 91640 MW; 3A978AD3A0742B88 CRC64;

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Query Match
Best Local Similarity 1.0%; Score 8; DB 16; Length 840;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 DGLVDPDA 294
DB 332 DGLVDPDA 339

RESULT 43
ID 026077 PRELIMINARY; PRT; 945 AA.
AC 026077;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Helicase.
GN HP1553.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Richardson J., Zhou L., Khairi S.E., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utecherback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
DR EMBL; AE000653; AAD08593.1; -.
DR TIGR; HP1553; -.
DR InterPro; IPR000212; UvrD-helicase.
DR Pfam; PF00580; UvrD-helicase; 1.
KW Hypothetical protein; Helicase; Complete proteome.
SQ SEQUENCE 945 AA; 108880 MW; 6EE53868566EB22 CRC64;

Query Match
Best Local Similarity 1.0%; Score 8; DB 16; Length 945;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 ERLGKPN 506
DB 657 ERLGKPN 664

RESULT 44
ID 08TMX4 PRELIMINARY; PRT; 1233 AA.
AC 08TMX4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE WD40-repeat containing protein.
GN MA2525.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., MacDonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Altnor D., Brown A.,

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RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
 RA Linton L., McMan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
 RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
 RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birren B.;
 RT "The genome of *Methanoscoccus acetivorans* reveals extensive metabolic
 RT and physiological diversity.";
 RL Genome Res. 12:532-542(2002).
 DR EMBL; AE010946; AAM05908.1; -.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 16.
 DR SMART; SM00320; WD40; 16.
 DR PROSITE; PS00678; WD_REPEATS_1; 13.
 DR PROSITE; PS50082; WD_REPEATS_2; 16.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Complete proteome.
 SQ SEQUENCE 1233 AA; 138558 MW; 49D207B08C3BB8A6 CRC64;

Query Match 1.0%; Score 8; DB 17; Length 1233;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 482 EKLVDL 489
 Db 236 EKLVDL 243

RESULT 45
 093HW0 PRELIMINARY; PRT; 1646 AA.
 AC 093HW0;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Endo-beta-N-acetylglucosaminidase D.
 GN ENDO D.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2128261; PubMed=11388907;
 RA Muramatsu H., Tachikui H., Ushida H., Song X., Qiu Y., Yamamoto S.,
 RA Muramatsu T.;
 RT "Molecular Cloning and Expression of Endo-beta-N-acetylglucosaminidase
 RT D, Which Acts on the Core Structure of Complex Type Asparagine-Linked
 RT Oligosaccharides.";
 RL J. Biochem. 129:923-928(2001).
 CC - SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
 CC AN AMIDE BOND (BY SIMILARITY).
 DR EMBL; AB055806; BAB62042.1; -.
 DR InterPro; IPR005201; Glyco_hydro_85.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR InterPro; IPR006192; LPXTG.
 DR Pfam; PF03644; Glyco_hydro_85; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Peptidoglycan-anchor.
 SQ SEQUENCE 1646 AA; 182121 MW; 5050E57B8E58D4 CRC64;

Query Match 1.0%; Score 8; DB 2; Length 1646;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 447 LTEAHKAL 454
 Db 1279 LTEAHKAL 1286

RESULT 46
 097S90 PRELIMINARY; PRT; 1659 AA.
 AC 097S90;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Endo-beta-N-acetylglucosaminidase, putative.
 GN SP0498.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapfel E., Khouli H., Wolf A.M., Uettermann T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of *Streptococcus*
 RT pneumoniae.";
 RL Science 293:498-506(2001).
 DR EMBL; AE007361; AAK74656.1; -.
 DR TIGR; SP0498; -.
 DR InterPro; IPR005201; Glyco_hydro_85.
 DR InterPro; IPR005877; Gpos_YsIRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR InterPro; IPR006192; LPXTG.
 DR Pfam; PF03644; Glyco_hydro_85; 1.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF04650; YsIRK_signal; 1.
 DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
 DR TIGRfams; TIGR01168; YsIRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 KW Complete proteome.
 SQ SEQUENCE 1659 AA; 183202 MW; 06A52DACA96AB074 CRC64;

Query Match 1.0%; Score 8; DB 16; Length 1659;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 447 LTEAHKAL 454
 Db 1292 LTEAHKAL 1299

RESULT 47
 08CZ52 PRELIMINARY; PRT; 1659 AA.
 AC 08CZ52;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN SP00440.
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=171101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21429245; PubMed=11544234;

RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
 RA DeHoff B.S., Estrem S.T., Filtz L., Fu D.-J., Fuller W., Geringer C.,
 RA Gilmore R., Glass J.S., Khoja H., Kratz A.R., Lagace R.E.,
 RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
 RA McArthur S.M., McHenry M., McMaster K., Mundy C.W., Niclas T.I.,
 RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
 RA Sun P.-M., Winkler W.E., Yang Y., Young-Bellido M., Zhao G.,
 RA Zook C.A., Baltz R.H., Jaskunas S.R., Roestek P.R. Jr., Skatrud P.L.,
 RA Glaes J.I.;
 RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
 RL J. Bacteriol. 183:5709-5717(2001).
 DR EMBL: AB008424; AKK9244.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1659 AA; 183107 MW; EF072B217E4AD32 CRC64;

Query Match 1.0%; Score 8; DB 16; Length 1659;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 447 LTEAHKAL 454
 Db 1292 LTEAHKAL 1299

RESULT 48

Q8SSW5 PRELIMINARY; PRT; 2621 AA.
 AC Q8SSW5;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-NOV-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE KIAA1058 protein.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 NCBI_Taxid=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MX4;
 RA Glockner G., Eichinger L., Szafranski K., Pachbat J., Dear P.,
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
 RA Tunngal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
 RT "Sequence and Analysis of Chromosome 2 of Dictyostelium.";
 DR Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AC115585; JAL92252.1; -;
 SQ SEQUENCE 2621 AA; 293740 MW; EF6A8B5C1B7D210 CRC64;

Query Match 1.0%; Score 8; DB 5; Length 2621;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 252 SNNSNTNS 259
 Db 19 SNNSNTNS 26

RESULT 49

O87936 PRELIMINARY; PRT; 42 AA.
 AC O87936;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ENV protein (Fragment).
 GN ENV.
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NCBI_Taxid=11723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=macC8;
 RX MEDLINE=95333295; PubMed=7609080;
 RA Whatmore A., Cook N., Hall G., Sharpe S., Rud E., Cranage M.;
 RT "Repair and evolution of nef in vivo modulates simian immunodeficiency

RT virus virulence.";
 RL J. Virol. 69:5117-5123(1995).
 DR EMBL: X86726; CA60398.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR Pfam: PF00517; Gp41; 1.
 KW Transmembrane.
 FT NON TER
 SQ SEQUENCE 42 AA; 4890 MW; F1E9ADB76A83E7A CRC64;

Query Match 0.9%; Score 7; DB 15; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 750 ATEYLAG 756
 Db 4 ATEYLAG 10

RESULT 50

O87948 PRELIMINARY; PRT; 42 AA.
 AC O87948;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ENV protein (Fragment).
 GN ENV.
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NCBI_Taxid=11723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=macC8;
 RX MEDLINE=95333295; PubMed=7609080;
 RA Whatmore A., Cook N., Hall G., Sharpe S., Rud E., Cranage M.;
 RT "Repair and evolution of nef in vivo modulates simian immunodeficiency
 virus virulence.";
 RL J. Virol. 69:5117-5123(1995).
 DR EMBL: X86731; CA60408.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR Pfam: PF00517; Gp41; 1.
 KW Transmembrane.
 FT NON TER
 SQ SEQUENCE 42 AA; 4890 MW; F1E9ADB76A83E7A CRC64;

Query Match 0.9%; Score 7; DB 15; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 750 ATEYLAG 756
 Db 4 ATEYLAG 10

RESULT 51

O87938 PRELIMINARY; PRT; 42 AA.
 AC O87938;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ENV protein (Fragment).
 GN ENV.
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NCBI_Taxid=11723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=macC8;
 RX MEDLINE=95333295; PubMed=7609080;
 RA Whatmore A., Cook N., Hall G., Sharpe S., Rud E., Cranage M.;
 RT "Repair and evolution of nef in vivo modulates simian immunodeficiency
 virus virulence.";

RL J. Virol. 69:5117-5123(1995).
 DR EMBL: X86724; CAA60394.1; -;
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00517; GP41; 1.
 KM Transmembrane.
 FT NON TER
 SQ SEQUENCE 42 AA; 4890 MW; F1E9ADB76A83E7A CRC64;

Query Match 0.9%; Score 7; DB 15; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 750 ATETLAG 756
 |||||
 Db 4 ATETLAG 10

RESULT 52
 Q88084 PRELIMINARY; PRT; 42 AA.
 ID 088084
 AC 088084
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ENV protein (Fragment).
 GN ENV.
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=macC8;
 RA Whatmore A.M.;
 RL Submitted (AUG-1995) to the EMBL/Genbank/DBJ databases.
 DR EMBL: X90853; CAA62360.1; -;
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00517; GP41; 1.
 KM Transmembrane.
 FT NON TER
 SQ SEQUENCE 42 AA; 4871 MW; F1F57C7676A83E7A CRC64;

Query Match 0.9%; Score 7; DB 15; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 750 ATETLAG 756
 |||||
 Db 4 ATETLAG 10

RESULT 53
 Q87952 PRELIMINARY; PRT; 42 AA.
 ID 087952
 AC 087952
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ENV protein (Fragment).
 GN ENV.
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=macC8;
 RA MEDLINE=95333295; PubMed=7609080;
 RT "Repair and evolution of nef in vivo modulates simian immunodeficiency virus virulence."
 RT J. Virol. 69:5117-5123(1995).
 DR EMBL: X86725; CAA60396.1; -;
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00517; GP41; 1.

KM Transmembrane.
 FT NON TER
 SQ SEQUENCE 42 AA; 4890 MW; F1E9ADB76A83E7A CRC64;

Query Match 0.9%; Score 7; DB 15; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 750 ATETLAG 756
 |||||
 Db 4 ATETLAG 10

RESULT 54
 Q87946 PRELIMINARY; PRT; 42 AA.
 ID 087946
 AC 087946
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ENV protein (Fragment).
 GN ENV.
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=macC8;
 RX MEDLINE=95333295; PubMed=7609080;
 RA Whatmore A., Cook N., Hall G., Sharpe S., Rud E., Cranage M.;
 RT "Repair and evolution of nef in vivo modulates simian immunodeficiency virus virulence."
 RT J. Virol. 69:5117-5123(1995).
 DR EMBL: X86730; CAA60406.1; -;
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00517; GP41; 1.
 KM Transmembrane.
 FT NON TER
 SQ SEQUENCE 42 AA; 4890 MW; F1E9ADB76A83E7A CRC64;

Query Match 0.9%; Score 7; DB 15; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 750 ATETLAG 756
 |||||
 Db 4 ATETLAG 10

RESULT 55
 Q88080 PRELIMINARY; PRT; 42 AA.
 ID 088080
 AC 088080
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ENV protein (Fragment).
 GN ENV.
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=macC8;
 RA Whatmore A.M.;
 RL Submitted (AUG-1995) to the EMBL/Genbank/DBJ databases.
 DR EMBL: X90851; CAA62356.1; -;
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00517; GP41; 1.
 KM Transmembrane.
 FT NON TER
 SQ SEQUENCE 42 AA; 4818 MW; F1EB8D9976A83E7A CRC64;

Query Match 0.9%; Score 7; DB 15; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 750 ATETLAG 756
|||||
Db 4 ATETLAG 10

RESULT 56
087944 PRELIMINARY; PRT; 43 AA.
AC 087944;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ENV protein (Fragment).
GN ENV.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=macC8;
RX MEDLINE=95333295; PubMed=7609080;
RA Whatmore A., Cook N., Hall G., Sharpe S., Rud E., Cranage M.;
RT "Repair and evolution of nef in vivo modulates simian immunodeficiency virus virulence".
RL J. Virol. 69:5117-5123(1995).
DR EMBL; X86729; CAA60404.1; -;
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4947 MW; F1E9FF5CE833E7A CRC64;

Query Match 0.9%; Score 7; DB 15; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 750 ATETLAG 756
|||||
Db 5 ATETLAG 11

RESULT 57
087942 PRELIMINARY; PRT; 44 AA.
ID 087942;
AC 087942;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ENV protein (Fragment).
GN ENV.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=macC8;
RX MEDLINE=95333295; PubMed=7609080;
RA Whatmore A., Cook N., Hall G., Sharpe S., Rud E., Cranage M.;
RT "Repair and evolution of nef in vivo modulates simian immunodeficiency virus virulence".
RL J. Virol. 69:5117-5123(1995).
DR EMBL; X86728; CAA60402.1; -;
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
SQ SEQUENCE 44 AA; 5046 MW; F1E9FF1A4A09507A CRC64;

Query Match 0.9%; Score 7; DB 15; Length 44;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 750 ATETLAG 756
|||||
Db 6 ATETLAG 12

RESULT 58
087940 PRELIMINARY; PRT; 49 AA.
ID 087940;
AC 087940;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ENV protein (Fragment).
GN ENV.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=macC8;
RX MEDLINE=95333295; PubMed=7609080;
RA Whatmore A., Cook N., Hall G., Sharpe S., Rud E., Cranage M.;
RT "Repair and evolution of nef in vivo modulates simian immunodeficiency virus virulence".
RL J. Virol. 69:5117-5123(1995).
DR EMBL; X86727; CAA60400.1; -;
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
SQ SEQUENCE 49 AA; 5601 MW; AAC9F81D7A5BF6A5 CRC64;

Query Match 0.9%; Score 7; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 750 ATETLAG 756
|||||
Db 11 ATETLAG 17

RESULT 59
Q45596 PRELIMINARY; PRT; 49 AA.
ID Q45596;
AC Q45596;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Function unknown.
GN YYDF.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96051385; PubMed=7584024;
RA Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin".
RL DNA Res. 1:1-14(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=94171085; PubMed=8125345;
RA Zhang J., Aronson A.L.;
RT "A Bacillus subtilis bglA gene encoding phospho-beta-glucosidase is inducible and closely linked to a NADH dehydrogenase-encoding gene".
RL Gene 140:85-90(1994).
RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=94156824; PubMed=8113162;
RA Calogero S., Gardan R., Glaser P., Schweizer J., Rapoport G.,
RA Debarbouille M.;
RT "RocR, a novel regulatory protein controlling arginine utilization in
RT Bacillus subtilis, belongs to the NtrC/NIFA family of transcriptional
RT activators.";
RL J. Bacteriol. 176:1234-1241 (1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=94236234; PubMed=8180695;
RA Hartford O.M., Dowds B.C.;
RT "Isolation and characterization of a hydrogen peroxide resistant
RT mutant of Bacillus subtilis.";
RL Microbiology 140:297-304 (1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96093926; PubMed=7584049;
RA Yoshida K., Seki S., Fujimura M., Miwa Y., Fujita Y.;
RT "Cloning and sequencing of a 36-Kb region of the Bacillus subtilis
RT genome between the gnt and tol operons.";
RL DNA Res. 2:61-69 (1995).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=95311309; PubMed=7540694;
RA Gardan R., Rapoport G., Debarbouille M.;
RT "Expression of the rocDEF operon involved in arginine catabolism in
RT Bacillus subtilis.";
RL J. Mol. Biol. 249:843-856 (1995).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX Kaahara Y., Nakai S., Yoshikawa H., Ogasawara N.;
RA Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brigelli S.C., Bron S.,
RA Brouillet S., Brunsch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Katamata D., Kasahara Y., Klaerr-Bianchard M., Klein C.,
RA Kobayashi Y., Koeltter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Paro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Pressac E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeder R., Scoffone F.,
RA Setiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Tokokin A., Tacconi E., Takagi T., Takahashi H., Takenaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambuit R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zunshein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256 (1997).

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RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; D78193; BA01276.1; -.
DR EMBL; Z99124; CAB16055.1; -.
RW Complete proteome.
SQ SEQUENCE 49 AA; 5781 MW; BA5F90DAD2982A86 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 406 ETVKNLE 412
DB 9 ETVKNLE 15

RESULT 60
O9AGM9 PRELIMINARY; PRT; 50 AA.
AC O9AGM9;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE GMP459 (Fragment).
GN GMP459.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=CM459et(M);
RX MEDLINE=2120755; PubMed=11320127;
RA Roberts A.P., Johannesen P.A., Lyras D., Mullany P., Rood J.I.;
RT "Comparison of Tn5397 from Clostridium difficile, Tn916 from
RT Enterococcus faecalis and the CM459et(M) element from Clostridium
RT perfringens shows that they have similar conjugation regions but
RT different insertion and excision modules.";
RL Microbiology 147:1243-1251 (2001).
DR EMBL; AF329848; AAK17959.1; -.
DR HSSP; P04079; 1GPM.
DR InterPro; IPR001674; GMP_synt_C.
DR Pfam; PF00958; GMP_synt_C; 1.
FT NON_TER 1
SQ SEQUENCE 50 AA; 5689 MW; 58A68ACE792DCAA0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 IVNEVKG 103
DB 25 IVNEVKG 31

RESULT 61
O8FHVO PRELIMINARY; PRT; 51 AA.
AC O8FHVO;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN C1740.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=06:HI / CFT073 / ATCC 700928;
 RA MEDLINE=22388234; PubMed=12471157;
 RX Welch R.A., Burland V., Plunkett G., III, Redford P., Roesch P.,
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL; AE016760; AAN80206.1; -;
 KW Hypothetical protein: Complete proteome.
 SQ SEQUENCE 51 AA; 603 MW; 7BCD4D2E0A509E0B CRC64;

QY Query Match 0.9%; Score 7; DB 16; Length 51;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 520 LADKYTT 526
 DB 18 LADKYTT 24

RESULT 62

Q90VA0 PRELIMINARY; PRT; 68 AA.
 AC Q90VA0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Nef protein (Negative factor) (27 kDa protein) (Fragment).
 GN NEF.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.
 OC NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B+48;
 RX MEDLINE=21160457; PubMed=11259184;
 RA Ibanez A., Cloet B., Martinez M.A.;
 RT "Absence of genetic diversity reduction in the HIV-1 integrated
 RT proviral LTR sequence population during successful combination
 RT therapy.";
 RL Virology. 282:1-5(2001).
 CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
 CC ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN (BY
 CC SIMILARITY).

DR EMBL; AF294070; AAK48560.1; -;
 DR InterPro; IPR001558; HIV_Nef.
 DR Pfam; PF00469; F-Protein; 1.
 DR Prodom; PD000031; HIV_Nef; 1.
 DR AIDS; GTP-binding; Lipoprotein; Myristate.
 FT NON_TER 1
 SQ SEQUENCE 68 AA; 8020 MW; F10ECTAB1A8D247F CRC64;

QY Query Match 0.9%; Score 7; DB 15; Length 68;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 722 VETEKVE 728
 DB 10 VETEKVE 16

RESULT 63

Q9A3B0 PRELIMINARY; PRT; 68 AA.
 AC Q9A3B0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein CC3294.
 GN CC3294.
 OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
 OC Caulobacteraceae; Caulobacter.
 OC NCBI_Taxid=155892;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.C., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Vamathevan J., Berry K.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL; AE005992; AAK25256.1; -;
 DR TIGR; CC3294; -;
 KW Hypothetical protein: Complete proteome.
 SQ SEQUENCE 68 AA; 7458 MW; FAB37837A43B2E82 CRC64;

QY Query Match 0.9%; Score 7; DB 16; Length 68;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 ELEERIA 328
 DB 31 ELEERIA 37

RESULT 64

Q977L2 PRELIMINARY; PRT; 71 AA.
 AC Q977L2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE Zn-ribbon protein.
 OS uncultured crenarchaeote 7444.
 OC Archaea; Crenarchaeota; environmental samples;
 OC marine archaeal group 1.
 OC NCBI_Taxid=166279;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Beja O., Koonin E.V., Aravind L., Taylor L.T., Seiz H., Stein J.L.,
 RA Bensen D.C., Feldman R.A., Swanson R.V., DeLong E.F.;
 RT "Comparative genomic analysis of coexisting archaeal genetic variants
 RT in an Antarctic marine microbial assemblage.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF393466; AAK96096.1; -;
 SQ SEQUENCE 71 AA; 8052 MW; C14F0FB3B9558FE CRC64;

QY Query Match 0.9%; Score 7; DB 1; Length 71;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 710 VETPAE 716
 DB 16 VETPAE 22

RESULT 65

Q96YD8 PRELIMINARY; PRT; 71 AA.
 AC Q96YD8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Putative integrase.
 GN STS236.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.

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OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankaï A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7."
RL DNA Res. 8:123-140(2001).
DR EMBL: AP000989; BAB67339.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 71 AA; 815 MW; 3D46F83EBB546E37 CRC64;

Query Match 0.9%; Score 7; DB 17; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 111 GKYYVYL 117
Db 18 GKYYVYL 24

RESULT 66
OY Q9HGR7 PRELIMINARY; PRT; 80 AA.
ID Q9HGR7
AC Q9HGR7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)
DE (Fragment).
GN GPD.
OS Gilbertella periscaria.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Gilbertellaceae;
OC Gilbertella.
OX NCBI_TaxID=101096;
RN [1]
RP SEQUENCE FROM N.A.
RA Tamas P.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Pap T., Vastag M., Acs K., Vagvolgyi C.;
RT "Phylogenetic relationships among Mucoraceae, Choanephoraceae and
RT Gilbertellaceae based on rDNA and glyceraldehyde-3-phosphate
RT dehydrogenase sequences."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + PHOSPHATE +
CC NAD(+) = 3-PHOSPHO-D-GLYCEROYL PHOSPHATE + NADH.
CC -1- PATHWAY: SECOND PHASE OF GLYCOLYSIS; FIRST STEP.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
CC DEHYDROGENASE FAMILY.
DR EMBL: AJ278316; GAC05663.1; -.
DR HSSP; P00354; 3GPD.
DR InterPro: IPR001173; GAP_dhhdhogenase.
DR Pfam; PF02800; gpdh_C; 1.
KW Glycolysis; NAD; Oxidoreductase.
FT NON_TER 1 1
FT NON_TER 80 80
SQ SEQUENCE 80 AA; 8609 MW; A571C27B7C915F0E CRC64;

Query Match 0.9%; Score 7; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 509 EYTEDEV 515
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Db 43 EYTEDEV 49

RESULT 67
OY Q8WYJ9 PRELIMINARY; PRT; 83 AA.
ID Q8WYJ9
AC Q8WYJ9;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE U6 snRNA-associated Sm-like protein Lsm6.
DE Dictyostelium discoidium (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and Analysis of Chromosome 2 of Dictyostelium."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116961; AAM3742.1; -.
DR InterPro: IPR006649; snRNP.
DR InterPro: IPR001163; snRNP_Sm.
DR Pfam; PF01423; Sm; 1.
DR ProDom; PD020287; snRNP; 1.
DR SMART; SM00511; Sm; 1.
SQ SEQUENCE 83 AA; 9411 MW; 8299A18276894BEA CRC64;

Query Match 0.9%; Score 7; DB 5; Length 83;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 250 NTSNNSN 256
Db 9 NTSNNSN 15

RESULT 68
OY Q73850 PRELIMINARY; PRT; 86 AA.
ID Q73850
AC Q73850;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Envelope glycoprotein, V1-V2 region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96251940; PubMed=8661394;
RA Palmer C., Balfe P., Fox D., May J.C., Frederiksen R., Fenyo E.M.,
RA McKeating J.A.;
RT "Functional characterization of the V1V2 region of human
RT immunodeficiency virus type 1."
RL Virology 220:436-449(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Blouin C.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U52268; AAB07922.1; -.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1 1
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9788 MW; 6241F1B599434EF3 CRC64;

Query Match 0.9%; Score 7; DB 15; Length 86;
```

Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 247 TNTNTSN 253
Db 25 TNTNTSN 31

RESULT 69
073851

ID 073851 PRELIMINARY; PRT; 86 AA.

AC 073851; 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DE Envelope glycoprotein, VI-V2 region (Fragment).

OS Human immunodeficiency virus 1.

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676; SEQUENCE FROM N.A.

RA Palmer C., Baile P., Fox D., May J.C., Frederiksson R., Fenyo E.M.,

RT "Functional characterization of the VIV2 region of human

RL Virology 220:436-449(1996).

RN [2] SEQUENCE FROM N.A.

RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; US2269; AAB07923.1; -

DR Interpro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

KW AIDS; Coat protein; Glycoprotein.

FT NON_TER 1 1

FT NON_TER 86 86

SO SEQUENCE 86 AA; 9788 MW; 6241F1E599434EF3 CRC64;

OY 247 TNTNTSN 253

Db 25 TNTNTSN 31

RESULT 70

073852

ID 073852 PRELIMINARY; PRT; 86 AA.

AC 073852; 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DE Envelope glycoprotein, VI-V2 region (Fragment).

OS Human immunodeficiency virus 1.

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676; SEQUENCE FROM N.A.

RA Palmer C., Baile P., Fox D., May J.C., Frederiksson R., Fenyo E.M.,

RT "Functional characterization of the VIV2 region of human

RL Virology 220:436-449(1996).

RN [2] SEQUENCE FROM N.A.

RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; US2270; AAB07924.1; -

DR Interpro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

KW AIDS; Coat protein; Glycoprotein.

FT NON_TER 1 1

FT NON_TER 86 86

SO SEQUENCE 86 AA; 9788 MW; 6241F1E599434EF3 CRC64;

OY 247 TNTNTSN 253

Db 25 TNTNTSN 31

RESULT 71

097W98

ID 097W98 PRELIMINARY; PRT; 90 AA.

AC 097W98; 01-OCT-2001 (TReMBLrel. 18, Created)

DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)

DE Hypothetical protein SSO10237.

OS Sulfolobus solfataricus.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

OX NCBI_TaxID=2287; SEQUENCE FROM N.A.

RA STRAIN=ATCC 35092 / DSM 1617 / P2;

RA MEDLINE=21332296; PubMed=11427726;

RA She Q., Singh R.K., Contaloni F., Zivanovic Y., Allard G.,

RA Aweyaz M.J., Chan-Welher C.C.-Y., Clausen I.G., Cutlis B.A.,

RA De Moers A., Erasuo G., Fletcher C., Gordon P.M.K.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.,

RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

DR EMBL; AE006836; AAK42490.1; -

KW Hypothetical protein; Complete proteome.

SO SEQUENCE 90 AA; 10208 MW; 5AE75F77EFED0635 CRC64;

OY 111 GKKYVYL 117

Db 18 GKKYVYL 24

RESULT 72

09RUG5

ID 09RUG5 PRELIMINARY; PRT; 93 AA.

AC 09RUG5; 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DE Hypothetical protein DR1421.

OS Deinococcus radiodurans.

OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;

OX NCBI_TaxID=1299; SEQUENCE FROM N.A.

RA STRAIN=R1; MEDLINE=20036896; PubMed=10567266;

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RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Uetreback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RA "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577(1999).
DR EMBL; AE001987; AAF11000.1; -.
DR TIGR; DR1421; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 93 AA; 10167 MW; 39DBF6FDEB24B5 CRC64;

Query Match 0.9%; Score 7; DB 16; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 487 DLAFLA 493
DB 6 DLAFLA 12

RESULT 73
Q9RY27 PRELIMINARY; PRT; 94 AA.
ID Q9RY27;
AC Q9RY27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein DR0124.
GN DR0124.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Uetreback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RA "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577(1999).
DR EMBL; AE001875; AAF09721.1; -.
DR TIGR; DR0124; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 94 AA; 11353 MW; 4DFCB8011DE91235 CRC64;

Query Match 0.9%; Score 7; DB 16; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 ELEERIA 328
DB 81 ELEERIA 87

RESULT 74
Q8FAP6 PRELIMINARY; PRT; 96 AA.
ID Q8FAP6;
AC Q8FAP6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Transposase incs for insertion element IS2A/D/F/H/I/K.

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GN C5196.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CPT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016771; AAN83618.1; -.
KW Complete proteome.
SQ SEQUENCE 96 AA; 10661 MW; 362073321AC7BD1B CRC64;

Query Match 0.9%; Score 7; DB 16; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 ASELAIA 208
DB 45 ASELAIA 51

RESULT 75
Q8U029 PRELIMINARY; PRT; 104 AA.
ID Q8U029;
AC Q8U029;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Small nucleolar rnp similar to gar1.
GN PF1791.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010277; AAL81915.1; -.
KW Complete proteome.
SQ SEQUENCE 104 AA; 12311 MW; EFOA25A67B14687C CRC64;

Query Match 0.9%; Score 7; DB 17; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 RTNWVPS 240
DB 26 RTNWVPS 32

RESULT 76
P88557 PRELIMINARY; PRT; 108 AA.
ID P88557;
AC P88557;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P17 (Gag polypeptide) (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97151115; PubMed=8995651;
RT Hughes E.S., Bell J.E., Simmonds P.;
RT "Investigation of the dynamics of the spread of human immunodeficiency
RT virus to brain and other tissues by evolutionary analysis of sequences
RT from the p17ag and env genes."
RL J. Virol. 71:1272-1280(1997).
DR EMBL; U79816; AAB46537.1; -
DR InterPro; IPR000071; Retrovir_p17.
DR Pfam; PF00540; Gag_p17.1.
DR PRINTS; PR00234; HIVMATRIX.
KM AIDS; Core Protein; Polyprotein.
FT NON_TER 1
FT TER 108
SQ SEQUENCE 108 AA; 12031 MW; 06C862CF21B76E42 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 15; Length 108;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 NSLSVSO 378
Db 85 NSLSVSO 91

RESULT 77
08VR72 PRELIMINARY; PRT; 109 AA.
AC 08VR72;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 21, Last annotation update)
DE Insertion sequence protein.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21458820; PubMed=11574920;
RA Rasio D.A., Phillips J.A., Li X., Mobley H.L.T.;
RT "Identification of DNA sequences from a second pathogenicity island of
RT uropathogenic Escherichia coli CFT073: probes specific for
RT uropathogenic populations."
RL J. Infect. Dis. 184:1041-1049(2001).
DR EMBL; AP447814; AAL67376.1; -
DR InterPro; IPR002514; Transposase_8.
DR Pfam; PF01527; Transposase_8; 1.
SQ SEQUENCE 109 AA; 12173 MW; 5546C66A2BB96F28 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 109;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 ASEILAA 208
Db 70 ASEILAA 76

RESULT 78
09A6S4 PRELIMINARY; PRT; 110 AA.
AC 09A6S4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE HsbR/Yadr/Yfhf family protein.
DE CC2009.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.

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OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gunn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Yamatevra H., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005874; AAK23984.1; -
DR TIGR; CC2009; -
DR InterPro; IPR000361; HsbR_Yadr_Yfhf.
DR Pfam; PF01521; HsbR-like; 1.
DR ProDom; PD002183; HsbR_Yadr_Yfhf; 1.
DR TIGRPFAM; TIGR00049; TIGR00049; 1.
DR PROSITE; PS01152; HSB; 1.
KM Complete proteome.
SQ SEQUENCE 110 AA; 11698 MW; D1DCD55226D91119 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 110;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 779 LALLKGS 785
Db 72 LALLKGS 78

RESULT 79
09CDT0 PRELIMINARY; PRT; 110 AA.
AC 09CDT0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Unknown protein.
GN YWAB OR IL2131.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Manger S., Jallion O., Malarne K.,
RA Weisenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
DR EMBL; AE006441; AAK06229.1; -
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF02699; YajC; 1.
DR TIGRPFAM; TIGR00739; YajC; 1.
DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
KM Complete proteome.
SQ SEQUENCE 110 AA; 11915 MW; FA8E3A9C84DAE2CE CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 110;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 710 VEETPAE 716
Db 94 VEETPAE 100

RESULT 80

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08FC10 PRELIMINARY; PRT; 111 AA.
 ID 08FC10: 01-MAR-2003 (TREMBlrel. 23, Created)
 AC 08FC10: 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Transposase insC for insertion element IS2A/D/F/H/I/K.
 GN C4552.
 OS Escherichia coli O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O6:H1 / ATCC 790928;
 RX MEDLINE=22388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Raeko D., Buckles E.L., Lion S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL; AE016769; AAN82986.1; -.
 KW Complete proteome.
 SQ SEQUENCE 111 AA; 12410 MW; 9A637F9998E413CA CRC64;

Query Match 0.9%; Score 7; DB 16; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 202 ASFLAA 208
 DB 85 ASFLAA 91

RESULT 81
 ID 08CMN4 PRELIMINARY; PRT; 115 AA.
 AC 08CMN4: 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Ribonuclease P protein component.
 GN SE2418.
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
 RA Chen Z., Wen Y.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE016752; AAO06061.1; -.
 KW Complete proteome.
 SQ SEQUENCE 115 AA; 13484 MW; 106B2592C400F18 CRC64;

Query Match 0.9%; Score 7; DB 16; Length 115;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 460 RNSDFOA 466
 DB 9 RNSDFOA 15

RESULT 82
 ID 08T4Z7 PRELIMINARY; PRT; 116 AA.
 AC 08T4Z7: 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Erythrocyte membrane protein 1 (Fragment).
 GN VAR.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH1;
 RX MEDLINE=21839615; PubMed=11849711;
 RA Fowler E.V., Peters J.M., Gatton M.L., Chen N., Cheng Q.;
 RT "Genetic diversity of the DBLalpha region in Plasmodium falciparum var
 genes among Asia-Pacific isolates.";
 RL Mol. Biochem. Parasitol. 120:117-126(2002).
 DR EMBL; AY054933; AAL1277.1; -.
 FT NON-TER
 FT NON-TER
 SQ SEQUENCE 116 AA; 13272 MW; 01F917589E19E327 CRC64;

Query Match 0.9%; Score 7; DB 5; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 649 TYKAPNG 655
 DB 71 TYKAPNG 77

RESULT 83
 ID 08L494 PRELIMINARY; PRT; 117 AA.
 AC 08L494: 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE OJ1316_H05.2 protein (P0038D11.19 protein).
 GN OJ1316_H05.2 OR P0038D11.19.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriocarpaceae; Oryzae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
 clone:OJ1316_H05.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 clone:P0038D11.19.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003340; BAC00607.1; -.
 DR EMBL; AP003344; BAC05543.1; -.
 DR Gramene; O8L494; -.
 SQ SEQUENCE 117 AA; 13260 MW; A03BF65BF4FE3194 CRC64;

Query Match 0.9%; Score 7; DB 10; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 381 RKGEGY 387
 DB 83 RKGEGY 89

RESULT 84
 ID 08YC21 PRELIMINARY; PRT; 117 AA.

AC 08YC21;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
 DE Transcriptional regulator.
 GN BMEI10712.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mijer C., Los T.,
 Ivanova N., Anderson I., Bhattacharya A., Lykdis A., Resnik G.,
 Selkov E., Elzer F.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 Haselkorn R., Kyriides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 Brucella melitensis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL; AE009706; AAL53954.1; -.
 KW Complete proteome.
 SQ SEQUENCE 117 AA; 12905 MW; B180B0A08BD6D49A CRC64;

Query Match 0.9%; Score 7; DB 16; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 200 LSASELA 206
 Db 88 LSASELA 94

RESULT 85
 Q8OUR7 PRELIMINARY; PRT; 120 AA.
 AC Q8OUR7;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
 DE ORF043L.
 OS Infectious spleen and kidney necrosis virus.
 OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae;
 OC Unclassified Iridoviridae.
 OX NCBI_TaxID=180170;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21874810; PubMed=11878882;
 RA He J.G., Deng M., Weng S.P., Li Z., Zhou S.Y., Long Q.X., Wang X.Z.,
 Chan S.M.;
 RT "Complete genome analysis of the mandarin fish infectious spleen and
 kidney necrosis Iridovirus.";
 RL Virology 291:126-139(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA He J.G., Deng M., Weng S.P., Li Z., Zhou S.Y., Long Q.X., Wang X.Z.,
 Chan S.M.;
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF371960; AAL98767.1; -.
 DR InterPro; IPR006863; Evtl.Alt.
 DR Pfam; PF04777; Evtl.Alt; I.
 SQ SEQUENCE 120 AA; 13326 MW; A06BFFDB695CB787 CRC64;

Query Match 0.9%; Score 7; DB 12; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 300 TARGAV 306
 Db 110 TARGAV 116

RESULT 86
 Q8FDX0 PRELIMINARY; PRT; 124 AA.
 AC Q8FDX0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
 DE Transposase insc for insertion element IS2A/D/F/H/I/K.
 GN C3612.
 OS Escherichia coli O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=06:HI / CFT073 / ATCC 700928;
 RX MEDLINE=22388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL; AE016766; AAN82060.1; -.
 KW Complete proteome.
 SQ SEQUENCE 124 AA; 13998 MW; F038388F93D92689 CRC64;

Query Match 0.9%; Score 7; DB 16; Length 124;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 202 ASELA 208
 Db 85 ASELA 91

RESULT 87
 Q9X6J3 PRELIMINARY; PRT; 126 AA.
 AC Q9X6J3;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
 DE Chorismate mutase.
 GN AROH.
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacillales; Geobacillus.
 OX NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCA 26;
 RA Chen X.P., Antson A.A., Yang M., Baumann C., Dodson E.J., Dodson G.G.,
 Gollnick P.;
 RT "Regulatory features of the trp operon and the crystal structure of
 the trp RNA-binding Attenuation Protein from Bacillus
 stearothermophilus.";
 RL J. Mol. Biol. 0:0-0(1999).
 DR EMBL; AF139534; AAD33790.1; -.
 DR HSSP; P19080; 1DBF.
 DR InterPro; IPR002701; Chorismate_mut.
 DR Pfam; PF01817; Chorismate_mut; I.
 SQ SEQUENCE 126 AA; 14101 MW; 0761341DF8BD7CB4 CRC64;

Query Match 0.9%; Score 7; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 VYLKAA 121
 Db 106 VYLKAA 112

RESULT 88

Q8FWA2 PRELIMINARY; PRT; 128 AA.
 AC Q8FWA2;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE 1566 family element, orf2, putative.
 GN BRA0557.
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1330 / Biovar 1;
 RX MEDLINE=22247741; PubMed=12271122;
 RA Paulsen I.T., Sehadati R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beaman M.J.,
 RA Daugherty S.C., Debey R.T., Durkin A.S., Kolony J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek U., Van Aken S.E.,
 RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
 RA Hoover D.B., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 DR EMBL; AE014552; AA03747.1; -.
 KW TIGR; BRA0557; -.
 KM Complete proteome.
 SQ SEQUENCE 128 AA; 13913 MW; B7072E85108AB0AA CRC64;

Query Match 0.9%; Score 7; DB 16; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 200 LSASELA 206
 |||||
 Db 99 LSASELA 105

RESULT 89

Q8EMH8 PRELIMINARY; PRT; 128 AA.
 AC Q8EMH8;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE 5-carboxymethyl-2-hydroxymuconate isomerase (EC 5.3.3.10).
 GN O82864.
 OS Oceanobacillus thelyensis.
 OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.
 OX NCBI_TaxID=182710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
 RX MEDLINE=22220767; PubMed=12235376;
 RA Takami H., Takaki Y., Uchiyama I.,
 RT "Genome sequence of Oceanobacillus thelyensis isolated from the Iheya
 RT Ridge and its unexpected adaptive capabilities to extreme
 RT environments."
 RL Nucleic Acids Res. 30:3927-3935(2002).
 DR EMBL; AP004602; BAC14820.1; -.
 KW Isomerase; Complete proteome.
 SQ SEQUENCE 128 AA; 14793 MW; D14491B1283783E CRC64;

Query Match 0.9%; Score 7; DB 16; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 660 DLFATIK 666
 |||||
 Db 84 DLFATIK 90

RESULT 90

Q9YAF7 PRELIMINARY; PRT; 128 AA.
 AC Q9YAF7;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein APE1982.
 GN APE1982.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcates;
 OC Desulfurococcaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,
 RA Jinno K., Takahashi M., Sekine M., Baba S.-I., Akai A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.,
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1."
 RL DNA Res. 6:83-101(1999).
 DR EMBL; AP000063; BAA80992.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 128 AA; 13557 MW; 9248C96789921467 CRC64;

Query Match 0.9%; Score 7; DB 17; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 785 SNPSVS 791
 |||||
 Db 43 SNPSVS 49

RESULT 91

Q9XBD3 PRELIMINARY; PRT; 129 AA.
 AC Q9XBD3;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE MutT-like protein.
 GN SC03260 OR SCE39.10.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Oliver K., Harris D.,
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Bentley S.D., Parkhill J., Barrett B.G., Rajandream N.A.,
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinash H., Hopwood D.A.,
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).

[4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitch E., Rajadream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL939115; CAB40318.1; -.
DR HSSP; P08337; ITDM.
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00293; NUDIX; 1.
DR PRINTS; PR00502; NUDIXFAMILY.
DR PROSITE; PS00893; NUDIX; 1.
KW Complete proteome.
SQ SEQUENCE 129 AA; 14108 MW; 1BD428B6F66D1911 CRC64;

Query Match 0.9%; Score 7; DB 16; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LTPDEV5 39
DB 89 LTPDEV5 95
P74726 PRELIMINARY; PRT; 130 AA.
ID P74726
AC P74726;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein slr0588.
GN SLR0588.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugita M., Sasegawa S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90917; BAA18846.1; -.
SQ SEQUENCE 130 AA; 14238 MW; 5C35184E0301910 CRC64;

Query Match 0.9%; Score 7; DB 16; Length 130;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 268 DSLKQL 274
DB 111 DSLKQL 117
RESULT 93
069802

ID 069802 PRELIMINARY; PRT; 131 AA.
AC 069802;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Orl31.
GN ORF131.
OS Streptomyces ambifaciens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomyces; Streptomyces.
OX NCBI_TaxID=1889;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15154;
RX MEDLINE=89265212; PubMed=2657820;
RA Boccard F., Smokvina T., Pernodet J.L., Friedmann A., Guerinneau M.;
RT "Structural analysis of loci involved in pSAM2 site-specific
RT integration in Streptomyces.";
RL Plasmid 21:59-70(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15154;
RX MEDLINE=9374848; PubMed=7934842;
RA Hagege J., Pernodet J.L., Friedmann A., Guerinneau M.;
RT "Mode and origin of replication of pSAM2, a conjugative integrating
RT element of Streptomyces ambifaciens.";
RL Mol. Microbiol. 10:799-812(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15154;
RX MEDLINE=9374848; PubMed=8366038;
RA Hagege J.M., Pernodet J.L., Gerbaud C., Sezonov G., Friedmann A.,
RA Guerinneau M.;
RT "Transfer function of the conjugative integrating element pSAM2 from
RT Streptomyces ambifaciens: characterization of a k11-kor system
RT associated with transfer.";
RL J. Bacteriol. 173:5529-5538(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15154;
RX MEDLINE=94302137; PubMed=8029324;
RA Hagege J., Boccard F., Smokvina T., Pernodet J.L., Friedmann A.,
RA Guerinneau M.;
RT "Identification of a gene encoding the replication initiator protein
RT of the Streptomyces integrating element, pSAM2.";
RL Plasmid 31:166-183(1994).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15154;
RX MEDLINE=96100452; PubMed=8559072;
RA Sezonov G., Hagege J., Pernodet J.L., Friedmann A., Guerinneau M.;
RT "Characterization of prx, a gene for replication control in pSAM2, the
RT integrating element of Streptomyces ambifaciens.";
RL Mol. Microbiol. 17:533-544(1995).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15154;
RX MEDLINE=98292736; PubMed=9620953;
RA Sezonov G., Duchene A.M., Friedmann A., Guerinneau M., Pernodet J.L.;
RT "Replicase, excisionase, and integrase genes of the Streptomyces
RT element pSAM2 constitute an operon positively regulated by the prx
RT gene.";
RL J. Bacteriol. 180:3056-3061(1998).
DR EMBL; AJ005260; CAA06447.1; -.

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DR InterPro: IPR000086; NUDIX_hydrolase.
DR Pfam: PF00293; NUDIX.1.
DR PRINTS: PR00502; NUDIXFAMILY.
DR PROSITE: PS00893; NUDIX.1.
KW p1asmid.
SQ SEQUENCE 131 AA; 14295 MW; E44DC7C113475BD1 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 131;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 LTPDEVS 39
    |||||
    91 LTPDEVS 97

RESULT 94
O92P78 PRELIMINARY; PRT; 131 AA.
ID O92P78;
AC O92P78;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE Putative zinc uptake regulation protein.
GN ZUR OR R01912 OR SMC04242.
OS Rhizobium melioli (Sinorhizobium melioli).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.
OK NCBI_taxid=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gonzy J., Bothe G., Ampe F., Barut J.,
RA Bolstad P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,
RA Pohl T., Portetel D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galbert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium melioli strain 1021."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL: AL591788; CAC46491.1; -.
DR InterPro: IPR002481; FUR.
DR Pfam: PF01475; FUR.1.
DR Prodom: PD002003; FUR.1.
KW Complete proteome.
SQ SEQUENCE 131 AA; 14643 MW; 8C8CCDA1B3E4CA88 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 131;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 ALDKLE 472
    |||||
    47 ALDKLE 53

RESULT 95
O86762 PRELIMINARY; PRT; 131 AA.
ID O86762;
AC O86762;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Mult-like protein.
GN SC05637 OR SC6A9.30C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OK NCBI_taxid=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);

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RA Murphy L., Harris D.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redendach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)."
RL Nature 417:141-147(2002).
DR EMBL: AL939124; CAA19915.1; -.
DR InterPro: IPR000086; NUDIX_hydrolase.
DR Pfam: PF00293; NUDIX.1.
DR PRINTS: PR00502; NUDIXFAMILY.
DR PROSITE: PS00893; NUDIX.1.
KW Complete proteome.
SQ SEQUENCE 131 AA; 14325 MW; F9F9BCB7C82AE791 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 131;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 LTPDEVS 39
    |||||
    91 LTPDEVS 97

RESULT 96
O9YL97 PRELIMINARY; PRT; 134 AA.
ID O9YL97;
AC O9YL97;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE PIX protein.
OS Human adenovirus type 9.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OK NCBI_taxid=10527;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99174004; PubMed=10074157;
RA Thomas D.L., Shin S., Jiang B.H., Vogel H., Ross M.A., Kapilt M.,
RA Shenk T.E., Javlier R.T.;
RT "Early region 1 transforming functions are dispensable for mammary
RT tumorigenesis by human adenovirus type 9."
RL J. Virol. 73:3071-3079(1999).
DR EMBL: AF099665; AAD16306.1; -.
DR InterPro: IPR005641; Adeno_PIX.
DR Pfam: PF03955; Adeno_PIX.1.
SQ SEQUENCE 134 AA; 13751 MW; 39EB34EB5C6CAD25 CRC64;

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Query Match 0.9%; Score 7; DB 12; Length 134;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 776 EKLALL 782
 DB 99 EKLALL 105

RESULT 97

QY 090640 PRELIMINARY; PRT; 134 AA.

AC 090640;
 DT 01-NOV-1998 (TEMBLrel. 08, Created)
 DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Simian-Human immunodeficiency virus.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=57667;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=SHIV-C2/1;
 RX MEDLINE=99281901; PubMed=10355770;
 RA Shinohara K., Sakai K., Ando S., Yoshino N., Takahashi E.,
 RA Someya K., Suzuki Y., Nakasone T., Sasaki Y., Kaizu M., Lu Y.,
 RA Honda M.;
 RT "A highly pathogenic simian/human immunodeficiency virus with genetic
 changes in cynomolgus monkey."
 RL J. Gen. Virol. 80:1231-1240(1999).
 DR EMBL; AF082832; AAC34101.1; -;
 DR InterPro; IPR000328; Env_Gp41.
 DR Pfam; PF00517; Gp41; 2. Env_Gp41.
 KW Transmembrane.
 FT NON_TER
 SQ SEQUENCE 134 AA; 15700 MW; CB92BE2FDB6C094A CRC64;

Query Match 0.9%; Score 7; DB 15; Length 134;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 750 ATETLG 756
 DB 96 ATETLG 102

RESULT 98

QY 08PN57 PRELIMINARY; PRT; 134 AA.

AC 08PN57;
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
 DE Hypothetical protein XAC1216.
 GN XAC1216.
 OS Xanthomonas axonopodis (pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=92829;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferris J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Canavaral F., Cardozo J., Chambergo F., Claphin L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferris M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Melanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Trufi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 host specificities."
 RL Nature 417:459-463(2002).
 DR EMBL; AF011751; AAM36088.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 134 AA; 14831 MW; 87247E2B424ECF8F CRC64;

Query Match 0.9%; Score 7; DB 16; Length 134;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 LKDAHA 123
 DB 101 LKDAHA 107

RESULT 99

QY 08VS19 PRELIMINARY; PRT; 136 AA.

AC 08VS19;
 DT 01-MAR-2002 (TEMBLrel. 20, Created)
 DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE Hypothetical 15.2 kDa protein.
 GN CP0106.
 OS Shigella flexneri 2a.
 OC plasmid pcpt301.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=42897;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=301;
 RA Jin Q., Zhang J.Y., Liu H., Yang J., Yang F., Zhang X.B., Wang J.H.,
 RA Yang G.W., Wu H.T., Dong J., Sun L.L., Xie Y., Zhao A.L., Gao Y.S.,
 RA Zhu J.P., Kan B., Chen S.X., Yao Z.J., He B.K., Chen R.S., Ma D.L.,
 RA Yuan Z.H., Xu J.G., Wang Y., Shen Y., Lu W.C., Qiang B.Q., Wen Y.M.,
 RA Hou Y.D.;
 RT "Complete DNA sequence and analysis of the large virulence plasmid
 PCP301 of Shigella flexneri."
 RL Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF386526; AAL72401.1; -;
 DR InterPro; IPR002514; Transposase_8.
 DR Pfam; PF01527; Transposase_8; 1.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 136 AA; 15159 MW; 8E2A0FA9317B3DF CRC64;

Query Match 0.9%; Score 7; DB 2; Length 136;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 ASBLAA 208
 DB 85 ASBLAA 91

RESULT 100

QY 017947 PRELIMINARY; PRT; 136 AA.

AC 017947;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE C13G3.1 protein.
 GN C13G3.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditiidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McMurray A.A.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL: Z74027; CAA98421.1; -.
 DR WormPep: C13G3.1; CE05277.
 SQ SEQUENCE 136 AA; 14914 MW; 804BDBAB75A6645F CRC64;
 Query Match 0.9%; Score 7; DB 5; Length 136;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 783 KGSNPSS 789
 |||||
 Db 96 KGSNPSS 102

Search completed: November 14, 2003, 11:01:14
 Job time : 109 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 10:58:50 ; Search time 112 Seconds

(without alignments)
300.709 Million cell updates/sec

Title: US-09-765-271-56

Perfect score: 796
Sequence: 1 SYELGLYQARTVKNRVS.....KLIALIKGSPNSVSKKIN 796

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 200 summaries

Database : Issued Patents_AA:*

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- 2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
- 4: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
- 5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/prodata/2/iaa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	795	99.9	796	3	US-08-961-083-56
2	795	99.9	796	4	US-09-536-784-56
3	695	87.3	819	4	US-09-468-656A-8
4	60	7.5	819	4	US-09-468-656A-10
5	60	7.5	838	4	US-09-468-656A-4
6	51	6.4	763	3	US-08-961-083-66
7	51	6.4	763	4	US-09-536-784-66
8	32	4.0	447	3	US-08-961-083-182
9	32	4.0	447	4	US-09-536-784-182
10	32	4.0	484	4	US-09-468-656A-6
11	9	1.1	795	4	US-09-328-582-6143
12	9	1.1	921	1	US-08-188-582-2
13	9	1.1	921	1	US-08-946-715-2
14	8	1.0	110	2	US-08-569-166-34
15	8	1.0	332	4	US-09-107-532A-5477
16	8	1.0	490	4	US-09-134-001C-5116
17	8	1.0	503	3	US-08-999-774A-10
18	8	0.9	15	1	US-08-221-583-57
19	7	0.9	15	1	US-08-221-583-58
20	7	0.9	15	1	US-08-221-583-59
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22	7	0.9	15	5	PCT-US95-04018-58
23	7	0.9	15	5	PCT-US95-04018-59
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25	7	0.9	27	4	US-09-608-902-4
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27	7	0.9	45	4	US-09-608-902-2

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30	7	0.9	66	4	US-09-608-902-1	Sequence 1, Appli
31	7	0.9	76	4	US-09-328-352-6019	Sequence 6019, Ap
32	7	0.9	117	4	US-09-134-001C-4585	Sequence 4585, Ap
33	7	0.9	149	4	US-09-252-991A-28698	Sequence 28698, A
34	7	0.9	158	2	US-08-917-456-2	Sequence 2, Appli
35	7	0.9	158	3	US-09-229-804-2	Sequence 2, Appli
36	7	0.9	163	4	US-09-252-991A-30622	Sequence 20622, A
37	7	0.9	191	4	US-09-252-991A-30217	Sequence 30217, A
38	7	0.9	198	4	US-09-613-303-35	Sequence 35, Appli
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40	7	0.9	201	2	US-08-916-901-8	Sequence 8, Appli
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43	7	0.9	226	3	US-08-908-332-5	Sequence 5, Appli
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45	7	0.9	235	4	US-09-580-235-6	Sequence 2, Appli
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52	7	0.9	235	4	US-09-580-181-8	Sequence 8, Appli
53	7	0.9	235	4	US-09-102-530-2	Sequence 2, Appli
54	7	0.9	235	4	US-09-102-530-4	Sequence 4, Appli
55	7	0.9	235	4	US-09-102-530-6	Sequence 6, Appli
56	7	0.9	235	4	US-09-102-530-8	Sequence 8, Appli
57	7	0.9	235	4	US-09-620-405B-487	Sequence 487, App
58	7	0.9	240	4	US-09-604-287A-487	Sequence 487, App
59	7	0.9	240	4	US-09-107-533A-6634	Sequence 6634, Ap
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61	7	0.9	257	4	US-09-579-845-10	Sequence 10, Appli
62	7	0.9	261	1	US-08-622-353-2	Sequence 2, Appli
63	7	0.9	261	2	US-08-622-353A-2	Sequence 2, Appli
64	7	0.9	261	3	US-08-826-390-2	Sequence 2, Appli
65	7	0.9	298	4	US-09-252-991A-21944	Sequence 21944, A
66	7	0.9	305	4	US-09-252-991A-31029	Sequence 31029, A
67	7	0.9	312	4	US-09-252-991A-29807	Sequence 29807, A
68	7	0.9	325	4	US-09-198-452A-745	Sequence 745, App
69	7	0.9	383	4	US-09-459-749D-17	Sequence 17, Appli
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82	7	0.9	461	4	US-09-758-124-2	Sequence 2, Appli
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84	7	0.9	465	4	US-09-328-352-4742	Sequence 4742, Ap
85	7	0.9	485	4	US-09-252-991A-17797	Sequence 17797, A
86	7	0.9	486	1	US-08-243-010-1	Sequence 1, Appli
87	7	0.9	498	4	US-09-252-991A-27183	Sequence 27183, A
88	7	0.9	505	4	US-09-620-405B-478	Sequence 478, App
89	7	0.9	505	4	US-09-604-287A-478	Sequence 485, App
90	7	0.9	505	4	US-09-252-991A-19121	Sequence 19121, A
91	7	0.9	511	3	US-08-991-677-4	Sequence 4, Appli
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93	7	0.9	512	4	US-08-232-545-16	Sequence 16, Appli
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95	7	0.9	513	4	US-09-564-808-6	Sequence 4, Appli
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 108 7 0.9 530 4 US-09-252-991A-21963 Sequence 21963, A
 109 7 0.9 539 1 US-08-399-696-122 Sequence 122, App
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 127 7 0.9 1289 4 US-09-546-934-1 Sequence 1, Appli
 128 7 0.9 2547 3 US-09-058-489-35 Sequence 35, Appli
 129 7 0.9 2736 4 US-09-252-991A-30227 Sequence 30227, A
 130 7 0.9 7 4 US-09-187-859-3833 Sequence 3833, Ap
 131 7 0.9 8 4 US-09-839-542B-3833 Sequence 3833, Ap
 132 7 0.9 8 4 US-09-187-859-3834 Sequence 3834, Ap
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 137 7 0.9 10 3 US-08-832-198-1 Sequence 1, Appli
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 143 7 0.9 11 4 US-09-025-596-44 Sequence 44, Appli
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 150 7 0.9 15 3 US-08-448-194-44 Sequence 44, Appli
 151 7 0.9 15 4 US-08-867-921-44 Sequence 44, Appli
 152 7 0.9 17 4 US-08-472-701-21 Sequence 21, Appli
 153 7 0.9 17 4 US-09-690-454-124 Sequence 124, App
 154 7 0.9 17 5 PCT-US95-08596-21 Sequence 21, Appli
 155 7 0.9 17 5 PCT-US95-08621-20 Sequence 20, Appli
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 170 7 0.9 40 1 US-08-313-075A-58 Sequence 58, Appli
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 175 6 0.8 50 4 US-09-752-510-2 Sequence 2, Appli
 176 6 0.8 53 4 US-08-861-476C-8 Sequence 8, Appli
 177 6 0.8 57 3 US-09-023-731-4 Sequence 4, Appli
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 189 6 0.8 63 4 US-09-017-947-19 Sequence 19, Appli
 190 6 0.8 64 4 US-09-722-210-491 Sequence 491, App
 191 6 0.8 69 2 US-08-245-511-27 Sequence 27, Appli
 192 6 0.8 69 2 US-08-600-993A-27 Sequence 27, Appli
 193 6 0.8 71 1 US-08-261-677-13 Sequence 13, Appli
 194 6 0.8 71 1 US-08-384-556A-9 Sequence 9, Appli
 195 6 0.8 71 2 US-08-331-355A-13 Sequence 13, Appli
 196 6 0.8 71 5 PCT-US94-12364-13 Sequence 13, Appli
 197 6 0.8 71 5 PCT-US95-07753-9 Sequence 9, Appli
 198 6 0.8 74 3 US-08-938-669A-31 Sequence 31, Appli
 199 6 0.8 74 4 US-09-306-828-11 Sequence 31, Appli
 200 6 0.8 78 4 US-09-107-532A-4405 Sequence 4405, Ap

ALIGNMENTS

RESULT 1
 US-08-961-083-56
 ; Sequence 56, Application US/08961083
 ; Patent No. 6159469
 ; GENERAL INFORMATION:
 ; APPLICANT: Chol et. al.
 ; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
 ; NUMBER OF SEQUENCES: 452
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 ; COMPUTER: HP Vectra 486/33
 ; OPERATING SYSTEM: MSDOS version 6.2
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/961,083
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brookes, A. Anders
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PB340P2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8512
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 796 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-08-961-083-56

Query Match 99.9%; Score 795; DB 3; Length 796;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 STELGIGYQARTYKNNRVSIDGKQATQKTEMLTPDEVSKEKREGINAEOIVIKITDGGYVT 60
DB 1 STELGIGYQARTYKNNRVSIDGKQATQKTEMLTPDEVSKEKREGINAEOIVIKITDGGYVT 60
QY 61 SHGDHYHYNGKVPYDAIISSEELMKDPNYKLDKEDI VNEVGGYVIKYDGYVYVYLKDA 120
DB 61 SHGDHYHYNGKVPYDAIISSEELMKDPNYKLDKEDI VNEVGGYVIKYDGYVYVYLKDA 120
QY 121 AHADVNRTEKEINRQKQEHSHREGTTPNDGAVALARSGRYTTDDGYIFNADIIEDT 180
DB 121 AHADVNRTEKEINRQKQEHSHREGTTPNDGAVALARSGRYTTDDGYIFNADIIEDT 180
QY 181 GDAYIVPHGDHYHYPKNELSASELAAPFLSGRGNLSNRTYRRQNSDNTSRTNWVS 240
DB 181 GDAYIVPHGDHYHYPKNELSASELAAPFLSGRGNLSNRTYRRQNSDNTSRTNWVS 240
QY 241 VSNPGTTNTNTSNNTNSQASQNSDIDSLKQLYKLPSQRHVESDGLVPFPAQITTSRT 300
DB 241 VSNPGTTNTNTSNNTNSQASQNSDIDSLKQLYKLPSQRHVESDGLVPFPAQITTSRT 300
QY 301 ARGVAVPHGDHYHFIPIYSQMSSELEERIIARILPLRYRSHNVWVDSRPEQSPPTPEPSPG 360
DB 301 ARGVAVPHGDHYHFIPIYSQMSSELEERIIARILPLRYRSHNVWVDSRPEQSPPTPEPSPG 360
QY 361 POPAPNLKIDSNSLSVSQLVRKVGEGYVEEKGISRYVFAKOLPSETVNLNLSKLSKQSS 420
DB 361 POPAPNLKIDSNSLSVSQLVRKVGEGYVEEKGISRYVFAKOLPSETVNLNLSKLSKQSS 420
QY 421 VSHITLAKKENAVAPRQOEYDYKAYNLLTEAHKALFYXKGRNSDFQALDKLRLNDESTN 480
DB 421 VSHITLAKKENAVAPRQOEYDYKAYNLLTEAHKALFYXKGRNSDFQALDKLRLNDESTN 480
QY 481 KEKLVDDLLAFIAPITHPERLQKPNQIETDEDEVIAQLADKYTSDGYIFDEHDIISD 540
DB 481 KEKLVDDLLAFIAPITHPERLQKPNQIETDEDEVIAQLADKYTSDGYIFDEHDIISD 540
QY 541 EGDAYVTPHMGSHWIGKDSLSDKEKVAQAAYTKEGILPPSPBDADVKNPTGDSAAAY 600
DB 541 EGDAYVTPHMGSHWIGKDSLSDKEKVAQAAYTKEGILPPSPBDADVKNPTGDSAAAY 600
QY 601 NRKGEKRIPLVRLPYMVEHTEVEKNGNLIIPKDHYNIKFAMFDDHTYKAPNGYTTLED 660
DB 601 NRKGEKRIPLVRLPYMVEHTEVEKNGNLIIPKDHYNIKFAMFDDHTYKAPNGYTTLED 660
QY 661 LFAATIKYVYEHDERPHSNDGNGNASEHILGKKHSDENKNPKADEEVEETPAPEVP 720
DB 661 LFAATIKYVYEHDERPHSNDGNGNASEHILGKKHSDENKNPKADEEVEETPAPEVP 720
QY 721 QVETEKVEAQLKEAEVLLAKVTDSILKANATELGLRNLLTLOIMDNNSIMAEAEKLIA 780
DB 721 QVETEKVEAQLKEAEVLLAKVTDSILKANATELGLRNLLTLOIMDNNSIMAEAEKLIA 780
QY 781 LKGSNPSSVSXEKIN 796
DB 781 LKGSNPSSVSXEKIN 796

```

RESULT 2

US-09-536-784-56

Sequence 56, Application US/09536784

Patent No. 6573082

GENERAL INFORMATION:

APPLICANT: Choi et. al.

TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines

NUMBER OF SEQUENCES: 452

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/536,784

FILING DATE: 30-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/961,083

FILING DATE: OCT-30-1997

ATTORNEY/AGENT INFORMATION:

NAME: Michelle S. Marks

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB340P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 796 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 56:

US-09-536-784-56

Query Match 99.9%; Score 795; DB 4; Length 796;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 STELGIGYQARTYKNNRVSIDGKQATQKTEMLTPDEVSKEKREGINAEOIVIKITDGGYVT 60
DB 1 STELGIGYQARTYKNNRVSIDGKQATQKTEMLTPDEVSKEKREGINAEOIVIKITDGGYVT 60
QY 61 SHGDHYHYNGKVPYDAIISSEELMKDPNYKLDKEDI VNEVGGYVIKYDGYVYVYLKDA 120
DB 61 SHGDHYHYNGKVPYDAIISSEELMKDPNYKLDKEDI VNEVGGYVIKYDGYVYVYLKDA 120
QY 121 AHADVNRTEKEINRQKQEHSHREGTTPNDGAVALARSGRYTTDDGYIFNADIIEDT 180
DB 121 AHADVNRTEKEINRQKQEHSHREGTTPNDGAVALARSGRYTTDDGYIFNADIIEDT 180
QY 181 GDAYIVPHGDHYHYPKNELSASELAAPFLSGRGNLSNRTYRRQNSDNTSRTNWVS 240
DB 181 GDAYIVPHGDHYHYPKNELSASELAAPFLSGRGNLSNRTYRRQNSDNTSRTNWVS 240
QY 241 VSNPGTTNTNTSNNTNSQASQNSDIDSLKQLYKLPSQRHVESDGLVPFPAQITTSRT 300
DB 241 VSNPGTTNTNTSNNTNSQASQNSDIDSLKQLYKLPSQRHVESDGLVPFPAQITTSRT 300
QY 301 ARGVAVPHGDHYHFIPIYSQMSSELEERIIARILPLRYRSHNVWVDSRPEQSPPTPEPSPG 360
DB 301 ARGVAVPHGDHYHFIPIYSQMSSELEERIIARILPLRYRSHNVWVDSRPEQSPPTPEPSPG 360
QY 361 POPAPNLKIDSNSLSVSQLVRKVGEGYVEEKGISRYVFAKOLPSETVNLNLSKLSKQSS 420
DB 361 POPAPNLKIDSNSLSVSQLVRKVGEGYVEEKGISRYVFAKOLPSETVNLNLSKLSKQSS 420
QY 421 VSHITLAKKENAVAPRQOEYDYKAYNLLTEAHKALFYXKGRNSDFQALDKLRLNDESTN 480
DB 421 VSHITLAKKENAVAPRQOEYDYKAYNLLTEAHKALFYXKGRNSDFQALDKLRLNDESTN 480
QY 481 KEKLVDDLLAFIAPITHPERLQKPNQIETDEDEVIAQLADKYTSDGYIFDEHDIISD 540
DB 481 KEKLVDDLLAFIAPITHPERLQKPNQIETDEDEVIAQLADKYTSDGYIFDEHDIISD 540

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Qy 541 EGDAYVTPHMGSHWIGKDSLSDKEKVAQAAYTKEKGLPPSPDADYKANPTGDSAAIY 600
Db 541 EGDAYVTPHMGSHWIGKDSLSDKEKVAQAAYTKEKGLPPSPDADYKANPTGDSAAIY 600
Qy 601 NRKGEKRIPLVRLPYVVEHTVEYKGNLII PHKDHYNIKFAMFDHTTYKAPNGYTLSD 660
Db 601 NRKGEKRIPLVRLPYVVEHTVEYKGNLII PHKDHYNIKFAMFDHTTYKAPNGYTLSD 660
Qy 661 LFATIKYVEHPDERPHSNDGNGNASEHVLGKDHSEDPNKNFKADEEPVEETPAEPVP 720
Db 661 LFATIKYVEHPDERPHSNDGNGNASEHVLGKDHSEDPNKNFKADEEPVEETPAEPVP 720
Qy 721 QVETEKVAQLKEAEVLLAKYTDSSLKANATETLAGLRNNLTLOIMDNNSIMAEAEKLLA 780
Db 721 QVETEKVAQLKEAEVLLAKYTDSSLKANATETLAGLRNNLTLOIMDNNSIMAEAEKLLA 780
Qy 781 LKGSNPSSVSKEKIN 796
Db 781 LKGSNPSSVSKEKIN 796

```

```

RESULT 3
US-09-468-656A-8
; Sequence 8, Application US/09468656A
; Patent No. 6582706
; GENERAL INFORMATION:
; APPLICANT: Johnson, Leslie S.
; TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
; TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
; FILE REFERENCE: 469201-444
; CURRENT APPLICATION NUMBER: US/09/468,656A
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/113,048
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 819
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-468-656A-8

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```

Query Match 87.3%; Score 695; DB 4; Length 819;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 SYELGLYQARTVKEKNNRVSYIDGKOATOKTENLTPDEVSKREGINAEOIIVIKITDOGYVT 60
Db 21 SYELGLYQARTVKEKNNRVSYIDGKOATOKTENLTPDEVSKREGINAEOIIVIKITDOGYVT 80
Qy 61 SHGDHYHYNKGVPYDAIISBELLMKDPNYKLKDEIDINEYKGVYIVKDGKYVYLLKDA 120
Db 81 SHGDHYHYNKGVPYDAIISBELLMKDPNYKLKDEIDINEYKGVYIVKDGKYVYLLKDA 140
Qy 121 AAHADVNRKKEIRINROKQSHSQHREGCTPRNDGAVLAASOGRYTTDDGYIFNASTIIDT 180
Db 141 AAHADVNRKKEIRINROKQSHSQHREGCTPRNDGAVLAASOGRYTTDDGYIFNASTIIDT 200
Qy 181 GDAYIVPBGDHYHYIPKNELSASELAAAEAFLSGNGNLSNSTRYRONSDMSTRNWPVS 240
Db 201 GDAYIVPBGDHYHYIPKNELSASELAAAEAFLSGNGNLSNSTRYRONSDMSTRNWPVS 260
Qy 241 VSNPCTTNTSNNSTNSOASQSNDDISLKLQYLKPLSQHVESDGLVFPDPAQITSTRT 300
Db 261 VSNPCTTNTSNNSTNSOASQSNDDISLKLQYLKPLSQHVESDGLVFPDPAQITSTRT 320
Qy 301 ARGVAVPHGDHYHFPYQMSLEKRIARIIPLRFRSNHWVPDSRPEQSPQPTPEBSPG 360
Db 321 ARGVAVPHGDHYHFPYQMSLEKRIARIIPLRFRSNHWVPDSRPEQSPQPTPEBSPG 380

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Qy 361 POPAPNLIKIDSSNSVSLQVARKVGEQVFEBEKISRVAFAKDLPSFTVKNLKESKQES 420
Db 381 POPAPNLIKIDSSNSVSLQVARKVGEQVFEBEKISRVAFAKDLPSFTVKNLKESKQES 440
Qy 421 VSHTLTAKKENVARDEPFDKAYNLLTEAHKALFXNKGKRSDDQALDKLERLNDSTN 480
Db 441 VSHTLTAKKENVARDEPFDKAYNLLTEAHKALFXNKGKRSDDQALDKLERLNDSTN 500
Qy 481 KEKLVDDLAFIATITPERLGPNSQIEXTEDVRIAOLADKTTSDGYIFDEHDIIISD 540
Db 501 KEKLVDDLAFIATITPERLGPNSQIEXTEDVRIAOLADKTTSDGYIFDEHDIIISD 560
Qy 541 EGDAYVTPHMGSHWIGKDSLSDKEKVAQAAYTKEKGLPPSPDADYKANPTGDSAAIY 600
Db 561 EGDAYVTPHMGSHWIGKDSLSDKEKVAQAAYTKEKGLPPSPDADYKANPTGDSAAIY 620
Qy 601 NRKGEKRIPLVRLPYVVEHTVEYKGNLII PHKDHYNIKFAMFDHTTYKAPNGYTLSD 660
Db 621 NRKGEKRIPLVRLPYVVEHTVEYKGNLII PHKDHYNIKFAMFDHTTYKAPNGYTLSD 680
Qy 661 LFATIKYVEHPDERPHSNDGNGNASEHVLGKDHSEDPNKNFKADEEPVEETPAEPVP 720
Db 681 LFATIKYVEHPDERPHSNDGNGNASEHVLGKDHSEDPNKNFKADEEPVEETPAEPVP 740
Qy 721 QVETEKVAQLKEAEVLLAKYTDSSLKANATETLAGLRNNLTLOIMDNNSIMAEAEKLLA 780
Db 741 QVETEKVAQLKEAEVLLAKYTDSSLKANATETLAGLRNNLTLOIMDNNSIMAEAEKLLA 800
Qy 781 LKGSNPSSVSKEKIN 796
Db 801 LKGSNPSSVSKEKIN 816

```

```

RESULT 4
US-09-468-656A-10
; Sequence 10, Application US/09468656A
; Patent No. 6582706
; GENERAL INFORMATION:
; APPLICANT: Adamou, John E.
; TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
; TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
; FILE REFERENCE: 469201-444
; CURRENT APPLICATION NUMBER: US/09/468,656A
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/113,048
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 819
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-468-656A-10

```

```

Query Match 7.5%; Score 60; DB 4; Length 819;
Best Local Similarity 100.0%; Pred. No. 1,3e-50;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 31 ENLTPDEVSKREGINAEOIIVIKITDOGYVTSHGHDHYHYNKGVPYDAIISBELLMKDPNY 90
Db 52 ENLTPDEVSKREGINAEOIIVIKITDOGYVTSHGHDHYHYNKGVPYDAIISBELLMKDPNY 111

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```

RESULT 5
US-09-468-656A-4
; Sequence 4, Application US/09468656A
; Patent No. 6582706
; GENERAL INFORMATION:
; APPLICANT: Adamou, John E.
; TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus

```

;; TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
;; TITLE OF INVENTION: Motifs
;; FILE REFERENCE: 469201-444
;; CURRENT APPLICATION NUMBER: US/09/468,656A
;; CURRENT FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: 60/113,048
;; PRIOR FILING DATE: 1998-12-21
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO: 4
;; LENGTH: 838
;; TYPE: PRT
;; ORGANISM: Streptococcus pneumoniae
US-09-468-656A-4

Query Match
Best Local Similarity 100.0%; Score 60; DB 4; Length 838;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ENLTPDEVSKRESINAEQIVIKITDQGYTSHGDHYHYNGKVPDAISELLMDPNY 90
Db 52 ENLTPDEVSKRESINAEQIVIKITDQGYTSHGDHYHYNGKVPDAISELLMDPNY 111

RESULT 6
US-08-961-083-66
; Sequence 66, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 763 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-083-66

Query Match
Best Local Similarity 100.0%; Score 51; DB 3; Length 763;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 160 QGRYTTDGYIFNASDIIEDTGDYIVPHGDHYHYIPKXELASSELAAEA 210
Db 160 QGRYTTDGYIFNASDIIEDTGDYIVPHGDHYHYIPKXELASSELAAEA 210

Db 159 QGRYTTDGYIFNASDIIEDTGDYIVPHGDHYHYIPKXELASSELAAEA 209

RESULT 7
US-09-536-784-66
; Sequence 66, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 763 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-536-784-66

Query Match
Best Local Similarity 100.0%; Score 51; DB 4; Length 763;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 160 QGRYTTDGYIFNASDIIEDTGDYIVPHGDHYHYIPKXELASSELAAEA 210
Db 159 QGRYTTDGYIFNASDIIEDTGDYIVPHGDHYHYIPKXELASSELAAEA 209

RESULT 8
US-08-961-083-182
; Sequence 182, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-083-182

Query Match 4.0%; Score 32; DB 3; Length 447;
Best Local Similarity 100.0%; Pred. No. 3.9e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AEQIVIKITDQGYVTSQDHYHYNGKVPYDA 77
DB 43 AEQIVIKITDQGYVTSQDHYHYNGKVPYDA 74

RESULT 9
US-09-536-784-182
Sequence 182, Application US/09536784
Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 182:
US-09-536-784-182

Query Match 4.0%; Score 32; DB 4; Length 447;
Best Local Similarity 100.0%; Pred. No. 3.9e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AEQIVIKITDQGYVTSQDHYHYNGKVPYDA 77
DB 43 AEQIVIKITDQGYVTSQDHYHYNGKVPYDA 74

RESULT 10
US-09-468-656A-6
Sequence 6, Application US/09468656A
Patent No. 6582706
GENERAL INFORMATION:
APPLICANT: Johnson, Leslie S.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 484
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-468-656A-6

Query Match 4.0%; Score 32; DB 4; Length 484;
Best Local Similarity 100.0%; Pred. No. 4.2e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AEQIVIKITDQGYVTSQDHYHYNGKVPYDA 77
DB 67 AEQIVIKITDQGYVTSQDHYHYNGKVPYDA 98

RESULT 11
US-09-328-352-6143
Sequence 6143, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Bretton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6143
LENGTH: 795
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-6143

Query Match 1.1%; Score 9; DB 4; Length 795;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 SASFLAAE 209
DB 428 SASFLAAE 436

RESULT 12
US-08-188-582-2
; Sequence 2, Application US/08188582
; Patent No. 5534410
; GENERAL INFORMATION:
; APPLICANT: Tjian, Robert
; APPLICANT: Comai, Lucio
; APPLICANT: Dynlacht, Brian D.
; APPLICANT: Hoey, Timothy
; APPLICANT: Ruppert, Siegfried
; APPLICANT: Tanese, Naoko
; APPLICANT: Weinzierl, Robert O.J.
; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,582
; FILING DATE: 28-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-188-582-2

Query Match 1.1%; Score 9; DB 1; Length 921;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 TINTSNNSNT 257
| | | | |
Db 178 TINTSNNSNT 186

RESULT 13
US-08-646-715-2
; Sequence 2, Application US/08646715
; Patent No. 5637686
; GENERAL INFORMATION:
; APPLICANT: Tjian, Robert
; APPLICANT: Comai, Lucio
; APPLICANT: Dynlacht, Brian D.
; APPLICANT: Hoey, Timothy
; APPLICANT: Ruppert, Siegfried
; APPLICANT: Tanese, Naoko
; APPLICANT: Wang, Edith
; APPLICANT: Weinzierl, Robert O.J.
; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE

; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,715
; FILING DATE: 09-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/188,582
; FILING DATE: 28-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-715-2

Query Match 1.1%; Score 9; DB 1; Length 921;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 TINTSNNSNT 257
| | | | |
Db 178 TINTSNNSNT 186

RESULT 14
US-08-569-166-34
; Sequence 34, Application US/08569166
; Patent No. 5830722
; GENERAL INFORMATION:
; APPLICANT: NICOLAS, LUC
; APPLICANT: CHARLES, JEAN-FRANCOIS
; APPLICANT: DELECLUSE, ARMELE
; APPLICANT: BARLOY, FREDERIQUE
; TITLE OF INVENTION: CLOSTRIDIUM BIFERMENTANS DNA FRAGMENT
; TITLE OF INVENTION: BEARING GENES CODING FOR PROTEINS LINKED TO AN
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,166

FILING DATE: 05-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00768
FILING DATE: 24-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93/07795
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-3220
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-166-34

Query Match 1.0%; Score 8; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 250 NTSNNSNT 257
|||||
Db 67 NTSNNSNT 74

RESULT 15
US-09-107-532A-5477
Sequence 5477, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Atinelli, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5477:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...332
SEQUENCE DESCRIPTION: SEQ ID NO: 5477:
US-09-107-532A-5477

Query Match 1.0%; Score 8; DB 4; Length 332;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 EFINRQK 137
|||||
Db 137 EFINRQK 144

RESULT 16
US-09-134-001C-5116
Sequence 5116, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5116
LENGTH: 490
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5116

Query Match 1.0%; Score 8; DB 4; Length 490;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 NDGAVALA 157
|||||
Db 72 NDGAVALA 79

RESULT 17
US-08-999-774A-10
Sequence 10, Application US/08999774A
Patent No. 6274312
GENERAL INFORMATION:
APPLICANT: Gish, Kurt C.
APPLICANT: Seghezzi, Wolfgang
APPLICANT: Shanahan, Frances
APPLICANT: Lees, Emma M.
APPLICANT: McClanahan, Terrill K.
TITLE OF INVENTION: Intracellular Regulatory Molecules;
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/999,774A
FILING DATE: 10-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,818
FILING DATE: 11-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: CHING, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0646
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-999-774A-10

Query Match 1.0%; Score 8; DB 3; Length 503;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 PSPGPQA 364
|||||
DB 244 PSPGPQA 251

RESULT 18
US-08-221-583-57
Sequence 57, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdccmod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-57

Query Match 0.9%; Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 QPTPEPS 358
|||||
DB 8 QPTPEPS 14

RESULT 19
US-08-221-583-58
Sequence 58, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdccmod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-58

Query Match 0.9%; Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 QPTPEPS 358
|||||
DB 5 QPTPEPS 11

RESULT 20
US-08-221-583-59
Sequence 59, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25:mdctcd.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-06-221-583-59

Query Match 0.9%; Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 352 QTRPEPS 358
Db 2 QTRPEPS 8

RESULT 21
PCT-US95-04018-57
Sequence 57, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCR-0232
TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-57

Query Match 0.9%; Score 7; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 352 QTRPEPS 358
Db 8 QTRPEPS 14

RESULT 22
PCT-US95-04018-58
Sequence 58, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-58

Query Match 0.9%; Score 7; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 OPTPEPS 358
Db 5 OPTPEPS 11

RESULT 23
PCT-US95-04018-59
; Sequence 59, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCCR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-04018-59

Query Match 0.9%; Score 7; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 OPTPEPS 358
Db 2 OPTPEPS 8

RESULT 24
US-09-020-116-4
; Sequence 4, Application US/09020116
; Patent No. 6084063
; GENERAL INFORMATION:
; APPLICANT: Vonakis, Becky
; APPLICANT: Metzger, Henry

; APPLICANT: Chen, Huaxian
; TITLE OF INVENTION: SIGNAL TRANSDUCTION INHIBITORS
; TITLE OF INVENTION: OF ALLERGIC REACTIONS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: SUITE 1200, 127 PEACHTREE STREET
; CITY: ATLANTA
; STATE: GA
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,116
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLER, MARY L
; REGISTRATION NUMBER: 39,303
; REFERENCE/DOCKET NUMBER: 14014.0285
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-020-116-4

Query Match 0.9%; Score 7; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 557 GKDSLSLSD 563
Db 8 GKDSLSLSD 14

RESULT 25
US-09-608-902-4
; Sequence 4, Application US/09608902
; Patent No. 6353097
; GENERAL INFORMATION:
; APPLICANT: Vonakis, Becky
; APPLICANT: Metzger, Henry
; APPLICANT: Chen, Huaxian
; TITLE OF INVENTION: SIGNAL TRANSDUCTION INHIBITORS OF
; TITLE OF INVENTION: ALLERGIC REACTIONS
; FILE REFERENCE: 14014.0285U2
; CURRENT APPLICATION NUMBER: US/09/608,902
; CURRENT FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 09/020,116
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /No. 6353097e = synthetic con-

Query Match 0.9%; Score 7; DB 4; Length 27;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 557 GKDSLSD 563
 |||||
 Db 8 GKDSLSD 14

RESULT 26
 US-09-020-116-2
 ; Sequence 2, Application US/09020116
 ; Patent No. 6084063
 ; GENERAL INFORMATION:
 ; APPLICANT: Vonakis, Becky
 ; APPLICANT: Metzger, Henry
 ; APPLICANT: Chen, Huaxian
 ; TITLE OF INVENTION: SIGNAL TRANSDUCTION INHIBITORS
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
 ; STREET: SUITE 1200, 127 PEACHTREE STREET
 ; CITY: ATLANTA
 ; STATE: GA
 ; COUNTRY: USA
 ; ZIP: 30303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: US/09/020,116
 ; APPLICATION NUMBER: US/09/020,116
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MILLER, MARY L
 ; REGISTRATION NUMBER: 39,303
 ; REFERENCE/DOCKET NUMBER: 14014.0285
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404/688-0770
 ; TELEFAX: 404/688-9880
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 45 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-020-116-2

Query Match 0.9%; Score 7; DB 3; Length 45;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 557 GKDSLSD 563
 |||||
 Db 8 GKDSLSD 14

RESULT 27
 US-09-608-902-2
 ; Sequence 2, Application US/09608902
 ; Patent No. 6353097
 ; GENERAL INFORMATION:
 ; APPLICANT: Vonakis, Becky
 ; APPLICANT: Metzger, Henry
 ; APPLICANT: Chen, Huaxian
 ; TITLE OF INVENTION: SIGNAL TRANSDUCTION INHIBITORS OF

; TITLE OF INVENTION: ALLERGIC REACTIONS
 ; FILE REFERENCE: 14014.0285U2
 ; CURRENT APPLICATION NUMBER: US/09/608,902
 ; CURRENT FILING DATE: 2000-07-03
 ; PRIOR APPLICATION NUMBER: 09/020,116
 ; PRIOR FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 45
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: /No. 6353097e = synthetic cons
 ; US-09-608-902-2

Query Match 0.9%; Score 7; DB 4; Length 45;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 557 GKDSLSD 563
 |||||
 Db 8 GKDSLSD 14

RESULT 28
 US-09-171-646-1
 ; Sequence 1, Application US/09171646A
 ; Patent No. 6235516
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghisalba, Oreste
 ; APPLICANT: Kittelmann, Mathias
 ; APPLICANT: Laumen, Kurt
 ; APPLICANT: Walser-Volken, Paula
 ; TITLE OF INVENTION: Biocatalysts with Amine Acylase Activity
 ; FILE REFERENCE: 4-20825/A/PCT
 ; CURRENT APPLICATION NUMBER: US/09/171,646A
 ; CURRENT FILING DATE: 1998-11-12
 ; EARLIER APPLICATION NUMBER: 96810266.5
 ; EARLIER FILING DATE: 1996-04-25
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 50
 ; TYPE: PRT
 ; ORGANISM: Rhodococcus globerulus
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (41)..)
 ; OTHER INFORMATION: amino acid is uncertain
 ; US-09-171-646-1

Query Match 0.9%; Score 7; DB 3; Length 50;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 201 SASLAA 207
 |||||
 Db 9 SASLAA 15

RESULT 29
 US-09-020-116-1
 ; Sequence 1, Application US/09020116
 ; Patent No. 6084063
 ; GENERAL INFORMATION:
 ; APPLICANT: Vonakis, Becky
 ; APPLICANT: Metzger, Henry
 ; APPLICANT: Chen, Huaxian
 ; TITLE OF INVENTION: SIGNAL TRANSDUCTION INHIBITORS
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: SUITE 1200, 127 PEACHTREE STREET
CITY: ATLANTA
STATE: GA
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,116
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, MARY L
REGISTRATION NUMBER: 39,303
REFERENCE/DOCKET NUMBER: 14014.0285
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEFAX: 404/688-9880
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-020-116-1

Query Match 0.9%; Score 7; DB 3; Length 66;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 557 GDSLSLSD 563
DB 8 GDSLSLSD 14

RESULT 30
US-09-608-902-1
Sequence 1, Application US/09608902
Patent No. 6353097
GENERAL INFORMATION:
APPLICANT: Vonakis, Becky
APPLICANT: Metzger, Henry
APPLICANT: Chen, Huaxian
TITLE OF INVENTION: SIGNAL TRANSDUCTION INHIBITORS OF
FILE REFERENCE: 14014.0285U2
CURRENT APPLICATION NUMBER: US/09/608,902
CURRENT FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 09/020,116
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 66
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: /No. 6353097e = synthetic cons
US-09-608-902-1

Query Match 0.9%; Score 7; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 557 GDSLSLSD 563

DB 8 GDSLSLSD 14

RESULT 31
US-09-328-352-6019
Sequence 6019, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6019
LENGTH: 76
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-6019

Query Match 0.9%; Score 7; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AIISEEL 83
DB 59 AIISEEL 65

RESULT 32
US-09-134-001C-4585
Sequence 4585, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4585
LENGTH: 117
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4585

Query Match 0.9%; Score 7; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 RNSDFQA 466
DB 11 RNSDFQA 17

RESULT 33
US-09-252-991A-28698
Sequence 28698, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28698
LENGTH: 149
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28698

Query Match 0.9%; Score 7; DB 4; Length 149;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 203 SELAAE 209
Db 56 SELAAE 62

RESULT 34

US-08-917-456-2
Sequence 2, Application US/08917456
Patent No. 586368
GENERAL INFORMATION:
APPLICANT: Greenwood, Rebecca C.
APPLICANT: Gentry, Daniel R.
TITLE OF INVENTION: NOVEL GRE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/917,456
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10046
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-917-456-2

Query Match 0.9%; Score 7; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 176 IIEDTGD 182
Db 77 IIEDTGD 83

RESULT 35

US-09-229-804-2
Sequence 2, Application US/09229804
Patent No. 6210674
GENERAL INFORMATION:
APPLICANT: Greenwood, Rebecca C.
APPLICANT: Gentry, Daniel R.
TITLE OF INVENTION: NOVEL GRE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,804
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/917,456
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10046
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

Query Match 0.9%; Score 7; DB 3; Length 158;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 176 IIEDTGD 182
Db 77 IIEDTGD 83

RESULT 36

US-09-252-991A-20622
Sequence 20622, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20622
LENGTH: 163
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-20622

Query Match 0.9%; Score 7; DB 4; Length 163;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 SQASQSN 265
DB 27 SQASQSN 33

RESULT 37

US-09-252-991A-30217
; Sequence 30217, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30217
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30217

Query Match 0.9%; Score 7; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 487 DLLAFLA 493
DB 174 DLLAFLA 180

RESULT 38

US-09-613-303-35
; Sequence 35, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-35

Query Match 0.9%; Score 7; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 GKRIFL 611
DB 55 GKRIFL 61

RESULT 39

US-08-916-901-3
; Sequence 3, Application US/08916901
; Patent No. 5892012
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: RAB PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,901
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0367 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LIVRIT04
; CLONE: 2514506
US-08-916-901-3

Query Match 0.9%; Score 7; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 PNLKIDS 371
DB 184 PNLKIDS 190

RESULT 40

US-08-916-901-8
; Sequence 8, Application US/08916901
; Patent No. 5892012
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: RAB PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 57006
US-08-916-901-8

Query Match 0.9%; Score 7; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 365 PNLKIDS 371
Db 184 PNLKIDS 190

RESULT 41
US-09-154-602-3
Sequence 3, Application US/09154602
Patent No. 6300472
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,602
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,901
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: L1VTRUT04
CLONE: 2514506
US-09-154-602-3

Query Match 0.9%; Score 7; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 365 PNLKIDS 371
Db 184 PNLKIDS 190

RESULT 42
US-09-154-602-8
Sequence 8, Application US/09154602
Patent No. 6300472
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,602
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,901
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 57006
US-09-154-602-8

Query Match 0.9%; Score 7; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 PNLKIDS 371
| | | | |
Db 184 PNLKIDS 190

RESULT 43
US-08-908-332-5
; Sequence 5, Application US/08908332
; Patent No. 6013515
; GENERAL INFORMATION:
; APPLICANT: Xiao, Hua
; APPLICANT: Greenblatt, Jacka F.
; APPLICANT: Roeder, Robert G.
; TITLE OF INVENTION: COFACTORS FOR HIV-1 PROTEIN TAT AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,332
; FILING DATE: 07-Aug-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 226 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: E. coli
; US-08-908-332-5

Query Match 0.9%; Score 7; DB 3; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 YNRVKE 606
| | | | |
Db 137 YNRVKE 143

RESULT 44
US-09-326-394-4
; Sequence 4, Application US/09326394
; Patent No. 6306820
; GENERAL INFORMATION:
; APPLICANT: Bendele, Alison M.
; APPLICANT: Semello, Regina M.
; APPLICANT: Edwards, Carl K.
; TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
; TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: US
ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/326,394
; FILING DATE: 08-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,587
; FILING DATE: 06-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,355
; FILING DATE: 23-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,315
; FILING DATE: 07-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/052,023
; FILING DATE: 09-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zindrick, Thomas K.
; REGISTRATION NUMBER: 32,185
; REFERENCE/DOCKET NUMBER: A-430D
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-326-394-4

Query Match 0.9%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 QPTPEPS 358
| | | | |
Db 206 QPTPEPS 212

RESULT 45
US-09-580-235-2
; Sequence 2, Application US/09580235
; Patent No. 6433158
; GENERAL INFORMATION:
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Site Specific Protein Modification
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C Henry
; STREET: 51 University
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,235
; FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/102,530
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-580-235-2

Query Match 0.9%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 QTPPEPS 358
|||||
Db 206 QTPPEPS 212

RESULT 46
US-09-580-235-4
Sequence 4, Application US/09580235
Patent No. 6433158
GENERAL INFORMATION:
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Site Specific Protein Modification
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C Henry
STREET: 51 University
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,235
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/102,530
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-580-235-4

Query Match 0.9%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 QTPPEPS 358

Db 206 QTPPEPS 212
|||||

RESULT 47
US-09-580-235-6
Sequence 6, Application US/09580235
Patent No. 6433158
GENERAL INFORMATION:
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Site Specific Protein Modification
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C Henry
STREET: 51 University
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,235
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/102,530
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-580-235-6

Query Match 0.9%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 QTPPEPS 358
|||||
Db 206 QTPPEPS 212

RESULT 48
US-09-580-235-8
Sequence 8, Application US/09580235
Patent No. 6433158
GENERAL INFORMATION:
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Site Specific Protein Modification
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C Henry
STREET: 51 University
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,235
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/102,530
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-580-235-8

Query Match 0.9%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 QTPPEPS 358
Db 206 QTPPEPS 212

RESULT 49
US-09-580-181-2
Sequence 2, Application US/09580181
Patent No. 6441136
GENERAL INFORMATION:
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Site Specific Protein Modification
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C Henry
STREET: 51 University
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,181
FILING DATE: 26-MAY-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/102,530
FILING DATE: 22-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-580-181-2

Query Match 0.9%; Score 7; DB 4; Length 235;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 QTPPEPS 358
Db 206 QTPPEPS 212

RESULT 50
US-09-580-181-4
Sequence 4, Application US/09580181
Patent No. 6441136
GENERAL INFORMATION:
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Site Specific Protein Modification
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C Henry
STREET: 51 University
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,181
FILING DATE: 26-MAY-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/102,530
FILING DATE: 22-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-580-181-4

Query Match 0.9%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 QTPPEPS 358
Db 206 QTPPEPS 212

RESULT 51
US-09-580-181-6
Sequence 6, Application US/09580181
Patent No. 6441136
GENERAL INFORMATION:
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Site Specific Protein Modification
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C Henry
STREET: 51 University
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,181
FILING DATE: 26-MAY-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/102,530
FILING DATE: 22-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-580-181-6

Query Match 0.9%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 352 QTPPEPS 358
|||
Db 206 QTPPEPS 212

RESULT 52
US-09-580-181-8
Sequence 8, Application US/09580181
Patent No. 6441136
GENERAL INFORMATION:
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Site Specific Protein Modification
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C Henry
STREET: 51 University
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,181
FILING DATE: 26-MAY-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/102,530
FILING DATE: 22-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-580-181-8

Query Match 0.9%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 352 QTPPEPS 358
|||
Db 206 QTPPEPS 212

RESULT 53
US-09-102-530-2
Sequence 2, Application US/09102530
Patent No. 6451986
GENERAL INFORMATION:
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Site Specific Protein Modification
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C Henry
STREET: 51 University
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,530
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-102-530-2

Query Match 0.9%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 352 QTPPEPS 358
|||
Db 206 QTPPEPS 212

RESULT 54
US-09-102-530-4
Sequence 4, Application US/09102530
Patent No. 6451986
GENERAL INFORMATION:
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Site Specific Protein Modification
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C Henry
STREET: 51 University
CITY: Seattle
STATE: WA
COUNTRY: US

ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,530
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-102-530-4

Query Match: 0.9%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 OPTPEPS 358
DB 206 OPTPEPS 212

RESULT 55
US-09-102-530-6
Sequence 6, Application US/09102530
Patent No. 6451986
GENERAL INFORMATION:
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Site Specific Protein Modification
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C Henry
STREET: 51 University
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,530
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-102-530-6

Query Match: 0.9%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 OPTPEPS 358
DB 206 OPTPEPS 212

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 OPTPEPS 358
DB 206 OPTPEPS 212

RESULT 56
US-09-102-530-8
Sequence 8, Application US/09102530
Patent No. 6451986
GENERAL INFORMATION:
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Site Specific Protein Modification
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C Henry
STREET: 51 University
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,530
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-102-530-8

Query Match: 0.9%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 OPTPEPS 358
DB 206 OPTPEPS 212

RESULT 57
US-09-620-405B-487
Sequence 487, Application US/09620405B
Patent No. 6528054
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jianshun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/620,405B
FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 495
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 487

LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-620-405B-487

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 235;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 RTKERIN 133
Db 47 RTKERIN 53

RESULT 58
US-09-604-287A-487
Sequence 487, Application US/09604287A
Patent No. 6586572
GENERAL INFORMATION:

APPLICANT: Jiang, Yugu
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jianshun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C7
CURRENT APPLICATION NUMBER: US/09/604,287A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 487
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-604-287A-487

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 235;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 RTKERIN 133
Db 47 RTKERIN 53

RESULT 59
US-09-107-532A-6634
Sequence 6634, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6634:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium

FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1..240
SEQUENCE DESCRIPTION: SEQ ID NO: 6634:
US-09-107-532A-6634

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 240;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 SNNSTN 258
Db 214 SNNSTN 220

RESULT 60
US-09-252-991A-29404
Sequence 29404, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29404
LENGTH: 245
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29404

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 245;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 NDGAVAL 156
Db 206 NDGAVAL 212

RESULT 61
US-09-579-845-10
Sequence 10, Application US/09579845
Patent No. 6537540
GENERAL INFORMATION:
APPLICANT: Burstein, Haim
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING

;; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
;; FILE REFERENCE: 226272004420
;; CURRENT APPLICATION NUMBER: US/09/579,845
;; CURRENT FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/150,688
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 10
;; LENGTH: 257
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-09-579-845-10

Query Match 0.9%; Score 7; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 QPTPEPS 358
DB 228 QPTPEPS 234

RESULT 62
US-08-622-353-2
; Sequence 2, Application US/08622353
; Patent No. 5700925
; GENERAL INFORMATION:
; APPLICANT: Bishai, William R.
; APPLICANT: Young, Douglas B.
; APPLICANT: Zhang, Ying
; APPLICANT: Demaio, James
; TITLE OF INVENTION: A STATIONARY PHASE, STRESS RESPONSE
; TITLE OF INVENTION: SIGMA FACTOR FROM MYCOBACTERIUM TUBERCULOSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Banner & Allegretti, LTD
; STREET: 1001 G Street, eleventh floor
; CITY: NW
; STATE: Washington DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/622,353
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoshcalt, Dale
; REGISTRATION NUMBER: 19090
; REFERENCE/DOCKET NUMBER: 3181.51220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
US-08-622-353-2

Query Match 0.9%; Score 7; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 SASLELAA 207
DB 143 SASLELAA 149

RESULT 63
US-08-622-352A-2
; Sequence 2, Application US/08622352A
; Patent No. 5824546
; GENERAL INFORMATION:
; APPLICANT: Bishai, William R.
; APPLICANT: Demaio, James
; TITLE OF INVENTION: REGULATION OF A SIGMA FACTOR
; TITLE OF INVENTION: FROM MYCOBACTERIUM TUBERCULOSIS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/622,352A
; FILING DATE: 27-MAR-1996
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
US-08-622-352A-2

Query Match 0.9%; Score 7; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 SASLELAA 207
DB 143 SASLELAA 149

RESULT 64
US-08-826-390-2
; Sequence 2, Application US/08826390
; Patent No. 6004764
; GENERAL INFORMATION:
; APPLICANT: Bishai, William R.
; APPLICANT: Young, Douglas B.
; APPLICANT: Zhang, Ying
; APPLICANT: Demaio, James
; TITLE OF INVENTION: Stationary Phase, Stress Response
; TITLE OF INVENTION: Sigma Factor From Mycobacterium tuberculosis, and
; TITLE OF INVENTION: Regulation Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826.390
; FILING DATE: 27-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/622,353
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/622,352
; FILING DATE: 27-MAR-1996
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
;
US-08-826-390-2
;
Query Match      0.9%; Score 7; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      201 SASIELAA 207
      |||||
Db      143 SASIELAA 149

RESULT 65
US-05-252-991A-21944
; Sequence 21944, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21944
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
;
US-09-252-991A-21944
;
Query Match      0.9%; Score 7; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      600 YNRVKGGE 606
      |||||
Db      210 YNRVKGGE 216

RESULT 66
US-09-252-991A-17702
; Sequence 17702, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17702
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
;
US-09-252-991A-17702
;
Query Match      0.9%; Score 7; DB 4; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      152 GAVALAR 158
      |||||
Db      276 GAVALAR 282

RESULT 67
US-09-252-991A-31029
; Sequence 31029, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31029
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
;
US-09-252-991A-31029
;
Query Match      0.9%; Score 7; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      151 DGAVALLA 157
      |||||
Db      283 DGAVALLA 289

RESULT 68
US-09-252-991A-29807
; Sequence 29807, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29807
; LENGTH: 325
; TYPE: PRT
```

```

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17702
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
;
US-09-252-991A-17702
;
Query Match      0.9%; Score 7; DB 4; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      152 GAVALAR 158
      |||||
Db      276 GAVALAR 282

RESULT 67
US-09-252-991A-31029
; Sequence 31029, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31029
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
;
US-09-252-991A-31029
;
Query Match      0.9%; Score 7; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      151 DGAVALLA 157
      |||||
Db      283 DGAVALLA 289

RESULT 68
US-09-252-991A-29807
; Sequence 29807, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29807
; LENGTH: 325
; TYPE: PRT
```


ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29807

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 325;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 SPGPOPA 364
DB 179 SPGPOPA 185

RESULT 69
US-09-198-452A-745
Sequence 745, Application US/09198452A
Patent No. 6559294

GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 745

LENGTH: 381

TYPE: PRT

ORGANISM: Chlamydia pneumoniae

FEATURE:
NAME/KEY: SITE

LOCATION: 1...381

OTHER INFORMATION: Xaa=unknown or other

QY 741 VTDSLSK 747
DB 353 VTDSLSK 359

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 381;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 70
US-09-459-749D-17

Sequence 17, Application US/09459749D
Patent No. 6464975

GENERAL INFORMATION:
APPLICANT: Millis, Albert J. T.

TITLE OF INVENTION: Compositions and Methods for Altering Cell Migration
FILE REFERENCE: 0794.016A

CURRENT APPLICATION NUMBER: US/09/459,749D
CURRENT FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: 60/111,856
PRIOR FILING DATE: 1998-12-11

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 17

LENGTH: 383

TYPE: PRT

ORGANISM: Sus scrofa

US-09-459-749D-17

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 383;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 573 TREKGL 579
DB 288 TREKGL 294

RESULT 71
US-08-861-774E-82

Sequence 82, Application US/08861774E
Patent No. 6297007

GENERAL INFORMATION:
APPLICANT: Waters, Barbara

APPLICANT: Miao, Yvian

APPLICANT: Ho, Yap

APPLICANT: Tong, Seow

TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
BIOACTIVE MOLECULES

FILE REFERENCE: 9993-006

CURRENT APPLICATION NUMBER: US/08/861,774E
CURRENT FILING DATE: 1997-05-22

NUMBER OF SEQ ID NOS: 94

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 82

LENGTH: 390

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Clone ps10

US-08-861-774E-82

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 390;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 GVAVPHG 309
DB 11 GVAVPHG 17

RESULT 72
US-08-311-731A-12

Sequence 12, Application US/08311731A
Patent No. 6583266

GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS

APPLICANT: MAO, JEN-I

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411

CORRESPONDENCE ADDRESS:
ADDRESSER: WOLF, GREENFIELD & SACKS, P.C.

STREET: 600 ATLANTIC AVENUE

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A

FILING DATE:
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.

REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500

TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM TUBERCULOSIS
US-08-311-731A-12

Query Match 0.9%; Score 7; DB 4; Length 406;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 AVALARS 159
DB 84 AVALARS 90

RESULT 73
US-09-252-991A-22113
Sequence 22113, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22113
LENGTH: 447
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22113

Query Match 0.9%; Score 7; DB 4; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 PGQPAP 365
DB 214 PGQPAP 220

RESULT 74
US-08-385-229-2
Sequence 2, Application US/08385229
Patent No. 5605690
GENERAL INFORMATION:
APPLICANT: Jacobs, Cindy A.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Method of Treating TNF-Dependent
TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,229
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946,236

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0606
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-385-229-2

Query Match 0.9%; Score 7; DB 1; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 QPTEPS 358
DB 228 QPTEPS 234

RESULT 75
US-08-650-000-2
Sequence 2, Application US/08650000
Patent No. 5945397
GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,000
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,453
FILING DATE:
APPLICATION NUMBER: US/08/038,765
FILING DATE:
APPLICATION NUMBER: US 403,241
FILING DATE: 05-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 405,370
FILING DATE: 11-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 421,417
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,635
FILING DATE: 10-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2501-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-650-000-2

Query Match 0.9%; Score 7; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 352 QTPERS 358
Db 228 QTPERS 234

RESULT 76
US-09-042-785A-7
; Sequence 7, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
US-09-042-785A-7

Query Match 0.9%; Score 7; DB 3; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 352 QTPERS 358
Db 228 QTPERS 234

RESULT 77
US-08-477-347-3
; Sequence 3, Application US/08477347

; Patent No. 6232446
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,347
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/115,685
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 106271
; FILING DATE: 08-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH=10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-347-3

Query Match 0.9%; Score 7; DB 3; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 352 QTPERS 358
Db 228 QTPERS 234

RESULT 78
US-09-006-353A-4
; Sequence 4, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: MEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: ROSEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF341
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-006-353A-4

Query Match 0.9%; Score 7; DB 3; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 QTPPEPS 358
|||||
DB 228 QTPPEPS 234

RESULT 79
US-08-476-862-2
Sequence 2, Application US/08476862
Patent No. 6262239
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
APPLICANT: ENGELMANN, Hartmut
TITLE OF INVENTION: TNF INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,862
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339

FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=12A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-862-2

Query Match 0.9%; Score 7; DB 3; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 QTPPEPS 358
|||||
DB 228 QTPPEPS 234

RESULT 80
US-09-573-986-4
Sequence 4, Application US/09573986
Patent No. 6455040
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488,1280004
CURRENT APPLICATION NUMBER: US/09/573,986
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-09-573-986-4

Query Match 0.9%; Score 7; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 QTPPEPS 358
|||||
DB 228 QTPPEPS 234

RESULT 81
US-08-406-824A-2
Sequence 2, Application US/08406824A
Patent No. 6541610
GENERAL INFORMATION:
APPLICANT: SMITH, Craig A.
TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
FILE REFERENCE: A-71592
CURRENT APPLICATION NUMBER: US/08/406,824A
CURRENT FILING DATE: 1995-03-20
PRIOR APPLICATION NUMBER: US 08/255,849
PRIOR FILING DATE: 1994-06-08
PRIOR APPLICATION NUMBER: US 07/860,710
PRIOR FILING DATE: 1992-03-30
PRIOR APPLICATION NUMBER: US 07/523,635
PRIOR FILING DATE: 1990-05-10
PRIOR APPLICATION NUMBER: US 07/421,417
PRIOR FILING DATE: 1989-10-13

;; PRIOR APPLICATION NUMBER: US 07/405,370
;; PRIOR FILING DATE: 1989-09-11
;; PRIOR APPLICATION NUMBER: US 07/403,241
;; PRIOR FILING DATE: 1989-09-05
;; NUMBER OF SEQ ID NOS: 29
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2
;; LENGTH: 461
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-08-406-824A-2

Query Match 0.9%; Score 7; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 OPTPEPS 358
DB 228 OPTPEPS 234

RESULT 82
US-09-800-909-2
; Sequence 2, Application US/09800909
; Patent No. 655511
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; APPLICANT: ENGELMANN, Hartmut
; TITLE OF INVENTION: TNF INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NETMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/800,909
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,862
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 94039
; FILING DATE: 06-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 91229
; FILING DATE: 06-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 90339
; FILING DATE: 18-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=12A
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

;; MOLECULE TYPE: protein
US-09-800-909-2

Query Match 0.9%; Score 7; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 OPTPEPS 358
DB 228 OPTPEPS 234

RESULT 83
US-09-758-124-2
; Sequence 2, Application US/09758124
; Patent No. 6572852
; GENERAL INFORMATION:
; APPLICANT: SMITH, Craig A.
; APPLICANT: GOODWIN, Raymond G.
; APPLICANT: BECKMANN, M. Patricia
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND -BETA RECEPTORS
; FILE REFERENCE: A7895
; CURRENT APPLICATION NUMBER: US/09/758,124
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 08/953,268
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 08/555,629
; PRIOR FILING DATE: 1995-11-09
; PRIOR APPLICATION NUMBER: 08/468,453
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/038,765
; PRIOR FILING DATE: 1993-03-13
; PRIOR APPLICATION NUMBER: 07/523,635
; PRIOR FILING DATE: 1990-05-10
; PRIOR APPLICATION NUMBER: 07/421,417
; PRIOR FILING DATE: 1989-10-13
; PRIOR APPLICATION NUMBER: 07/405,370
; PRIOR FILING DATE: 1989-09-11
; PRIOR APPLICATION NUMBER: 07/403,241
; PRIOR FILING DATE: 1989-09-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-124-2

Query Match 0.9%; Score 7; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 OPTPEPS 358
DB 228 OPTPEPS 234

RESULT 84
US95760-2
; Patent No. 5395760
; APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN, M. PATRICIA
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND -B-RECEPTORS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/523,635
; FILING DATE: 10-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 421,417
; FILING DATE: 13-OCT-1989
; APPLICATION NUMBER: 405,370
; FILING DATE: 11-SEP-1989

APPLICATION NUMBER: 403,241
FILING DATE: 05-SEP-1989
SEQ ID NO: 2
LENGTH: 461
5395760-2

Query Match 0.9%; Score 7; DB 6; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 QPTPEPS 358
|||||
Db 228 QPTPEPS 234

RESULT 65
US-09-328-352-4742
Sequence 4742, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4742
LENGTH: 462
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4742

Query Match 0.9%; Score 7; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 415 LSKOESV 421
|||||
Db 42 LSKOESV 48

RESULT 86
US-09-252-991A-17797
Sequence 17797, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17797
LENGTH: 485
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17797

Query Match 0.9%; Score 7; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 357 PSPGPOP 363
|||||
Db 2 PSPGPOP 8

RESULT 87
US-08-243-010-1
Sequence 1, Application US/08243010
Patent No. 5639597

GENERAL INFORMATION:
APPLICANT: Lautifer, Leander
APPLICANT: Zettlmeissel, Gerd
APPLICANT: Oquendo, Patricia
TITLE OF INVENTION: Cell-free Receptor Binding Assays, The
TITLE OF INVENTION: Production and Use Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,010
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/798,564
FILING DATE: 26-NOV-1991
APPLICATION NUMBER: DE P 40 37 837.3
FILING DATE: 28-NOV-1990

ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481-1132-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 486 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-243-010-1

Query Match 0.9%; Score 7; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 QPTPEPS 358
|||||
Db 228 QPTPEPS 234

RESULT 88
US-09-252-991A-27183
Sequence 27183, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27183
LENGTH: 498
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27183

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 498;
Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 DEDIVNE 100
DB 406 DEDIVNE 412

RESULT 89
US-09-620-405B-478
Sequence 478, Application US/09620405B

Patent No. 6528054
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiaqichun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C8
CURRENT APPLICATION NUMBER: US/09/620,405B
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 495
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 478
LENGTH: 505
TYPE: PRT
ORGANISM: Homo sapien
US-09-620-405B-478

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 505;
Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 RTKEIN 133
DB 317 RTKEIN 323

RESULT 90
US-09-620-405B-485
Sequence 485, Application US/09620405B
Patent No. 6528054
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiaqichun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C8
CURRENT APPLICATION NUMBER: US/09/620,405B
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 495
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 485
LENGTH: 505
TYPE: PRT
ORGANISM: Homo sapiens
US-09-620-405B-485

Query Match 0.9%; Score 7; DB 4; Length 505;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 RTKEIN 133
DB 317 RTKEIN 323

RESULT 91
US-09-604-287A-478
Sequence 478, Application US/09604287A
Patent No. 6586572
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiaqichun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C7
CURRENT APPLICATION NUMBER: US/09/604,287A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 478
LENGTH: 505
TYPE: PRT
ORGANISM: Homo sapien
US-09-604-287A-478

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 505;
Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 RTKEIN 133
DB 317 RTKEIN 323

RESULT 92
US-09-604-287A-485
Sequence 485, Application US/09604287A
Patent No. 6586572
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiaqichun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C7
CURRENT APPLICATION NUMBER: US/09/604,287A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 485
LENGTH: 505
TYPE: PRT
ORGANISM: Homo sapiens
US-09-604-287A-485

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 505;
Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 RTKEIN 133
DB 317 RTKEIN 323

```
RESULT 93
US-09-252-991A-19121
; Sequence 19121, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19121
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19121

Query Match      0.9%; Score 7; DB 4; Length 506;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      205 LAAAEAF 211
Db      104 LAAAEAF 110

RESULT 94
US-09-991-677-4
; Sequence 4, Application US/08991677A
; Patent No. 6252135
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent L.
; APPLICANT: Carraway, Daniel T.
; APPLICANT: Smeltzer, Richard H.
; TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
; FILE REFERENCE: 50617
; CURRENT APPLICATION NUMBER: US/08/991,677A
; CURRENT FILING DATE: 1997-12-16
; EARLIER APPLICATION NUMBER: US 60/033,381
; EARLIER FILING DATE: 1996-12-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Liquidambar styraciflua
US-08-991-677-4

Query Match      0.9%; Score 7; DB 3; Length 511;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      485 VDDLLAF 491
Db      270 VDDLLAF 276

RESULT 95
US-08-426-509A-16
; Sequence 16, Application US/08426509A
; Patent No. 6326469
; GENERAL INFORMATION:
; APPLICANT: Ulirich, Axel
; APPLICANT: Gishizsky, Mikhail
; APPLICANT: Sures, Irman G.
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
; TITLE OF INVENTION: TYROSINE KINASES
```

```
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York,
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,509A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/232,545
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-0074-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: No. 6326469e
US-08-426-509A-16

Query Match      0.9%; Score 7; DB 4; Length 512;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      557 GKDSLSD 563
Db      8 GKDSLSD 14

RESULT 96
US-08-232-545-16
; Sequence 16, Application US/08232545
; Patent No. 6506578
; GENERAL INFORMATION:
; APPLICANT: Ulirich, Axel
; APPLICANT: Gishizsky, Mikhail
; APPLICANT: Sures, Irman G.
; TITLE OF INVENTION: No. 6506578e1 Megakaryocytic Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,545
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
```


ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-232-545-16

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 512;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 557 GKDSLSD 563
Db 8 GKDSLSD 14

RESULT 97
PCT-US95-05008-16
Sequence 16, Application PC/TUS9505008
GENERAL INFORMATION:
APPLICANT: Sugen, Inc.
APPLICANT: 515 Galveston Drive
APPLICANT: Redwood City, California 94063-4720
APPLICANT: United States of America
APPLICANT: Wissenschaften E.V.
APPLICANT: Hofgarten Str. 2
APPLICANT: Munchen 80539
APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
FILING DATE: 24-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid

STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-05008-16

Query Match
Best Local Similarity 100.0%; Score 7; DB 5; Length 512;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 557 GKDSLSD 563
Db 8 GKDSLSD 14

RESULT 98
US-09-564-808-6
Sequence 6, Application US/09564808
Patent No. 6501004
GENERAL INFORMATION:
APPLICANT: Selvaraj, Gopalan
APPLICANT: Nair, Ramesh B
APPLICANT: Joy IV, Richard W
APPLICANT: Keller, Wilfred A
APPLICANT: Dattla, Raju S
TITLE OF INVENTION: Transgenic Reduction of Sinapine in Crucifera
FILE REFERENCE: 44618 Sequence Listing
Patent No. 6501004
CURRENT APPLICATION NUMBER: US/09/564,808
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,800
PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: 2,270,417
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 6
LENGTH: 513
TYPE: PRT
ORGANISM: Brassica napus
US-09-564-808-6

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 513;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 VDDLIAF 491
Db 271 VDDLIAF 277

RESULT 99
US-08-385-229-4
Sequence 4, Application US/08385229
Patent No. 5605690
GENERAL INFORMATION:
APPLICANT: Jacobs, Cindy A.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Method of Treating TNF-Dependent
TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/385,229
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946,236
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0606
TELEFAX: (206) 587-0430
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 518 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-385-229-4

Query Match 0.9%; Score 7; DB 1; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 OPTPEPS 358
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Db 257 OPTPEPS 263

RESULT 100
US-05-579-845-1
Sequence 1, Application US/09579845
Patent No. 6537540
GENERAL INFORMATION:
APPLICANT: Birstein, Haim
APPLICANT: Stepan, Anthony M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 226272004420
CURRENT APPLICATION NUMBER: US/09/579,845
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/150,688
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 20
SOFTWARE: fastseq for windows Version 4.0
SEQ ID NO: 1
LENGTH: 518
TYPE: PRT
ORGANISM: Homo sapien
US-09-579-845-1

Query Match 0.9%; Score 7; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 257 OPTPEPS 263

Search completed: November 14, 2003, 11:04:05
Job time : 122 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 11:02:11 ; Search time 69 Seconds
(without alignments)
2106.049 Million cell updates/sec

Title: US-09-765-271-56

Perfect score: 796
Sequence: 1 SYELGLYQARTVKNRVS.....KLIALIKSNPSVSKKIN 796

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Gapop 60.0 , Gapext 60.0

Searched: 666188 seqs, 182559486 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 200 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	60	7.5	838	11	US-09-884-465A-8
5	51	6.4	763	9	US-09-765-272-66
6	32	4.0	42	11	US-09-884-465A-12
7	32	4.0	447	9	US-09-765-272-182
8	32	4.0	484	11	US-09-769-787-38
9	32	4.0	484	12	US-09-744A-24
10	32	4.0	840	11	US-09-884-465A-10
11	32	4.0	1039	11	US-09-884-465A-6
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13	27	3.4	1378	11	US-09-884-465A-378
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18	24	3.0	1365	11	US-09-884-465A-382	Sequence 382, App
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20	17	2.1	381	12	US-09-769-736-24	Sequence 24, Appl
21	17	2.1	793	11	US-09-252-088-15	Sequence 15, Appl
22	17	2.1	822	12	US-09-769-726-18	Sequence 18, Appl
23	12	1.5	715	11	US-09-252-088-16	Sequence 16, Appl
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79	7	0.9	235	15	US-10-242-230-2	Sequence 2, Appl
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85	7	0.9	257	15	US-10-313-852-10	Sequence 10, Appl
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97	7	0.9	272	11	US-09-884-465A-301	Sequence 301, App
98	7	0.9	285	12	US-10-017-161-910	Sequence 910, App
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102	7	0.9	311	12	US-10-219-810-49	Sequence 49, App
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104	7	0.9	311	12	US-10-044-643-18	Sequence 18, App
105	7	0.9	311	12	US-10-044-643-20	Sequence 20, App
106	7	0.9	311	15	US-10-220-382-10	Sequence 10, App
107	7	0.9	336	10	US-09-738-626-4819	Sequence 4819, App
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109	7	0.9	356	15	US-10-220-382-9	Sequence 9, App
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115	7	0.9	390	10	US-09-924-256A-82	Sequence 82, App
116	7	0.9	410	12	US-10-238-075-1228	Sequence 1228, App
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125	7	0.9	461	9	US-09-800-909-2	Sequence 2, App
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174	7	0.9	670	15	US-10-156-761-14107	Sequence 14107, A
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176	7	0.9	679	10	US-09-738-626-5995	Sequence 5995, App
177	7	0.9	694	11	US-09-842-758-75	Sequence 75, App
178	7	0.9	694	12	US-10-345-680-26	Sequence 26, App
179	7	0.9	720	12	US-10-363-427-8	Sequence 8, App
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181	7	0.9	754	15	US-10-128-714-3448	Sequence 3448, App
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188	7	0.9	821	10	US-09-882-529-3	Sequence 3, App
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191	7	0.9	870	9	US-09-815-242-4993	Sequence 5993, App
192	7	0.9	870	9	US-09-815-242-12637	Sequence 12637, A
193	7	0.9	879	9	US-09-872-733-16	Sequence 16, App
194	7	0.9	879	15	US-10-263-020-16	Sequence 16, App
195	7	0.9	886	8	US-08-781-986A-5235	Sequence 535, App
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199	7	0.9	894	11	US-09-884-465A-340	Sequence 340, App
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RESULT 1
US-09-765-272-56
Sequence 56, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765, 272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders

RESULT 4
US-09-884-465A-8
Sequence 8, Application US/09884465A
Publication No. US2003007293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 838
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-884-465A-8

Query Match
Best Local Similarity 100.0%; Score 60; DB 11; Length 838;
Best Local Similarity 100.0%; Pred. No. 3.6e-50;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 31 ENLTDEVSKEGNAEQIVKITDQGYVTSQDHYHYNGKVPYDAIISBELMKDPNY 90
Db 52 ENLTDEVSKEGNAEQIVKITDQGYVTSQDHYHYNGKVPYDAIISBELMKDPNY 111

RESULT 5
US-09-765-272-66
Sequence 66, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 763 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-765-272-66

Query Match
Best Local Similarity 100.0%; Score 51; DB 9; Length 763;
Best Local Similarity 100.0%; Pred. No. 2.7e-41;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 160 QGRYTTDDGYIFNNSDIIEDTGDAYIVPHGDIHYHYIPKNEISASELAAEA 210
Db 159 QGRYTTDDGYIFNNSDIIEDTGDAYIVPHGDIHYHYIPKNEISASELAAEA 209

RESULT 6
US-09-884-465A-12
Sequence 12, Application US/09884465A
Publication No. US2003007293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 42
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Unknown Organism
US-09-884-465A-12

Query Match
Best Local Similarity 100.0%; Score 32; DB 11; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 46 AEQIVIKITDQGYVTSQDHYHYNGKVPYDA 77
Db 4 AEQIVIKITDQGYVTSQDHYHYNGKVPYDA 35

RESULT 7
US-09-765-272-182
Sequence 182, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272

```

; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 182:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 182:
US-09-765-272-182
```

```

Query Match          4.0%; Score 32; DB 9; Length 447;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      46 AEOIVIKITDGGYVTSHGHDHYHYNGKVPYDA 77
         |||||||
DB      43 AEOIVIKITDGGYVTSHGHDHYHYNGKVPYDA 74
```

```

RESULT 8
US-09-769-787-38
; Sequence 38, Application US/09769787
; Publication No. US20030091577A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PMC/P21129WO
; CURRENT APPLICATION NUMBER: US/09/769,787
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-787-38
```

```

Query Match          4.0%; Score 32; DB 11; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      46 AEOIVIKITDGGYVTSHGHDHYHYNGKVPYDA 77
         |||||||
DB      67 AEOIVIKITDGGYVTSHGHDHYHYNGKVPYDA 98
```

```

RESULT 9
US-09-769-744A-24
; Sequence 24, Application US/09769744A
; Publication No. US20030134407A1
; GENERAL INFORMATION:
; APPLICANT: Ie Page, Richard WF
; APPLICANT: Wells, Jeremy M
; APPLICANT: Hamblift, Sean B
; APPLICANT: Hansbro, Philip M
```

```

; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PMC/P21122WO
; CURRENT APPLICATION NUMBER: US/09/769,744A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/GB99/02452
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: GB 9816336.3
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/125329
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-744A-24
```

```

Query Match          4.0%; Score 32; DB 12; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      46 AEOIVIKITDGGYVTSHGHDHYHYNGKVPYDA 77
         |||||||
DB      67 AEOIVIKITDGGYVTSHGHDHYHYNGKVPYDA 98
```

```

RESULT 10
US-09-884-465A-10
; Sequence 10, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Joseph
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 840
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-884-465A-10
```

```

Query Match          4.0%; Score 32; DB 11; Length 840;
Best Local Similarity 100.0%; Pred. No. 1.8e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      46 AEOIVIKITDGGYVTSHGHDHYHYNGKVPYDA 77
         |||||||
DB      47 AEOIVIKITDGGYVTSHGHDHYHYNGKVPYDA 78
```

```

RESULT 11
US-09-884-465A-6
; Sequence 6, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Joseph
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
```

```

; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1039
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-884-465A-6

```

```

Query Match      4.0%; Score 32; DB 11; Length 1039;
Best Local Similarity 100.0%; Pred. No. 2,2e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      46 AEOIVIKITDQGYVTSKGDHYHYNGKVPYDA 77
      |||||
Db      67 AEOIVIKITDQGYVTSKGDHYHYNGKVPYDA 98

```

```

RESULT 12
; US-09-884-465A-380
; Sequence 380, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 380
; LENGTH: 1139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (570)..(570)
; OTHER INFORMATION: Xaa = Glycine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (571)..(571)
; OTHER INFORMATION: Xaa = Proline or nothing
; US-09-884-465A-380

```

```

Query Match      3.4%; Score 27; DB 11; Length 1139;
Best Local Similarity 100.0%; Pred. No. 2,1e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      326 RIARIIPLRYSNMHWVPSRPEQSPQ 352
      |||||
Db      63 RIARIIPLRYSNMHWVPSRPEQSPQ 89

```

```

RESULT 13
; US-09-884-465A-378
; Sequence 378, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.

```

```

; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 378
; LENGTH: 1378
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (570)..(570)
; OTHER INFORMATION: Xaa = Glycine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (571)..(571)
; OTHER INFORMATION: Xaa = Proline or nothing
; US-09-884-465A-378

```

```

Query Match      3.4%; Score 27; DB 11; Length 1378;
Best Local Similarity 100.0%; Pred. No. 2,6e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      326 RIARIIPLRYSNMHWVPSRPEQSPQ 352
      |||||
Db      63 RIARIIPLRYSNMHWVPSRPEQSPQ 89

```

```

RESULT 14
; US-09-884-465A-376
; Sequence 376, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 376
; LENGTH: 999
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (430)..(430)
; OTHER INFORMATION: Xaa = Glycine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (431)..(431)
; OTHER INFORMATION: Xaa = Proline or nothing

```


US-09-884-465A-376

Query Match 3.0%; Score 24; DB 11; Length 999;

Best Local Similarity 100.0%; Pred. No. 1.8e-14;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DIDSLLKQLYKPLPSQRHVESDGL 289

DB 2 DIDSLLKQLYKPLPSQRHVESDGL 25

RESULT 15

US-09-884-465A-377

Sequence 377, Application US/09884465A

Publication No. US20030077293A1

GENERAL INFORMATION:

APPLICANT: Shire Biochem, Inc.

APPLICANT: Hamel, Josee

APPLICANT: Brodeur, Bernard

APPLICANT: Martin, Denis

APPLICANT: Charland, Nathalie

APPLICANT: Ouellet, Catherine

TITLE OF INVENTION: Streptococcus Antigens

FILE REFERENCE: 055190-0044

CURRENT APPLICATION NUMBER: US/09/884,465A

PRIOR FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: 60/212,683

NUMBER OF SEQ ID NOS: 384

SOFTWARE: PatentIn version 3.1

SEQ ID NO 377

LENGTH: 999

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (1)..(1)

OTHER INFORMATION: Xaa = Methionine or nothing

NAME/KEY: MISC_FEATURE

LOCATION: (570)..(570)

OTHER INFORMATION: Xaa = Glycine or nothing

NAME/KEY: MISC_FEATURE

LOCATION: (571)..(571)

OTHER INFORMATION: Xaa = Proline or nothing

US-09-884-465A-377

Query Match 3.0%; Score 24; DB 11; Length 999;

Best Local Similarity 100.0%; Pred. No. 1.8e-14;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DIDSLLKQLYKPLPSQRHVESDGL 289

DB 572 DIDSLLKQLYKPLPSQRHVESDGL 595

RESULT 16

US-09-884-465A-383

Sequence 383, Application US/09884465A

Publication No. US20030077293A1

GENERAL INFORMATION:

APPLICANT: Shire Biochem, Inc.

APPLICANT: Hamel, Josee

APPLICANT: Brodeur, Bernard

APPLICANT: Martin, Denis

APPLICANT: Charland, Nathalie

APPLICANT: Ouellet, Catherine

TITLE OF INVENTION: Streptococcus Antigens

FILE REFERENCE: 055190-0044

CURRENT APPLICATION NUMBER: US/09/884,465A

PRIOR FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: 60/212,683

NUMBER OF SEQ ID NOS: 384

SOFTWARE: PatentIn version 3.1

SEQ ID NO 383

LENGTH: 1126

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (1)..(1)

OTHER INFORMATION: Xaa = Methionine or nothing

NAME/KEY: MISC_FEATURE

LOCATION: (557)..(557)

OTHER INFORMATION: Xaa = Glycine or nothing

NAME/KEY: MISC_FEATURE

LOCATION: (558)..(558)

OTHER INFORMATION: Xaa = Proline or nothing

US-09-884-465A-383

Query Match 3.0%; Score 24; DB 11; Length 1126;

Best Local Similarity 100.0%; Pred. No. 2e-14;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DIDSLLKQLYKPLPSQRHVESDGL 289

DB 2 DIDSLLKQLYKPLPSQRHVESDGL 25

RESULT 17

US-09-884-465A-381

Sequence 381, Application US/09884465A

Publication No. US20030077293A1

GENERAL INFORMATION:

APPLICANT: Shire Biochem, Inc.

APPLICANT: Hamel, Josee

APPLICANT: Brodeur, Bernard

APPLICANT: Martin, Denis

APPLICANT: Charland, Nathalie

APPLICANT: Ouellet, Catherine

TITLE OF INVENTION: Streptococcus Antigens

FILE REFERENCE: 055190-0044

CURRENT APPLICATION NUMBER: US/09/884,465A

PRIOR FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: 60/212,683

NUMBER OF SEQ ID NOS: 384

SOFTWARE: PatentIn version 3.1

SEQ ID NO 381

LENGTH: 1238

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (1)..(1)

OTHER INFORMATION: Xaa = Methionine or nothing

NAME/KEY: MISC_FEATURE

LOCATION: (430)..(430)

OTHER INFORMATION: Xaa = Glycine or nothing

NAME/KEY: MISC_FEATURE

LOCATION: (431)..(431)

OTHER INFORMATION: Xaa = Proline or nothing

US-09-884-465A-381

Query Match 3.0%; Score 24; DB 11; Length 1238;

Best Local Similarity 100.0%; Pred. No. 2.2e-14;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DIDSLLKQLYKPLPSQRHVESDGL 289

DB 2 DIDSLLKQLYKPLPSQRHVESDGL 25

RESULT 18

US-09-884-465A-382
; Sequence 382, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 382
; LENGTH: 1365
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC FEATURE
; LOCATION: (557)-(557)
; OTHER INFORMATION: Xaa = Glycine or nothing
; NAME/KEY: MISC FEATURE
; LOCATION: (558)-(558)
; OTHER INFORMATION: Xaa = Proline or nothing

US-09-884-465A-382

Query Match 3.0%; Score 24; DB 11; Length 1365;
Best Local Similarity 100.0%; Pred. No. 2,4e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 266 DIDSLLKQLYKLPISQRHVESDGL 289

Db 2 DIDSLLKQLYKLPISQRHVESDGL 25

RESULT 19

US-09-884-465A-11
; Sequence 11, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-11

Query Match 2.9%; Score 23; DB 11; Length 94;

Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 DQGVTSQDHYHYNGKVPYDA 77

Db 1 DQGVTSQDHYHYNGKVPYDA 23

RESULT 20

US-09-769-736-24
; Sequence 24, Application US/09769736
; Publication No. US20030138775A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Le Page, Richard WF
; APPLICANT: Wells, Jeremy M
; APPLICANT: Hamillity, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PMC/P210890
; CURRENT APPLICATION NUMBER: US/09/769,736
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: GB 9816335.5
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/125163
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-09-769-736-24

Query Match 2.1%; Score 17; DB 12; Length 381;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 YNGKVPYDAIISELLM 85

Db 92 YNGKVPYDAIISELLM 108

RESULT 21

US-09-252-088-15
; Sequence 15, Application US/09252088
; Publication No. US20030031682A1
; GENERAL INFORMATION:
; APPLICANT: BRODEUR, Bernard R.
; APPLICANT: RIOUX, Clement
; APPLICANT: BOYER, Martine
; APPLICANT: CHARLEBOIS, Isabelle
; APPLICANT: HAMEL, Josee
; APPLICANT: MARTIN, Denis
; TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
; FILE REFERENCE: 8331-9002
; CURRENT APPLICATION NUMBER: US/09/252,088
; PRIOR FILING DATE: 1998-02-18
; EARLIER APPLICATION NUMBER: US/60/075,425
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 793
; TYPE: PRT
; ORGANISM: group B streptococcus
US-09-252-088-15

Query Match 2.1%; Score 17; DB 11; Length 793;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 YNGKVPYDAIISELLM 85

|||||

```
Db          63 YNGKVPYDAIISELLM 79

RESULT 22
US-09-769-736-18
; Sequence 18, Application US/09769736
; Publication No. US20030138775A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Le Page, Richard WF
; APPLICANT: Wells, Jeremy M
; APPLICANT: Hannify, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PMC/P21089WO
; CURRENT APPLICATION NUMBER: US/09/769,736
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: GB 9816335.5
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/125163
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 18
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-09-769-736-18

Query Match          2.1%; Score 17; DB 12; Length 822;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          69 YNGKVPYDAIISELLM 85
|||||
Db          92 YNGKVPYDAIISELLM 108

RESULT 23
US-09-252-088-16
; Sequence 16, Application US/09252088
; Publication No. US20030031682A1
; GENERAL INFORMATION:
; APPLICANT: BRODEUR, Bernard R.
; APPLICANT: RIOUX, Clement
; APPLICANT: BOYER, Martine
; APPLICANT: CHARLEBOIS, Isabelle
; APPLICANT: HAMEL, Jose
; APPLICANT: MARTIN, Denis
; TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
; FILE REFERENCE: 8331-9002
; CURRENT APPLICATION NUMBER: US/09/252,088
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: US/60/075,425
; EARLIER FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 16
; LENGTH: 715
; TYPE: PRT
; ORGANISM: group B streptococcus
US-09-252-088-16

Query Match          1.5%; Score 12; DB 11; Length 715;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          160 QGRYTTDDGYIF 171
|||||
Db          84 QGRYTTDDGYIF 95

RESULT 24
US-09-884-465A-384

; Sequence 384, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 384
; LENGTH: 913
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (344)..(344)
; OTHER INFORMATION: Xaa = Glycine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (345)..(345)
; OTHER INFORMATION: Xaa = Proline or nothing
US-09-884-465A-384

Query Match          1.5%; Score 12; DB 11; Length 913;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          539 SDEGDVYVTPHM 550
|||||
Db          54 SDEGDVYVTPHM 65

RESULT 25
US-09-884-465A-379
; Sequence 379, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 379
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = Methionine or nothing
; NAME/KEY: MISC_FEATURE
; LOCATION: (344)..(344)
```

OTHER INFORMATION: Xaa = Glycine or nothing
NAME/KEY: MISC FEATURE
LOCATION: (345)..(345)
OTHER INFORMATION: Xaa = Proline or nothing
US-09-884-465A-379

Query Match 1.5%; Score 12; DB 11; Length 1152;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 307 PHGDHYHPIPS 318
DB 421 PHGDHYHPIPS 432

RESULT 26
US-09-769-736-72
Sequence 72, Application US/09769736
Publication No. US2003013875A1
GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Le Page, Richard WP
APPLICANT: Wells, Jeremy M
APPLICANT: Hamifly, Sean B
TITLE OF INVENTION: Proteins
FILE REFERENCE: PMC/P21089wo
CURRENT APPLICATION NUMBER: US/09/769,736
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: GB 9816335.5
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125163
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 72
LENGTH: 485
TYPE: PRT
ORGANISM: Streptococcus agalactiae
US-09-769-736-72

Query Match 1.4%; Score 11; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 523 KYTSDGYIFD 533
DB 110 KYTSDGYIFD 120

RESULT 27
US-09-884-465A-300
Sequence 300, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 300
LENGTH: 272
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Unknown Organism
US-09-884-465A-300

Query Match 1.1%; Score 9; DB 11; Length 272;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 634 KDHYNIKF 642
DB 110 KDHYNIKF 118

RESULT 28
US-09-884-465A-22
Sequence 22, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 86
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Unknown Organism
US-09-884-465A-22

Query Match 1.0%; Score 8; DB 11; Length 86;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 635 DHYNIKF 642
DB 52 DHYNIKF 59

RESULT 29
US-09-884-465A-374
Sequence 374, Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 374
LENGTH: 259
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Unknown Organism

US-09-884-465A-374

Query Match 1.0%; Score 8; DB 11; Length 259;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 DHYHNKIF 642

DB 98 DHYHNKIF 105

RESULT 30

US-09-884-465A-302
; Sequence 302, Application US/09884465A
; Publication No. US2003007293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 302
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-302

Query Match 1.0%; Score 8; DB 11; Length 270;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 DHYHNKIF 642

DB 109 DHYHNKIF 116

RESULT 31

US-09-884-465A-258
; Sequence 258, Application US/09884465A
; Publication No. US2003007293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 258
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-258

Query Match 1.0%; Score 8; DB 11; Length 272;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 DHYHNKIF 642

DB 111 DHYHNKIF 118

RESULT 32

US-09-884-465A-293
; Sequence 293, Application US/09884465A
; Publication No. US2003007293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 293
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-293

Query Match 1.0%; Score 8; DB 11; Length 272;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 DHYHNKIF 642

DB 111 DHYHNKIF 118

RESULT 33

US-10-156-761-13480
; Sequence 13480, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 13480
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13480

Query Match 1.0%; Score 8; DB 15; Length 400;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 669 VEHDPERP 676
 |||||
 Db 70 VEHDPERP 77

RESULT 34

US-09-815-242-5401
 ; Sequence 5401, Application US/09815242
 ; Patent No. US2002061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; FILE OF INVENTION: Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5401
 ; LENGTH: 482
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-09-815-242-5401

Query Match 1.0%; Score 8; DB 9; Length 482;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 NDGAVALA 157
 |||||
 Db 69 NDGAVALA 76

RESULT 35

US-09-815-242-12564
 ; Sequence 12564, Application US/09815242
 ; Patent No. US2002061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; FILE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12564
 ; LENGTH: 488
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-09-815-242-12564

OY 150 NDGAVALA 157
 |||||
 Db 72 NDGAVALA 79

RESULT 36

US-09-884-465A-336
 ; Sequence 336, Application US/09884465A
 ; Publication No. US2003007293A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shire Biochem, Inc.
 ; APPLICANT: Hamel, Josee
 ; APPLICANT: Brodeur, Bernard
 ; APPLICANT: Martin, Denis
 ; APPLICANT: Charland, Nathalie
 ; APPLICANT: Ouellet, Catherine
 ; TITLE OF INVENTION: Streptococcus Antigens
 ; FILE REFERENCE: 055190-0044
 ; CURRENT APPLICATION NUMBER: US/09/884,465A
 ; CURRENT FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 60/212,683
 ; PRIOR FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 384
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 336
 ; LENGTH: 894
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Unknown Organism
 ; US-09-884-465A-336

Query Match 1.0%; Score 8; DB 11; Length 894;
 Best Local Similarity 100.0%; Pred. No. 11e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 635 DRYHNKIF 642
 |||||
 Db 111 DRYHNKIF 118

RESULT 37

US-09-884-465A-344
 ; Sequence 344, Application US/09884465A

```
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 344
; LENGTH: 895
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-344
```

```
Query Match          1.0%; Score 8; DB 11; Length 895;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
QY      635 DHHYNIKF 642
        |||||
Db       111 DHHYNIKF 118
```

```
RESULT 38
US-09-884-465A-335
; Sequence 335, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 335
; LENGTH: 900
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-335
```

```
Query Match          1.0%; Score 8; DB 11; Length 900;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
QY      635 DHHYNIKF 642
        |||||
Db       111 DHHYNIKF 118
```

```
RESULT 39
US-09-884-465A-343
; Sequence 343, Application US/09884465A
; Publication No. US20030077293A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 343
; LENGTH: 901
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-343
```

```
Query Match          1.0%; Score 8; DB 11; Length 901;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
QY      635 DHHYNIKF 642
        |||||
Db       111 DHHYNIKF 118
```

```
RESULT 40
US-09-884-465A-332
; Sequence 332, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 332
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-332
```

```
Query Match          1.0%; Score 8; DB 11; Length 906;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
QY      635 DHHYNIKF 642
        |||||
Db       111 DHHYNIKF 118
```

```
RESULT 41
US-09-884-465A-369
; Sequence 369, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 369
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-369
```

```
Query Match 1.0%; Score 8; DB 11; Length 906;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 635 DHYNIKF 642
DB 745 DHYNIKF 752
```

```
RESULT 42
US-09-884-465A-370
; Sequence 370, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 370
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-370
```

```
Query Match 1.0%; Score 8; DB 11; Length 906;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 635 DHYNIKF 642
DB 111 DHYNIKF 118
```

```
RESULT 43
US-09-884-465A-371
; Sequence 371, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
```

```
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 371
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-371
```

```
Query Match 1.0%; Score 8; DB 11; Length 906;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 635 DHYNIKF 642
DB 745 DHYNIKF 752
```

```
RESULT 44
US-09-884-465A-372
; Sequence 372, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 372
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-372
```

```
Query Match 1.0%; Score 8; DB 11; Length 906;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 635 DHYNIKF 642
DB 111 DHYNIKF 118
```

```
RESULT 45
US-09-884-465A-373
; Sequence 373, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
```


APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 373
LENGTH: 906
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Unknown Organism
US-09-884-465A-373

Query Match 1.0%; Score 8; DB 11; Length 906;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 DRYHNKIF 642
|||||
DB 745 DRYHNKIF 752

RESULT 46
US-10-128-714-3262
Sequence 3262, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:

APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengji
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US/10/128,714
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3262
LENGTH: 1104
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-10-128-714-3262

Query Match 1.0%; Score 8; DB 15; Length 1104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 707 EEPVEETP 714
|||||
DB 952 EEPVEETP 959

RESULT 47

US-09-712-363-259
Sequence 259, Application US/09712363
Patent No. US20020164588A1
GENERAL INFORMATION:

APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
CURRENT FILING DATE: US/09/712,363
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 259
LENGTH: 1289
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-712-363-259

Query Match 1.0%; Score 8; DB 10; Length 1289;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 SELAAEA 210
|||||
DB 756 SELAAEA 763

RESULT 48
US-10-128-714-8262
Sequence 8262, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengji
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT FILING DATE: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31

```

; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 8262
; LENGTH: 1353
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8262
```

```
Query Match      1.0%; Score 8; DB 15; Length 1353;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
QY      707 EEPVEETP 714
      |||||
Db      1201 EEPVEETP 1208
```

```

RESULT 49
US-09-884-465A-23
; Sequence 23, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US/09/884,465A
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 23
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-23
```

```
Query Match      0.9%; Score 7; DB 11; Length 41;
Best Local Similarity 100.0%; Pred. No. 59;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
QY      666 KYVEHP 672
      |||||
Db      19 KYVEHP 25
```

```

RESULT 50
US-09-864-761-38022
; Sequence 38022, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
```

```

; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 38022
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010734.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.93
US-09-864-761-38022
```

```
Query Match      0.9%; Score 7; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. No. 69;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
QY      492 LAPITHP 498
      |||||
Db      34 LAPITHP 40
```

```

RESULT 51
US-10-106-698-5438
; Sequence 5438, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide.
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO: 5438
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
```

FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (72)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5438

Query Match 0.9%; Score 7; DB 15; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 787 PSSVSKE 793
|||||
DB 57 PSSVSKE 63

RESULT 52
US-09-764-891-3850
Sequence 3850, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3850
LENGTH: 91
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (74)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-3850

Query Match 0.9%; Score 7; DB 11; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 AQLKEAE 735
|||||
DB 21 AQLKEAE 27

RESULT 53
US-10-103-313-297
Sequence 297, Application US/10103313
Publication No. US20030082758A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJ207C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 297
LENGTH: 97
TYPE: PRT
ORGANISM: Homo sapiens
US-10-103-313-297

Query Match 0.9%; Score 7; DB 15; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 LIERLND 476
|||||
DB 68 LIERLND 74

RESULT 54
US-10-103-313-467
Sequence 467, Application US/10103313
Publication No. US20030082758A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJ207C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 467
LENGTH: 97
TYPE: PRT
ORGANISM: Homo sapiens
US-10-103-313-467

Query Match 0.9%; Score 7; DB 15; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 LIERLND 476
|||||
DB 68 LIERLND 74

RESULT 55
US-09-712-363-272
Sequence 272, Application US/09712363
Patent No. US20020164588A1
GENERAL INFORMATION:
APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
Prior Application Number: PCT/US00/02246
Prior Filing Date: 2000-01-28
Prior Application Number: 60/179,531
Prior Filing Date: 2000-02-01
Prior Application Number: 60/117,844
Prior Filing Date: 1999-01-29
Prior Application Number: 60/118,206,
Prior Filing Date: 1999-02-01
Prior Application Number: 60/126,593
Prior Filing Date: 1999-03-26
Prior Application Number: 60/134,093
Prior Filing Date: 1999-05-14
Prior Application Number: 60/134,092
Prior Filing Date: 1999-05-14
Prior Application Number: 60/165,124
Prior Filing Date: 1999-11-12
Prior Application Number: 60/165,086
Prior Filing Date: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 272
LENGTH: 100
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-712-363-272

Query Match 0.9%; Score 7; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 605 GEXRIPL 611
Db 55 GEXRIPL 61

RESULT 56
US-10-252-945-57
; Sequence 57, Application US/10252945
; Publication No. US20030134904A1
; GENERAL INFORMATION:
; APPLICANT: Giordano, Tony
; APPLICANT: Sturges, Michael A.
; APPLICANT: Rao, Samala, J.
; TITLE OF INVENTION: Inhibitors of RNASE P Proteins as
; TITLE OF INVENTION: Antibacterial Compounds
; FILE REFERENCE: 50093/026002
; CURRENT APPLICATION NUMBER: US/10/252,945
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/323,853
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Staphylococcus epidermis
US-10-252-945-57

Query Match 0.9%; Score 7; DB 12; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 460 RNSDFOA 466
Db 9 RNSDFOA 15

RESULT 57
US-10-156-761-7659
; Sequence 7659, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 7659
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-7659

Query Match 0.9%; Score 7; DB 15; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 733 EAEVLLA 739
Db 130 EAEVLLA 136

RESULT 58
US-09-820-843A-94
; Sequence 94, Application US/09820843A
; Publication No. US20030039963A1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI

; FILE REFERENCE: 063915
; CURRENT APPLICATION NUMBER: US/09/820,843A
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 94
; LENGTH: 143
; TYPE: PRT
; ORGANISM: R. prowazekii
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; OTHER INFORMATION: g1|3860651
US-09-820-843A-94

Query Match 0.9%; Score 7; DB 11; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 133 NRQOEH 139
Db 106 NRQOEH 112

RESULT 59
US-09-817-414-2
; Sequence 2, Application US/09817414
; Patent No. US20020058308A1
; GENERAL INFORMATION:
; APPLICANT: Greenwood, Rebecca C.
; TITLE OF INVENTION: NOVEL GRE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/817,414
; FILING DATE: 26-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/229,804
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Dickinson, Todd O
; REGISTRATION NUMBER: 28,354
; REFERENCE/DOCKET NUMBER: GM10046
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2252
; TELEFAX: 215-994-2222
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-817-414-2

Query Match 0.9%; Score 7; DB 9; Length 158;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 IIEDTGD 182
Db 77 IIEDTGD 83

RESULT 60
US-10-043-487-355
; Sequence 355, Application US/10043487
; Publication No. US2003005220A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, LEGRAIN
; TITLE OF INVENTION: Protein-protein interactions between Shigella flexneri polypeptides
; FILE REFERENCE: B4778A
; CURRENT APPLICATION NUMBER: US/10/043,487
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/261,130
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 561
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 355
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Shigella flexneri
US-10-043-487-355

Query Match 0.9%; Score 7; DB 15; Length 158;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 776 EKLALL 782
Db 3 EKLALL 9

RESULT 61
US-09-738-626-6669
; Sequence 6669, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATESHI, NAKO
; APPLICANT: SENOH, AKIHRO
; APPLICANT: IKEDA, MASARO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6669

LENGTH: 166
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-6669

Query Match 0.9%; Score 7; DB 10; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 SQASQSN 265
Db 55 SQASQSN 61

RESULT 62
US-09-882-529-5
; Sequence 5, Application US/09882529
; Patent No. US20020132317A1
; GENERAL INFORMATION:
; APPLICANT: Peyman, John A
; APPLICANT: da Silva, Antonio
; TITLE OF INVENTION: NOVEL INTERFERON-INDUCED TETRASPAN PROTEIN AND NUCLEIC
; FILE REFERENCE: 15966-771
; CURRENT APPLICATION NUMBER: US/09/882,529
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 60/211,565
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-882-529-5

Query Match 0.9%; Score 7; DB 10; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 NNLTLOI 765
Db 3 NNLTLOI 9

RESULT 63
US-09-882-529-6
; Sequence 6, Application US/09882529
; Patent No. US20020132317A1
; GENERAL INFORMATION:
; APPLICANT: Peyman, John A
; APPLICANT: da Silva, Antonio
; APPLICANT: Hockman, Paula
; TITLE OF INVENTION: NOVEL INTERFERON-INDUCED TETRASPAN PROTEIN AND NUCLEIC
; FILE REFERENCE: 15966-771
; CURRENT APPLICATION NUMBER: US/09/882,529
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 60/211,565
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-882-529-6

Query Match 0.9%; Score 7; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 773 AEAEXKL 779
|||
Db 91 AEAEXKL 97

RESULT 64

US-09-882-529-8
; Sequence 8, Application US/09882529
; Patent No. US20020132317A1
; GENERAL INFORMATION:
; APPLICANT: Peyman, John A
; APPLICANT: da Silva, Antonio
; APPLICANT: Hockman, Paula
; TITLE OF INVENTION: NOVEL INTERFERON-INDUCED TETRASPAN PROTEIN AND NUCLEIC
; FILE REFERENCE: 15966-771
; CURRENT APPLICATION NUMBER: US/09/882,529
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 60/211,565
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-882-529-8

Query Match 0.9%; Score 7; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 773 AEAEXKL 779
|||
Db 91 AEAEXKL 97

RESULT 65

US-10-156-761-9896
; Sequence 9896, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9896
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9896

Query Match 0.9%; Score 7; DB 15; Length 178;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 515 VRIAOA 521
|||
Db 133 VRIAOA 139

RESULT 66

US-10-267-311-35
; Sequence 35, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-35

Query Match 0.9%; Score 7; DB 15; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 605 GEKRIPL 611
|||
Db 55 GEKRIPL 61

RESULT 67

US-09-967-736-3
; Sequence 3, Application US/09967736
; Patent No. US20020103340A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: RAB PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/967,736
; FILING DATE: 28-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/154,602
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0367 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LVRTUT04
CLONE: 2514506
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-967-736-3

Query Match 0.9%; Score 7; DB 10; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 365 PNLKIDS 371
Db 184 PNLKIDS 190

RESULT 68

US-09-967-736-8
Sequence 8, Application US/09967736
Patent No. US20020103340A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Lal, Preeti
Corley, Neil C.
Shah, Purvi

TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/967,736
FILING DATE: 28-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/154,602
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 57006

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-967-736-8

Query Match 0.9%; Score 7; DB 10; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 365 PNLKIDS 371
Db 184 PNLKIDS 190

Db 184 PNLKIDS 190

RESULT 69

US-10-156-761-11020
Sequence 11020, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OKURA, SATOSHI
APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761

PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 11020
LENGTH: 209
TYPE: PRT

ORGANISM: Streptomyces avermitilis
US-10-156-761-11020

Query Match 0.9%; Score 7; DB 15; Length 209;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 488 LIAFLAP 494
Db 100 LIAFLAP 106

RESULT 70

US-09-925-301-1048
Sequence 1048, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301

PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1048
LENGTH: 217
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE

LOCATION: (122)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE
LOCATION: (186)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE
LOCATION: (200)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-301-1048
Query Match 0.9%; Score 7; DB 9; Length 217;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 127 RTKEIN 133
Db 72 RTKEIN 78

RESULT 71

US-10-102-806-466
; Sequence 466, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103PIC1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 466
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-466

Query Match 0.9%; Score 7; DB 15; Length 224;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 365 PNLKIDS 371
Db 207 PNLKIDS 213

RESULT 72

US-09-604-287A-487
; Sequence 487, Application US/09604287A
; Patent No. US20020064872A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 487
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-287A-487

Query Match 0.9%; Score 7; DB 9; Length 235;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 127 RTKEIN 133
Db 47 RTKEIN 53

RESULT 73

US-09-907-263-4
; Sequence 4, Application US/09907263
; Patent No. US20020119924A1
; GENERAL INFORMATION:
; APPLICANT: Bendele, Alison M.
; APPLICANT: Semello, Regina M.
; APPLICANT: Edwards, Carl K.
; TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
; PROTEIN FOR TREATING TNF-MEDIATED DISEASES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/907,263
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/326,394
; FILING DATE: 1999-06-04
; APPLICATION NUMBER: US 60/036,355
; FILING DATE: 23-JAN-1997
; APPLICATION NUMBER: US 60/039,315
; FILING DATE: 07-FEB-1997
; APPLICATION NUMBER: US 60/052,023
; FILING DATE: 09-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zindrick, Thomas K.
; REGISTRATION NUMBER: 32,185
; REFERENCE/DOCKET NUMBER: A-430D
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-907-263-4

Query Match 0.9%; Score 7; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 352 QPTPEPS 358
Db 206 QPTPEPS 212

RESULT 74

US-09-882-735-16
; Sequence 16, Application US/09882735
; Publication No. US20030054439A1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary
; TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I and
; FILE REFERENCE: 02-006
; CURRENT APPLICATION NUMBER: US/09/882,735
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/214,613
; PRIOR FILING DATE: 1999-01-08


```

; PRIOR APPLICATION NUMBER: PCT/US97/12244
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: 60/039,792
; PRIOR FILING DATE: 1997-03-04
; PRIOR APPLICATION NUMBER: 60/039,314
; PRIOR FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: 60/037,737
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 60/032,354
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: 60/021,443
; PRIOR FILING DATE: 1996-07-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-882-735-16

```

```

Query Match          0.9%; Score 7; DB 11; Length 235;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      352 QPTPEPS 358
Db      206 QPTPEPS 212

```

```

RESULT 75
US-10-124-805-487
; Sequence 487, Application US/10124805
; Publication No. US2003016022A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C12
; CURRENT APPLICATION NUMBER: US/10/124,805
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 487
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-124-805-487

```

```

Query Match          0.9%; Score 7; DB 12; Length 235;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      127 RTKEIN 133
Db      47 RTKEIN 53

```

```

RESULT 76
US-10-436-826-75
; Sequence 75, Application US/10436826
; Publication No. US2003018722A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Wooden, Scott
; FILE REFERENCE: 06843.0034-01000
; CURRENT APPLICATION NUMBER: US/10/436,826
; CURRENT FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 88/850,188
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 88

```

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Human
US-10-436-826-75

```

```

Query Match          0.9%; Score 7; DB 12; Length 235;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      352 QPTPEPS 358
Db      206 QPTPEPS 212

```

```

RESULT 77
US-10-007-805-487
; Sequence 487, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Uiang, Yogiin
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepner, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 487
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-805-487

```

```

Query Match          0.9%; Score 7; DB 14; Length 235;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      127 RTKEIN 133
Db      47 RTKEIN 53

```

```

RESULT 78
US-10-076-622-487
; Sequence 487, Application US/10076622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 487
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-10-076-622-487

Query Match 0.9%; Score 7; DB 15; Length 235;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 RTKEIN 133
|||||
47 RTKEIN 53

RESULT 79

US-10-243-230-2
; Sequence 2, Application US/10243230
; Publication No. US20030023049A1

GENERAL INFORMATION:

APPLICANT: Pettit, Dean
TITLE OF INVENTION: Site Specific Protein Modification
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Janis C Henry
STREET: 51 University
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/243,230
FILING DATE: 12-Sep-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/102,530
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-243-230-2

Query Match 0.9%; Score 7; DB 15; Length 235;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 QTPPEPS 358
|||||
Db 206 QTPPEPS 212

RESULT 80

US-10-243-230-4
; Sequence 4, Application US/10243230
; Publication No. US20030023049A1

GENERAL INFORMATION:

APPLICANT: Pettit, Dean
TITLE OF INVENTION: Site Specific Protein Modification
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Janis C Henry
STREET: 51 University

CITY: Seattle

STATE: WA
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/243,230
FILING DATE: 12-Sep-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/102,530
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-243-230-4

Query Match 0.9%; Score 7; DB 15; Length 235;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 QTPPEPS 358
|||||
Db 206 QTPPEPS 212

RESULT 81

US-10-243-230-6
; Sequence 6, Application US/10243230
; Publication No. US20030023049A1

GENERAL INFORMATION:

APPLICANT: Pettit, Dean
TITLE OF INVENTION: Site Specific Protein Modification
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Janis C Henry
STREET: 51 University
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/243,230
FILING DATE: 12-Sep-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/102,530
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-243-230-6

Query Match
Best Local Similarity 100.0%; Pred. No. 3e+02; Length 235;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 352 QPTPEPS 358
Db 206 QPTPEPS 212

RESULT 82
US-10-243-230-8
; Sequence 8, Application US/10243230
; Publication No. US20030023049A1

GENERAL INFORMATION:
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Site Specific Protein Modification
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/243,230
; FILING DATE: 12-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,530
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-243-230-8

Query Match
Best Local Similarity 100.0%; Pred. No. 3e+02; Length 235;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 352 QPTPEPS 358
Db 206 QPTPEPS 212

RESULT 83
US-10-156-761-12784
; Sequence 12784, Application US/10156761
; Publication No. US20030119018A1

GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12784
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12784

Query Match
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Length 247;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 487 DLLAFIA 493
Db 164 DLLAFIA 170

RESULT 84
US-10-032-585-7603
; Sequence 7603, Application US/10032585
; Publication No. US20030180953A1
GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiaang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Busey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 7603
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7603

Query Match
Best Local Similarity 100.0%; Pred. No. 3.2e+02; Length 248;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 373 SSLVSQL 379
Db 27 SSLVSQL 33

RESULT 85
US-10-313-852-10
; Sequence 10, Application US/10313852
; Publication No. US20030103942A1
GENERAL INFORMATION:
; APPLICANT: Burslein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; FILE REFERENCE: 226272004420

; CURRENT APPLICATION NUMBER: US/10/313,852
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-313-852-10

Query Match 0.9%; Score 7; DB 15; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 OPTPEPS 358
|||
Db 228 OPTPEPS 234

RESULT 86
US-10-314-033-10
; Sequence 10, Application US/10314033
; Publication No. US20030113295A1
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/10/314,033
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-314-033-10

Query Match 0.9%; Score 7; DB 15; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 OPTPEPS 358
|||
Db 228 OPTPEPS 234

RESULT 87
US-10-156-761-11174
; Sequence 1174, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 11174
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-11174

Query Match 0.9%; Score 7; DB 15; Length 264;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 LSASELA 206
|||
Db 142 LSASELA 148

RESULT 88
US-09-884-465A-304
; Sequence 304, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 304
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-304

Query Match 0.9%; Score 7; DB 11; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 598 AIVNRVK 604
|||
Db 74 AIVNRVK 80

RESULT 89
US-09-884-465A-303
; Sequence 303, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20

```

; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 303
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-303
```

```

Query Match          0.9%; Score 7; DB 11; Length 268;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      598 AIYNRVK 604
      |||||
Db       74 AIYNRVK 80
```

```

RESULT 90
US-09-884-465A-375
; Sequence 375, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 375
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-375
```

```

Query Match          0.9%; Score 7; DB 11; Length 268;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      598 AIYNRVK 604
      |||||
Db       74 AIYNRVK 80
```

```

RESULT 91
US-09-884-465A-294
; Sequence 294, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
```

```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 294
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-294
```

```

Query Match          0.9%; Score 7; DB 11; Length 272;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      598 AIYNRVK 604
      |||||
Db       74 AIYNRVK 80
```

```

RESULT 92
US-09-884-465A-295
; Sequence 295, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 295
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-295
```

```

Query Match          0.9%; Score 7; DB 11; Length 272;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      598 AIYNRVK 604
      |||||
Db       74 AIYNRVK 80
```

```

RESULT 93
US-09-884-465A-296
; Sequence 296, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
```

```
; SEQ ID NO 296
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-296
```

```
Query Match
Best Local Similarity 100.0%; Score 7; DB 11; Length 272;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 598 AIYNRVK 604
|||
Db 74 AIYNRVK 80
```

```
RESULT 94
US-09-884-465A-297
; Sequence 297, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 297
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-297
```

```
Query Match
Best Local Similarity 100.0%; Score 7; DB 11; Length 272;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 598 AIYNRVK 604
|||
Db 74 AIYNRVK 80
```

```
RESULT 95
US-09-884-465A-298
; Sequence 298, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 298
```

```
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-298
```

```
Query Match
Best Local Similarity 100.0%; Score 7; DB 11; Length 272;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 598 AIYNRVK 604
|||
Db 74 AIYNRVK 80
```

```
RESULT 96
US-09-884-465A-299
; Sequence 299, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 299
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-09-884-465A-299
```

```
Query Match
Best Local Similarity 100.0%; Score 7; DB 11; Length 272;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 598 AIYNRVK 604
|||
Db 74 AIYNRVK 80
```

```
RESULT 97
US-09-884-465A-301
; Sequence 301, Application US/09884465A
; Publication No. US20030077293A1
; GENERAL INFORMATION:
; APPLICANT: Shire Biochem, Inc.
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard
; APPLICANT: Martin, Denis
; APPLICANT: Charland, Nathalie
; APPLICANT: Ouellet, Catherine
; TITLE OF INVENTION: Streptococcus Antigens
; FILE REFERENCE: 055190-0044
; CURRENT APPLICATION NUMBER: US/09/884,465A
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/212,683
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 301
; LENGTH: 272
```

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Unknown Organism
US-09-884-465A-301

Query Match
Best Local Similarity 100.0%; Score 7; DB 11; Length 272;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 598 AAYNRVK 604
DB 74 AAYNRVK 80

RESULT 98
US-10-017-161-910
Sequence 910, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 910
LENGTH: 285
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-161-910

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 285;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 733 EAEVLLA 739
DB 87 EAEVLLA 93

RESULT 99
US-10-032-585-7197
Sequence 7197, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jlang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7197
LENGTH: 293
TYPE: PRT
ORGANISM: Candida albicans
US-10-032-585-7197

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 293;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 773 AEAEXKL 779

DB 9 AEAEXKL 15

RESULT 100
US-09-886-055-113
Sequence 113, Application US/09886055
Patent No. US20020132273A1
GENERAL INFORMATION:
APPLICANT: STRYER, LUBERT
APPLICANT: ZOZULIA, SERGEY
TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
FILE REFERENCE: 078003-0277150
CURRENT APPLICATION NUMBER: US/09/886,055
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/213,812
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 522
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 113
LENGTH: 311
TYPE: PRT
ORGANISM: Homo sapiens
US-09-886-055-113

Query Match
Best Local Similarity 100.0%; Score 7; DB 10; Length 311;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 733 EAEVLLA 739
DB 113 EAEVLLA 119

Search completed: November 14, 2003, 11:38:27
Job time : 79 secs

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